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**FIGURE 1**

GTTACTCGGTGGTGGCGGAGTCTACGGAAGCCGTTTTTCGCTTCACTTTTCCTGGCTGTAGAGC  
GCTTTCCCCCTGGCGGGTGAGAGTGCAGAGACGAAGGTGCGAGATGAGCACTATGTTTCGCGGA  
CACTCTCCTCATCGTTTTTTATCTCTGTGTGCACGGCTCTGCTCGCAGAGGGCATAACCTGGGT  
CCTGGTTTACAGGACAGACAAGTACAAGAGACTGAAGGCAGAAGTGGAACAGAGTAAAAA  
ATTGGAAGAAGAAGGAAACAATAACAGAGTCAGCTGGTCGACAACAGAAAAAGAAAATAGA  
GAGACAAGAAGAGAACTGAAGAATAACAACAGAGATCTATCAATGGTTCGAATGAAATCCAT  
GTTTGCTATTGGCTTTTGTTTTACTGCCCTAATGGGAATGTTCAATTCCATATTTGATGGTAG  
AGTGGTGGCAAAGCTTCCTTTTACCCCTCTTTCTTACATCCAAGGACTGTCTCATCGAAATCT  
GCTGGGAGATGACACCACAGACTGTTTCCTTCATTTTCCTGTATATTCTCTGTACTATGTCGAT  
TCGACAGAACATTGAGAAGATTCTCGGCCTTGCCCTTCACGAGCCGCCACCAAGCAGGCAGG  
TGGATTTCTTGGCCCACCACCTCCTTCTGGGAAGTTCTCTTGAACTCAAGAACTCTTTATTTT  
CTATCATTCTTTCTAGACACACACACATCAGACTGGCAACTGTTTTGTAGCAAGAGCCATAGG  
TAGCCTTACTACTTGGGCCTCTTTCTAGTTTTGAATTATTTCTAAGCCTTTTGGGTATGATTA  
GAGTGAAAATGGCAGCCAGCAAACCTGATAGTGCTTTTGGTCCTAGATGATTTTTATCAAATA  
AGTGGATTGATTAGTTAAGTTCAGGTAATGTTTATGTAATGAAAAACAAATAGCATCCTTCTT  
GTTTCATTTACATAAGTATTTTCTGTGGGACCGACTCTCAAGGCACTGTGTATGCCCTGCAAG  
TTGGCTGTCTATGAGCATTTAGAGATTTAGAAGAAAAATTTAGTTTGTTTAACCCTTGTAAC  
GTTTGTTTTGTTGTTGTTTTTTTTTCAAGCCAAATACATGACATAAGATCAATAAAGAGGCCA  
AATTTTATAGCTGTTTTATGTACAAGGAGAGATCTGTTTCATTTTGTGTTTGCCGTATTTCTAGA  
TATAAGTTTTAGCATGGGCCAGGAAGGACTAAAATAAAAGTTTTTAAGGTACAAAAA  
AAAA

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**FIGURE 2**

MSTMFADTLLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAGR  
QQKKKIERQEEKLKNNNRDLMSVRMKSMFAIGFCFTALMGMFNSIFDGRVVAKLPFTPLSYIQ  
GLSHRNLLGDDTTDCSFIFLYILCTMSIRQNIQKILGLAPSRAATKQAGGFLGPPPPSGKFS

**Important features:****Signal peptide:**

amino acids 1-22

**N-myristoylation sites..**

amino acids 103-109, 163-169

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 53-57

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**FIGURE 3**

AGCCGGGGGCGGGTTTGAAGACGCGTCGTTGGGTTTTGGAGGCCGTGAAACAGCCGTTTGAGT  
TTGGCTGCGGGTGGAGAACGTTTGT CAGGGGCCCCGGCCAAGAAGGAGGCCCGCCTGTTACGAT  
GGTGTCCATGAGTTTCAAGCGGAACCGCAGTGACCGTTCTACAGCACCCGGTGCTGCGGCTG  
TTGCCATGTCCGCACCGGGACGATCATCCTGGGGACCTGGTACATGGTAGTAAACCTATTGAT  
GGCAATTTTGCTGACTGTGGAAGTGACTCATCAAACCTCCATGCCAGCTGTCAACATTCAGTA  
TGAAGTCATCGGTAATTACTATTTCGTCTGAGAGAATGGCTGATAATGCCTGTGTTCTTTTTGC  
CGTCTCTGTTCTTATGTTTATAATCAGTTCAATGCTGGTTTATGGAGCAATTTCTTATCAAGT  
GGGTTGGCTGATTCCATTCTTCTGTTACCGACTTTTTGACTTCGTCCCTCAGTTGCCTGGTTGC  
TATTAGTTCTCTCACCTATTTGCCAAGAATCAAAGAATATCTGGATCAACTACCTGATTTTCC  
CTACAAAGATGACCTCCTGGCCTTGGACTCCAGCTGCCTCCTGTTCAATTGTTCTTGTGTTCTT  
TGCCTTATTCATCATTTTTTAAGGCTTATCTAATTAAGTGTGTTTGGAACTGCTATAAATACAT  
CAACAACCGAAACGTGCCGGAGATTGCTGTGTACCCTGCCTTTGAAAGCACCTCCTCAGTACG  
TTTTGCCAACCTATGAAATGGCCGTGAAAATGCCTGAAAAAGAACCACCACCTCCTTACTTAC  
CTGCCTGAAGAAATTCTGCCTTTGACAATAAATCCTATAACCAGCTTTTTGTTTGTATGTTA  
CAGAATGCTGCAATTCAGGGCTCTTCAAACCTGTTTGATATAAAATATGTTGTCTTTTGTTTA  
AGCATTTATTTCAAACACTAAGGAGCTTTTTGACATCTGTTAAACGTCTTTTTGTTTTTTG  
TTAAGTCTTTTACATTTTAATAGTTTTTGAAGACAATCTAGGTTAAGCAAGAGCAAAGTGCCA  
TTGTTTGCCTTTAATTGGGGGTGGGAAGGGAAAGAGGGTACTTGCCACATAGTTTCCTTTTT  
AACTGCACTTTCCTTTATATAATCGTTTGCATTTTGTTACTTGCTACCCTGAGTACTTTCAGGA  
AGACTGACTTAAATATTCGGGGTGAGTAAGTAGTTGGGTATAAGATCTGAACTTTTCATCTGC  
AGAGGCAAGAAAAATATTTGACATTGTGACTTGACTGTGGAAGATGATGGTTGCATGTTTCTA  
GTTTGTATATGTTTCCATCTTTGTGATAAGATGATTTAATAAATCTCTTTAAATACTAAAAA  
AAAAA

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**FIGURE 4**

MVSMSEFKRNRSDRFYSTRCCGCCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAVNIQ  
YEVIGNYYSSERMADNACVLFAVSVMFIISMLVYGAIQVGVLPFFCYRLFDVLSCLV  
AISSLTYLPRIKEYLDQLPDFPYKDDLLALDSSCLLFIVLVFFALFIIFKAYLINCWNCYKY  
INNRRNVPEIAVYPAFESTSSVRFANL

**Important features of the protein:**

**Transmembrane domain (Possible type II transmembrane protein):**

amino acids 30-49, 81-100, 111-131, 158-175

**N-glycosylation site.**

amino acids 9-13

**Tyrosine kinase phosphorylation sites.**

amino acids 8-16, 193-202

**N-myristoylation site.**

amino acids 68-74



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**FIGURE 5**

CCCGCTGGCCCGTCACTGCTCTCCCCGTCGTTTGCCCTCTCCAGTTCCCCCAGTGCCTGCCCT  
ACGCACCCCGATGGCGGAGCTGCGGCCTAGCGGCGCCCCCGGCCCCACCGCGCCCCCGGCC  
TGCCCCGACTGCCCCCCCCGGCCTTCGCTTCGCTCTTTCCCCCGGGACTGCACGCCATCTACGG  
AGAGTGCCGCCGCCTTTACCCTGACCAGCCGAACCCGCTCCAGGTTACCGCTATCGTCAAGTA  
CTGGTTGGGTGGCCCAGACCCCTTGACTATGTTAGCATGTACAGGAATGTGGGGAGCCCTTC  
TGCTAACATCCCCGAGCACTGGCACTACATCAGCTTCGGCCTGAGTGATCTCTATGGTGACAA  
CAGAGTCCATGAGTTTACAGGAACAGATGGACCTAGTGTTTGGCTTTGAGTTGACCTTTCG  
TCTGAAGAGAGAACTGGGGAGTCTGCCCCACCAACATGGCCCGCAGAGTTAATGCAGGGCTT  
GGCAGGATACGTGTTCCAGTCAGAGAACACCTTCTGCAGTGGGGACCATGTGTCTTGGCACAG  
CCCTTTGGATAACAGTGAGTCAAGAATTGAGCACATGCTGCTGACAGAGGACCCACAGATGCA  
GCCCCGTGCAGACACCCCTTTGGGGTAGTTACCTTCCTCCAGATCGTTGGTGTCTGCACTGAAGA  
GCTACACTCAGCCCAGCAGTGGAACGGGCAGGGCATCCTGGAGCTGCTGCGGACAGTGCCTAT  
TGCTGGCGGCCCTGGCTGATAACTGACATGCGGAGGGGAGAGACCATATTTGAGATCGATCC  
ACACCTGCAAGAGAGAGTTGACAAAGGCATCGAGACAGATGGCTCCAACCTGAGTGGTGTGAG  
TGCCAAGTGTGCCTGGGATGACCTGAGCCGGCCCCCGAGGATGACGAGGACAGCCGGAGCAT  
CTGCATCGGCACACAGCCCCGGCGACTCTCTGGCAAAGACACAGAGCAGATCCGGGAGACCCT  
GAGGAGAGGACTCGAGATCAACAGCAAACCTGTCCTTCCACCAATCAACCCTCAGCGGCAGAA  
TGGCCTCGCCCACGACCGGGCCCCGAGCCGCAAAGACAGCCTGGAAAGTGACAGCTCCACGGC  
CATCATTCCCCATGAGCTGATTGCGACGCGGCAGCTTGAGAGCGTACATCTGAAATTCAACCA  
GGAGTCCGGAGCCCTCATTCTCTGCTAAGGGGCAGGCTCCTGCATGGACGGCACTTTAC  
ATATAAAAGTATCACAGGTGACATGGCCATCACGTTTGTCTCCACGGGAGTGGAAGGCGCCTT  
TGCCACTGAGGAGCATCCTTACGCGGCTCATGGACCCTGGTTACAACTCTGAACCTATCCTCG  
GAGCTCTGCCCTCCCGTCCTGGAACGTCTTTCTGCCCTGAGGAGAGGGTAGTCAGCATCTCCA  
ATTTTCAGCAGCTCAAGAACCTTGGCCCCCACAGGACTTCGCAGATGTCACATTGCCCCCTCAG  
TCCCCTGAATGCCCTTCGGACCCAACCCCAATTCCCCAAGCCCCTGACCCCTAGCTGCCGGG  
GTTCCCCTCCAGTGCCACAAACCCCTCACCTCCCCTGGCAGCCCCCTCAGCGAGCCTGAGGC  
CCAGCACCCGCTGGCTCCCCAGCACATGGTCCCCTCCCATGGGCTGTTGCCAGGGGAACCGGG  
GCGCGGTGGGAACGAGCTGCTGGCCTCGGCATGTTTCAATAAAGTTGCTGTGCTGGGAG

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**FIGURE 6**

MAELRPSGAPGPTAPPAPGPTAPPAFASLFPPGLHAIYGECRRLYPDQPNPLQVTAIVKYWLG  
GPDPLDYVSMYRNVGSPSANIPEHWHYISFGLSDLYGDNRVHEFTGTDGPGSGFGFELTFRLKR  
ETGESAPPTWPAELMQGLARYVFQSENTFCSGDHVSWHSPLDNSESRIQHMLLTEDPQMOPVQ  
TPFGVVTFLQIVGVCTEELHSAQQWNGQGILELLRTVPIAGGPWLITDMRRGETIFEIDPHLQ  
ERVDKGIETDGSNLSGVSAKCAWDDLSPPEDEDSRSICIGTQPRRLSGKDTEQIRETLRRG  
LEINSKPVLPPINPQRQNGLAHDRAPSRKDSLESSTAIIPHELIRTRQLESVHLKFNQESG  
ALIPLCLRGRLHGRHFTYKSITGDMAITFVSTGVEGAFATEEHPYAAHGPWLQL

**Important features:****N-glycosylation site.**

amino acids 265-268

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**FIGURE 7**

CGCGAATGAAGTTTGCATTTTCCTCTGTTCTTGAGCCCAGCTTCTTCTCGTCTCCCACCCCAG  
CTTCCCGGCATTGGAAGAAGGGACCGTCCTCTTCCTTGTCTTGGCCACCCAAATCCTGGTATC  
GAAAGGGTTGAACGGACCGGAAGTGTGCAGCAGCGACGGGTCCCCAGCTAATCGACGCCGGAA  
GTAGCAATTACTAGACAAGCATTCCGCCGCCGGCTTCGCTATGGCGGCAATTCCCCCAGATTC  
CTGGCAGCCACCCAACGTTTACTTGGAGACCAGCATGGGAATCATTGTGCTGGAGCTGTACTG  
GAAGCATGCTCCAAAGACCTGTAAGAACTTTGCTGAGTTGGCTCGTCGAGGTTACTACAATGG  
CACAAAATTCCACAGAATTATCAAAGACTTCATGATCCAAGGAGGTGACCCAACAGGGACAGG  
TCGAGGTGGTGCATCTATCTATGGCAAACAATTTGAAGATGAACTTCATCCAGACTTGAAATT  
CACGGGGGCTGGAATTCTCGCAATGGCCAATGCGGGGCCAGATACCAATGGCAGCCAGTTCTT  
TGTGACCCCTCGCCCCACCCAGTGGCTTGACGGCAAACACACCATTTTTTGGCCGAGTGTGTCA  
GGGCATAGGAATGGTGAATCGCGTGGGAATGGTAGAAACAACTCCCAGGACCGCCCTGTGGA  
CGACGTGAAGATCATTAAGGCATACCCTTCTGGGTAGACTTGCTACCCTCTTGAGCAGCTCTT  
CTGAGATGGCCCCAGTGAACCAGCTTCTAGATGACATAGAATGACATGTAATGCTAAATTTCA  
TTTTGGCTTTGCAAGTCATGAAGCTTAGGAGGCCTGGCATCTTGGGTGAGTTAGAGATGGAAG  
TACATTTTAATAGGATGCTTCTTTTCTCTTCCCCAGTGCCTAGGTTGCCAGAGCATTTCAC  
AAATGCCCCCTGTTTATCAATAGGTGACTACTTACTACACATGAACCATAATGCTGCTTCTTGT  
GCATGTCTGCTCTGATATACGTCGAACAATGTAGCAGCCACTGTCATTTCTCAGTGGTTTTGC  
CTAACCAAACCTTCTTCCTAAGGAGATTTATATTCTGGCCTACACAGCAGTCCTTGATGGCTGA  
CAGCCACAGAATTCCAAACCAAGTAGTGTCTGTGAGCCCTCTTAACCTCTGTGCACGCCCTATT  
TCAGTCTTTTACATTTGTTCTTCTAGGGAATGTATGCATCTCTATATATATTTTCCCTCTCAA  
AACCAGAACATCAACAGTGCTGTTTCTGACACTTCAGACATCCACGCAAAGCCACATTGAAT  
TTTTGCCAAATGAAAAACACATCCAACAATCAAGTTTCTAAGAAGGTGTCAAGTGGGGAATAA  
TAATAATGTATAATAATCAAGAAATTAGTTTATTTAAAGGAAGCAGAAGCATTGACCATTTTT  
TCCCAGAGAAGAGGAGAAATCTGTAGTGAGCAAAGGACAGACCATGAATCCTCCTTGAGAAGT  
AGTACTCTCAGAAAGGAGAAGCGCCACTCAAGTTCTTTTAACCCAAGACTTTAGAGAAATTAG  
GTCCAAGATTTTTATATGTTTCAGTTGTTTATGTATAAAAATAACTTTCTGGATTTTGTGGGGA  
GGAGCAGGAGAGGAAGGAAGTTAATACCTATGTAATACATAGAACTTCCACAATAAAATGCC  
ATTGATGGTTAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 8**

MAAIPDPSWQPPNVYLETSMGIIIVLELYWKHAPKTCKNFAELARRGYNGTKFHRIKDFMIQ  
GGDPTGTGRGGASIYGKQFEDELHPDLKFTGAGILAMANAGPDTNGSQFFVTLAPTQWLDGKH  
TIFGRVCQGIGMVNRVGMVETNSQDRPVDDVKIIKAYPSG

**Important features:****N-glycosylation sites:**

amino acids 49-52, 108-111

**N-myristoylation sites:**

amino acids 64-69, 69-74, 143-148

**Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature:**

amino acids 48-65



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**FIGURE 10**

MWHEARKHERKLRGMMVDYKKRAERRREYYEKIKKDPAQFLQVHGRACKVHLDSAVALAAESP  
VNMMPWQGDTNNMIDRFDVRAHLDHIPDYTPPLTTISPEQESDERKCNERYRGLVQNDFAG  
ISEEQCLYQIYIDELYGGLQRPSEDEKKKLAEEKKASIGYTYEDSTVAEVEKAAEKPEEEESAA  
EEESNSDEDEVIPDIDVEVDVDELNQEQVADLNKQATTYGMADGDFVRMLRKDKKEAEAIKHA  
KALEEEKAMYSGRRSRRQRREFREKRLRGRKISPPSYARRDSPTYDPYKRSPSESSSESRSRS  
RSPTPGREEKITFITSFGGSDEEAAAAAAAAAASGVTTGKPPAPPQPGGPAPGRNASARRRSS  
SSSSSSASRTSSSRSSSRSSSRSGGGYYRSGRHARSRSRSWSRSRSRSTRYSRSRSRGRR  
HSGGGSRDGHRYSRSPARRGGYGPRRRSRSRSHSGDRYRRGGRGLRHHSSSRSSWSLSPSR  
SRSLTRSRSHSPSPSQSRSRSRSSQSPSPSPAREKLTRPAASPAVGEKLLKTEPAAGKETGA  
AKVTQADASGEAETEDAEGAEQAVQGG

**Important features:****N-glycosylation site:**

amino acids 370-373

**Glycosaminoglycan attachment site:**

amino acids 443-446

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**amino acids 159-162, 282-285, 291-294, 374-377, 375-378, 430-433,  
440-443, 466-469**Casein kinase II phosphorylation site:**amino acids 149-152, 166-169, 171-174, 187-190, 193-196, 195-198,  
303-306, 307-310, 335-338, 571-574**N-myristoylation sites:**

amino acids 118-123, 229-234, 350-355, 446-451, 586-591

**Amidation sites:**

amino acids 263-266, 280-283, 438-441

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**FIGURE 11**

GGTAGGCGCGCCAGACCTGAGACGGGTTGGGACTGGGCTGCGTCACGCGCGGGCTCTAAGCG  
CCCGGGGCCCCGCCAGTGGCCGGCACAGCCAATCGCAGCGCGGGAAGGCGGTGGGGGCGGGG  
AAGGCCGCCTGGAACTTAAATCCCGAGGCGGGCGAACCTGCACCAGACCGCGGACGTCTGTA  
ATCTCAGAGGCTTGTTTGCTGAGGGTGCCTGCGCAGCTGCGACGGCTGCTGGTTTTGAAACAT  
GAATCTTTCGCTCGTCCCTGGCTGCCTTTTGCTTGGAATAGCCTCCGCTGTTCCAAAATTTGA  
CCAAAATTTGGATACAAAGTGGTACCAGTGGAAAGCAACACACAGAAGATTATATGGCGCGAA  
TGAAGAAGGATGGAGGAGAGCAGTGTGGGAAAAGAATATGAAAATGATTGAACTGCACAATGG  
GGAATACAGCCAAGGGAAACATGGCTTCACAATGGCCATGAATGCTTTTGGTGACATGACCAA  
TGAAGAATTCAGGCAGATGATGGGTGCTTTCGAAACCAGAAATTCAGGAAGGGGAAAGTGTT  
CCGTGAGCCTCTGTTTCTTGATCTTCCCAAATCTGTGGATTGGAGAAAGAAAGGCTACGTGAC  
GCCAGTGAAGAATCAGAAACAGTGTGGTTCTTGTTGGGCTTTTAGTGCGACTGGTGCTCTTGA  
AGGACAGATGTTCCGGAAAACCTGGGAACTTGTCTCACTGAGCGAGCAGAATCTGGTGGACTG  
TTCGCGTCCTCAAGGCAATCAGGGCTGCAATGGTGGCTTCATGGCTAGGGCCTTCCAGTATGT  
CAAGGAGAACGGAGGCCTGGACTCTGAGGAATCCTATCCATATGTAGCAGTGGATGAAATCTG  
TAAGTACAGACCTGAGAATTCTGTTGCTAATGACACTGGCTTCACAGTGGTCGCACCTGGAAA  
GGAGAAGGCCCTGATGAAAGCAGTCGCAACTGTGGGGCCCATCTCCGTTGCTATGGATGCAGG  
CCATTCGTCCCTCCAGTTCTACAAATCAGGCATTTATTTTGAACCAGACTGCAGCAGCAAAAA  
CCTGGATCATGGTGTTCTGGTGGTTGGCTACGGCTTTGAAGGAGCAAATTCGAATAACAGCAA  
GTATTGGCTCGTCAAAAACAGCTGGGGTCCAGAATGGGGCTCGAATGGCTATGTAAAAATAGC  
CAAAGACAAGAACAACCACTGTGGAATCGCCACAGCAGCCAGCTACCCCAATGTGTGAGCTGA  
TGGATGGTGAGGAGGAAGGACTTAAGGACAGCATGTCTGGGGAAATTTTATCTTGAAACTGAC  
CAAACGCTTATTGTGTAAGATAAACCAGTTGAATCATGGAGGATCCAAGTTGAGATTTTAATT  
CTGTGACATTTTTTACAAGGGTAAAATGTTACCACTACTTTAATTATTGTTATACACAGCTTTA  
TGATATCAAAGACTCATTGCTTAATTCTAAGACTTTTGAATTTTCATTTTTTAAAAAGATGTA  
CAAAACAGTTTGAAATAAATTTTAATTCGTATATA

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**FIGURE 12**

MNLSLVLA AFCLGIASAVPKFDQNLDTKWYQWKATHRRLYGANEEGWRRRAVWEKNMKMIELHN  
GEYSQGKHGFTMAMNAFGDMTNEEFRQMMGCERNQKFRKGKVFREPLFLDLPKSVDWRKKGYV  
TPVKNQKQCGSCWAFSATGALEGQMFRKTGKLVSLSEQNLVDCSRPOGNQGCNGGFMARAFQY  
VKENGGLDSEESYPYVAVDEICKYRPENSVANDTGFTVVAPGKEKALMKAVATVGPISVAMDA  
GHSSFQFYKSGIYFEPDCSSKNLDHGVLVVGYGFE GANSNNSKYWLVKNSWGP EWGSNGYVKI  
AKDKNNHCGIATAASYPNV

**Important features:****Signal sequence**

amino acids 1-17

**N-glycosylation sites.**

amino acids 2-6, 221-225, 292-296

**N-myristoylation sites.**amino acids 13-19, 93-99, 136-142, 145-151, 174-180, 177-183,  
180-186, 194-200, 288-294, 324-330**Eukaryotic thiol (cysteine) proteases cysteine active site.**

amino acids 132-144

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 275-286



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**FIGURE 13**

GGCGGCGTCATGTGATCCGCTTCCCTGCTCCTTTAAGCGTCCACAGGCGGCGGAGCGGCCACA  
ATCACAGCTCCGGGCATTGGGGGAACCCGAGCCGGCTGCGCCGGGGGAATCCGTGCGGGCGCC  
TTCCGTCCCGGTCCCATCCTCGCCGCGCTCCAGCACCTCTGAAGTTTTGTCAGCGCCCAGAAAG  
GAGGCGAGGAAGGAGGGAGTGTGTGAGAGGAGGGAGCAAAAAGCTCACCCCTAAAACATTTATT  
TCAAGGAGAAAAGAAAAAGGGGGGGCGCAAAAATGCGCTGGGGCAATTATAGAAAACATGAGCA  
CCAAGAAGCTGTGCATTGTTGGTGGGATTCTGCTCGTGTTCCAAATCATCGCCTTTCTGGTGG  
GAGGCTTGATTGCTCCAGGGCCACAACGGCAGTGTCTACATGTCTGGTGAATGTGTGGATG  
CCCGTAAGAACCATCACAAGACAAAATGGTTCGTGCCTTGGGGACCCAATCATTGTGACAAGA  
TCCGAGACATTGAAGAGGCAATTCCAAGGGAAATTGAAGCCAATGACATCGTGTTCCTGTTC  
ACATTCCCCTCCCCACATGGAGATGAGTCTTGGTTCCAATTCATGCTGTTTATCCTGCAGC  
TGGACATTGCCTTCAAGCTAAACAACCAAATCAGAGAAAATGCAGAAGTCTCCATGGACGTTT  
CCCTGGCTTACCGTGATGACGCATTTGCTGAGTGGACTGAAATGGCCCATGAAAGAGTACCAC  
GGAAACTCAAATGCACCTTCACATCTCCCAAGACTCCAGAGCATGAGGGCCGTTACTATGAAT  
GTGATGTCCTTCCTTTCATGGAAATTGGGTCTGTGGCCCATAGTTTTACCTTTTAAACATCC  
GGCTGCCTGTGAATGAGAAGAAGAAAATCAATGTGGGAATTGGGGAGATAAAGGATATCCGGT  
TGGTGGGGATCCACCAAAATGGAGGCTTACCAAGGTGTGGTTTGCCATGAAGACCTTCCTTA  
CGCCAGCATCTTCATCATTATGGTGTGGTATTGGAGGAGGATCACCATGATGTCCCAGCCCC  
CAGTGCTTCTGGAAAAAGTCATCTTGGCCTTGGGATTTCCATGACCTTTATCAATATCCCAG  
TGGAATGGTTTTCCATCGGGTTTACTGGACCTGGATGCTGCTGTTTGGTGACATCCGACAGG  
GCATCTTCTATGCGATGCTTCTGTCTTCTGGATCATCTTCTGTGGCGAGCACATGATGGATC  
AGCACGAGCGGAACCACATCGCAGGGTATTGGAAGCAAGTCGGACCCATTGCCGTTGGCTCCT  
TCTGCCTCTTCATATTTGACATGTGTGAGAGAGGGGTACAACCTCACGAATCCCTTCTACAGTA  
TCTGGACTACAGACATTGGAACAGAGCTGGCCATGGCCTTCATCATCGTGGCTGGAATCTGCC  
TCTGCCTCTACTTCTGTTCCTATGCTTCATGGTATTTTCAGGTGTTTCGGAACATCAGTGGGA  
AGCAGTCCAGCCTGCCAGCTATGAGCAAAGTCCGGCGGCTACACTATGAGGGGCTAATTTTTTA  
GGTTCAAGTTCCTCATGCTTATCACCTTGGCCTGCGCTGCCATGACTGTATCTTCTTCATCG  
TTAGTCAGGTAACGGAAGGCCATTGGAAATGGGGCGGCGTCACAGTCCAAGTGAACAGTGCCT  
TTTTTCACAGGCATCTATGGGATGTGGAATCTGTATGTCTTTGCTCTGATGTTCTTGATGCAC  
CATCCCATAAAAATATGGAGAAGACCAGTCCAATGGCGATCTGGGTGTCCATAGTGGGGAAG  
AACTCCAGCTCACCACCACTATCACCCATGTGGACGGACCCACTGAGATCTACAAGTTGACCC  
GCAAGGAGGCCCAGGAGTAGGAGGCTGCAGCGCCCGGCTGGGACGGTCTCTCCATACCCAGC  
CCCTCTAACTAGAGTGGGGAGCATGCCAGAGAGAGCTCAATGTACAAATGAATGCCTCATGGC  
TCTTAGCTGTGGTTTTCTTGGACCAGCGGCATGGACATTTGTCAGTTTGCCTTCTGACGGTAGC  
TTTTGGAGGAAGATTCTTGCAGCCACTAATGCATTGTGTATGATAACAAAACTCTGGTATGA  
CACATTTTCTGTGATCATTGTTAATTAGTGACATAGTAACATCTGTAGCAGCTGGTTAGTAAA  
CCTCATGTGGGGGTGGGGTGGGGGTGTATTCCCTTGGGGGATGGTTTGGGCCGAATGGGGAGTG  
GAATATTTGACATTTTTCCTGTTTTAAATTCTAGGATAGATTTTAAACATCCTTTGCGGTCCCA  
GTCCAAGGTAGGCTGGTGTATAGTCTTCTCACTCCTAATCCATGACCACTGTTTTTTTCTTA  
TTTATATCACAGGTAGCCTACTGAGTTAATATTTAAGTTGTCAATAGATAAGTGTCCCTGTT  
TTGTGGCATAATATAACTGAATTTTCATGAGAAGATTTATTCACCAGGGGTATTTTCAGCTTTG  
AAACCAAAATCTGTGTATCTAATACTAACCAATCTGTTGGATGTGGATTTTAAAAAATGTTTGC  
TAACTACCCAAGTAAGATTTACTGTATTAAATGGCCTTCGGGTCTGAAAAGCTTTTTTAAACC  
TCTTGCTTAAATGCGTTTTATTTTGATAAGATACTTCAAATAGCCTCCAAAAGTGATAGATCC  
AATCACTTAAATAAACCTGTATGTATATGCAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 14**

MAGAI IENMSTKKLCIVGGILLVFQIIAFLVGGLIAPGPTTAVSYMSVKCVDARKNHHKTKWF  
VPWGNHCDKIRDIEEAIPREIEANDIVFSVHIPLPHMEMSPWFQFMLFILQLDIAFKLNNQI  
RENAEVSM DVSLAYRDDAFAEWTEMAHERVPRKLKCTFTSPKTPEHEGRYYECDVLPFMEIGS  
VAHKFYLLNIRLPVNEKKKINVGIGEIKDIRLVGIHQNGGFTKVWFAMKTFLTPSIFIIMVWY  
WRRITMMSRPPVLLEKVIFALGISMTFINIPVEWFSIGFDWTWMLLFGDIRQGIFYAMLLSFW  
IIFCGEHMMDQHERNHIAGYWKQVGPIAVGSFCLFIFDMCERGVQLTNPFIYSIWTTDIGTELA  
MAFIIVAGICLCLYFLFLCFMVVFQVFRNISGKQSSLPAMSKVRRRLHYEGLIFRFKFLMLITLA  
CAAMTVIFFIVSQVTEGHWKWGGVTVQVNSAFFGTGIYGMWNLYVFALMFLYAPSHKNYGEDQS  
NGDLGVHSGEELQLTTTITHVDGPTEIYKLTTRKEAQE

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**Transmembrane domains:**amino acids 239-253, 269-284, 302-318, 338-352, 377-399, 434-452,  
471-488**N-glycosylation sites.**

amino acids 8-12, 406-410

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 254-258

**N-myristoylation sites.**amino acids 223-229, 274-280, 305-311, 358-364, 374-380, 386-392,  
509-515

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**FIGURE 15**

GTGAGGGGAACAGCTGATCCGTCTGTTGGGAGGACAGATATCTCAAGGCCAGG**ATG**GGAAGAAT  
CACCAC TAAGCCGGGCACCATCCCGTGGTGGAGTCAACTTTCTCAATGTAGCCCGGACCTACA  
TCCCCAACACCAAGGTGGAATGTCACTACACCCTTCCCCCAGGCACCATGCCCAGTGCCAGTG  
ACTGGATTGGCATCTTCAAGGTGGAGGCTGCCTGTGTTCCGGATTACCACACATTTGTGTGGT  
CTTCCGTGCCTGAAAGTACAAGTATGATGGTTCCCCCATTCACACCAGTGTCAGTTCCAAGCCA  
GCTACCTGCCCCAAACCAGGAGCTCAGCTCTACCAGTTCCGATATGTGAACCGCCAGGGCCAGG  
TGTGTGGGCAGAGCCCCCTTTCCAGTTCCGAGAGCCAAGGCCCATGGATGAACTGGTGACCC  
TGGAGGAGGCTGATGGGGGCTCTGACATCCTGCTGGTTGTCCCCAAGGCAACTGTGTTACAGA  
ACCAGCTCGATGAGAGCCAGCAAGAACGGAATGACCTGATGCAGCTGAAGCTACAGCTGGAGG  
GACAGGTGACAGAGCTGAGGAGCCGAGTGCAGGAGCTCGAGAGGGCTCTGGCAACTGCCAGGC  
AGGAGCACACGGAGCTGATGGAACAGTACAAGGGGATTTCCCGGTCCCATGGGGAGATCACAG  
AAGAGAGGGACATCCTGAGCCGGCAACAGGGAGACCATGTGGCACGCATCCTGGAGCTAGAGG  
ATGACATCCAGACCATCAGTGAGAAAGTGCTGACGAAGGAAGTGGAGCTGGACAGGCTTAGAG  
ACACAGTGAAGGCCCTGACTCGGGAACAAGAGAAGCTCCTTGGGCAACTGAAAGAAGTACAAG  
CAGACAAGGAGCAAAGTGAGGCTGAGCTCCAAGTGGCACAACAGGAGAACCATCACTTAAATT  
TGGACCTGAAGGAGGGCGAAGAGCTGGCAAGAGGAGCAGAGTGCTCAGGCTCAGCGACTGAAAG  
ACAAGGTGGCCAGATGAAGGACACCCTAGGCCAGGCCAGCAGCGGGTGGCCGAGCTGGAGC  
CCTTGAAGGAGCAGCTTCGAGGGGGCCAGGAGCTTGCGAGCCTCAAGCCAGCAGAAAGCCACCC  
TTCTTGGGGAGGAGTTGGCCAGTGCAGCAGCAGCCAGGGACCGCACCATAGCCGAACTACACC  
GCAGCCGCCTGGAAGTGGCTGAAGTTAACGGCAGGCTGGCTGAGCTCGGTTTGCACCTTGAAGG  
AAGAAAAATGCCAATGGAGCAAGGAGCGGGCAGGGCTGCTGCAGAGTGTGGAGGCAGAGAAGG  
ACAAGATCCTGAAGCTGAGTGCAGAGATACTTCGATTGGAGAAGGCAGTTCAGGAGGAGAGGA  
CCCAAACCAAGTGTTCAAGACTGAGCTGGCCCCGGGAGAAGGATTCTAGCCTGGTACAGTTGT  
CAGAAAGTAAGCGGGAGCTGACAGAGCTGCGGTGAGCCCTGCGTGTGCTCCAGAAGGAAAAGG  
AGCAGTTACAGGAGGAGAAACAGGAATTGCTAGAGTACATGAGAAAGCTAGAGGCCCGCCTGG  
AGAAGGTGGCAGATGAGAAGTGAATGAGGATGCCACCACAGAGGATGAGGAGGCCGCTGTGG  
GGCTGAGCTGCCCGGCAGCTCTGACAGACTCAGAGGACGAGTCCCCAGAAGACATGAGGCTCC  
CACCCTATGGCCTTTGTGAGCGTGGAGACCCAGGCTCCTCTCCTGCTGGGCCTCGAGAGGCTT  
CTCCCCTTGTTGTATCAGCCAGCCGGCTCCCATTTCTCCTCACCTCTCTGGGCCAGCTGAGG  
ACAGTAGCTCTGACTCGGAGGCTGAAGATGAGAAGTCAGTCTGATGGCAGCTGTGCAGAGTG  
GGGTGAGGAGGCCAACTTACTGCTTCTGAACTGGGCAGTGCCTTCTATGACATGGCCAGTG  
GCTTTACAGTGGGTACCCTGTGAGAAACCAGCACTGGGGGGCCCTGCCACCCCCACATGGAAGG  
AGTGTCTATCTGTAAGGAGCGCTTTCCTGCTGAGAGTGACAAGGATGCCCTGGAGGACCACA  
TGGATGGACACTTCTTTTTTCAGCACCCAGGACCCCTTACCTTTGAG**TGA**TCTTACTCCCTCG  
TACATGCACAAATACACACTCATGCACACACACACTCACACACATGCATACACTTAGGTTTCA  
TGCCCATTTTCTATCACACTGGGCTCCATGATATTCTGTTCCCTAAGAACTGCTTCTGTGTGC  
CCTGTTTTTCATCCCAAGATTTCTCACTTCATCCTCTCCTACCTGGCTCTTTTGTCCCAGGGAG  
GGGTCCTGTTTCGGAAGCAGTGGCTGAATTTATCCCCTGAAAGTGGTTTGGAGGAACCGGGAT  
GGAGGAGGCCCTTCCCCTGTGGGAATAGAATCGTCCACTCCTAGCCCTGGTTGCTTCTGATACA  
CAGCCACTGCACACACACACTCACACTCACACTCCCTTGTCTGATGCCCCAAAGCCAATTCTCT  
GGGGCACCCCTACCCTCTCTTATTTGGAGTTTCCGTTGGTTTACCTGAGTTTCTCTGGGGTCT  
GCACAGAGGCAGCAGCATGGACATCATGGCCTCTCAGGTCCCTTTTGGTTCTCAGTTTCATTG  
GTTCTCTTTCTGTTCCCCCATTTGACTTCTGTGCCCCACCCTAGCCTTTTCCATAACCTTAGG  
TATTCAGTTTGGAGGGGTTTTTTGTATTTTTGAGGATTCTGTATTCTGTATCCTCTCCTCGC  
ATCTCCTCACATGGAAAGAAATAATGTATTTGTGCCTTCTGTGAGGAATGGGGGGAACAAGTG  
GTCCCAGGTATCCCCATTTCCAAGGCCCCCTCCCTCTCCAGGTCCCCCACAGCAATAAAAG  
CTTCCCCCTGATATCCATCCCTTTGTAGTTTGAACAAATATATTTATATGATATGTAA

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**FIGURE 16**

MEESPLSRAPSRGGVNFLNVARTYIPNTKVECHYTLPPGTMPASDWDWIGIFKVEAACVRDYHT  
FVWSSVPESTTDGSPIHSTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFREPRPMDE  
LVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLMQLKLQLEGQVTELRSRVQELERALA  
TARQEHTELMEQYKGISRSHGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD  
RLRDTVKALTREQEKLKGQLKEVQADKEQSEAEQVAQQENHHLNLDLKEAKSWQEEQSAQAQ  
RLKDKVAQMKDTLGQAQQRVAELEPLKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIA  
ELHRSRLVAEVNGRLAELGLHLKEEKQWSKERAGLLQSVEAEKDKILKLSAEILRLEKAVQ  
EERTQNQVFKTELAREKDSSLVQLSESKRELTELSALRVLQKEKEQLQEEKQELLEMYMRKLE  
ARLEKVADEKWNEDATTEDEEAAGVGLSCPAALTDSEDESPEDMRLPPYGLCERGDGSSPAGP  
REASPLVVISQPAPISPHLSGPAEDSSSDSEAEDEKSVLMAAVQSGGEEANLLLPELGSAFYD  
MASGFTVGTLSSETSTGGPATPTWKECPICKERFPAESDKDALEDHMDGHFFSTQDPFTFE

**Important features:****Casein kinase II phosphorylation sites:**

amino acids 28-31, 43-46, 68-71, 72-75, 129-132, 156-159, 208-211, 239-242, 282-285, 305-308, 376-379, 383-383, 468-471, 520-523, 521-524, 537-540, 539-542, 543-546, 593-596, 595-598, 597-600, 612-615, 639-642, 652-655, 667-670, 683-686

**N-myristoylation sites:**

amino acids 39-44, 107-112, 204-209, 414-419, 561-566, 613-618

**Cell attachment sequence:**

amino acids 557-559

**Leucine zipper pattern sequence:**

amino acids 163-184, 475-496, 482-503

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**FIGURE 17**

GCAAGTTGGGAATTTTAGACTGTCACTGCACATGGACCTCTGGGAAGACGTCTGGCGAGAGCT  
AGGCCCCTGGCCCTACAGACGGATCTTGCTGGCTCACCTGTCCCTGTGGAGGTTCCCCTGGG  
AAGGCAAGATGCCCAACAACAGCACTGCTCTGTCAATTGGCCAATGTTACCTACATCACCATGG  
AAATTTTCATTGGACTCTGCGCCATAGTGGGCAACGTGCTGGTCATCTGCGTGGTCAAGCTGA  
ACCCAGCCTGCAGACCACCACCTTCTATTTTCATTGTCTCTCTAGCCCTGGCTGACATTGCTG  
TTGGGGTGCTGGTCATGCCTTTGGCCATTGTTGTGAGCCTGGGCATCACAATCCACTTCTACA  
GCTGCCTTTTTATGACTTGCCTACTGCTTATCTTTACCCACGCCTCCATCATGTCCCTTGCTGG  
CCATCGCTGTGGACCGATACTTGCGGGTCAAGCTTACCGTCAGATTCAGAATTCCTGGGCTCC  
CTGGGTGCATTCTATCATTCCAGTTGAAAGTTTGCTTCCCTCCAGTCATGTGGCTCTTCATTC  
TACTCTCCTTGCTCTCATTTTCAGATGCCATGGTCATGGATGAAAAGGTCAAGAGAAGCTTTG  
TGCTGGACACGGCTTCTGCCATCTGCAACTACAATGCCCACTACAAGAATCACCCCCAAATACT  
GGTGCCGAGGCTATTTCCGTGACTACTGCAACATCATCGCCTTCTCCCCTAACAGCACCAATC  
ATGTGGCCCTGAGGGACACAGGGAACCAGCTCATTGTCACTATGTCTCTGCCTGACCAAAGAGG  
ACACGGGCTGGTACTGGTGTGGCATCCAGCGGGACTTTGCCAGGGATGACATGGATTTTACAG  
AGCTGATTGTAAGTACGACAAAGGAACCCTGGCCAATGACTTTTGGTCTGGGAAAGACCTAT  
CAGGCAACAAAACCAGAAGCTGCAAGGCTCCCAAAGTTGTCCGCAAGGCTGACCGCTCCAGGA  
CGTCCATTCTCATCATTTGCATACTGATCACGGGTTTGGGAATCATCTCTGTAATCAGTCATT  
TGACCAAAGGAGGAGAAGTCAAAGGAATAGAAGGGTAGGCAACACTTTGAAGCCCTTCTCGC  
GTGTCCTGACTCCAAAGGAAATGGCTCCTACTGAACAGATGTGACTGAAGATTTTTTTAATTT  
AGTTCATAAAGTGATGCTACAACAGAATAATCACCATGACAACCTGGCCCACACCTCAGAGACT  
GATTCTGATCTCCAGGAATTCTGAAGGACCTCTATCCTTGACAACAATCATTTCAGCCAG  
GTAGCAACGGCGGTAGTCAGAGGAGCTATGATAGACCACACCCAAGCAAGGCTGCCCTCAAAT  
AACATCTCAAGATCTTAGTTCTTATGCATTCCATCAGTCAGAAGTGAAGAAGAGGTGGAGAAT  
CTGGATTGGGGACCAGGAAATCACTTGTATTTTGTAGCCAATAAATTCCTAGCCAGTGTTGA  
ATGAAAAAAAAAAAAA

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**FIGURE 18**

MPNNSTALSLANVTYITMEIFIGLCAIVGNVLVICVVKLNPSLQTTTFYFIVSLALADIAVGV  
LVMP LAIVVSLGITIHFYSCLFMTCLLLIFTHASIMSL LAIVDRYL RVKLTVRFRIPGLPGC  
ILSFQLKVCFLPVMWLFILLSLALISDAMVMDEKVKRSFVLDTASAICNYN AHYKNHPKYWCR  
GYFRDYCNIIAFSPNSTNHVALRDTGNQLIVTMSCLTKEDTGWYWCGIQRDFARDDMDFT ELI  
VTDDKGT LANDFWSGKDL SGNKTR SCKAPKVVRKADRSRTS ILIICILITGLGIISVISHLTK  
RRRSQRNRRVGNTLKPFSRVLTPKEMAPTEQM

**Important features of the protein:****Transmembrane domains:**

amino acids 16-35, 62-80, 89-101, 134-152, 292-311

**N-glycosylation sites.**

amino acids 3-7, 4-8, 12-16, 204-208, 273-277

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 316-320

**N-myristoylation sites.**

amino acids 122-128, 125-131, 258-264

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 214-225

**G-protein coupled receptors proteins.**

amino acids 29-59, 76-116

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**FIGURE 19**

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCTGCGATTGAGCTGCGGGTCGCGGCCGGCGCCGGCCTCTCCAATG  
GCAAATGTGTGTGGCTGGAGGCGAGCGCGAGGCTTTCGGCAAAGGCAGTCGAGTGTTTGCAGACCGGGGCGAGTC  
CTGTGAAAGCAGATAAAAGAAAACATTTATTAACGTGTCTATTACGAGGGGAGCGCCCGGGGCTGTGCGACT  
CCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGAAAGCGGAAAAGAGGCAGATTACAGTCG  
TTTCCAGCCAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGATTTATTAGCGATGCCCCCTG  
GTTTGTGTGTTACGACACACACAGTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCCAGCTCCTGGGCG  
AATCCACATCTGTTTCAACTCTCCGCCGAGGGCGAGCAGGAGCGAGAGTGTGTGGAATCTGCGAGTGAAGAGGG  
ACGAGGGGAAAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAGAAGCACCAGATCAGCAAAA  
AAAGAAGATGGGCCCCCCGAGCCTCGTGCTGTGCTTGCTGTCCGCAACTGTGTTCTCCCTGCTGGGTGGAAGCTC  
GGCCTTCTGTGCGACCACCGCCTGAAAGGCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCCAACATCATCCT  
GGTGTGACGGACGACCAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAAGACCCGGCGCATCATGGAGCA  
GGGCGGGGCGCACTTCATCAACGCCTTCGTGACCACACCCATGTGCTGCCCTCAGCTCCTCCATCCTCACTGG  
CAAGTACGTCCACAACCACAACCTACACCAACAATGAGAACTGCTCCTCGCCCTCCTGGCAGGCACAGCACGA  
GAGCGGCACCTTTGCCGTGTACCTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAGTATCTTAATGAATA  
CAACGGCTCCTACGTCACCCGGCTGGAAGGAGTGGGTGCGACTCCTTAAAAACTCCCGCTTTTATAACTACAC  
GCTGTGTGCGAACGGGGTGAAGAGAAGCAGGCTCCGACTACTCCAAGGATTACCTCACAGACCTCATACCAA  
TGACAGCGTGAGCTTCTTCCGCACGTCCAAGAAGATGTACCCGCACAGGCCAGTCTCATGGTTCATAGCCATGC  
AGCCCCCAGCGCCCTGAGGATTACGCCCCACAATATTCACGCCTCTTCCCAAACGCATCTCAGCACATCACGCC  
GAGCTACAACCTACGCGCCCAACCCGGACAACACTGGATCATGCGCTACACGGGGCCCATGAAGCCCATCCACAT  
GGAATTCACCAACATGCTCCAGCGGAAGCGCTTGACAGCCCTCATGTGCGGTGGACGACTCCATGGAGACGATTTA  
CAACATGCTGGTTGAGACGGGCGAGCTGGACAACACGTACATCGTATACACCGCCGACCACGGTTACCACATCGG  
CCAGTTTGGCCTGGTGAAGGGAAATCCATGCCATATGAGTTTGACATCAGGGTCCCGTTCTACGTGAGGGGCCC  
CAACGTGGAAGCCGGCTGTCTGAATCCCCACATCGTCTCAACATTGACCTGGCCCCCACCATCCTGGACATTGC  
AGGCCTGGACATACCTGCGGATATGGACGGGAAATCCATCCTCAAGCTGCTGGACACGGAGCGGCCGGTGAATCG  
GTTTCACTTGAAAAAGAAGATGAGGGTCTGGCGGGACTCCTTCTTGGTGGAGAGAGGCAAGCTGTACACAAGAG  
AGACAATGACAAGGTGGACGCCAGGAGGAGAACTTTCTGCCCAAGTACCAGCGTGTGAAGGACCTGTGTGTCAGCG  
TGCTGAGTACCAGACGGCGTGTGAGCAGCTGGGACAGAAGTGGCAGTGTGTGGAGGACGCCACGGGGAAGCTGAA  
GCTGCATAAGTGCAAGGGCCCCATGCGGCTGGGCGGCAGCAGAGCCCTCTCCAACCTCGTGCCCAAGTACTACGG  
GCAGGGCAGCGAGGCCGTGCACCTGTGACAGCGGGGACTACAAGCTCAGCCTGGCCGGACGCCGGAAGAACTCTT  
CAAGAAGAAGTACAAGGCCAGCTATGTCCGCAGTGCCTCCAGTCCGCTCAGTGGCCATCGAGGTGGACGGCAGGCT  
GTACCAGTAGGCTGGGTGATGCCGCCAGCCCGAAACCTCACCAGCGGCACTGGCCAGGGCCCCCTGAGGA  
CCAAGATGACAAGGATGGTGGGACTTCAGTGGCACTGGAGGCCTTCCGACTACTCAGCCGCCAACCCCATTA  
AGTGACACATCGGTGCTACATCCTAGAGAACGACACAGTCCAGTGTGACCTGGACCTGTACAAGTCCCTGCAGGC  
CTGGAAAGACCACAAGCTGCACATCGACCACGAGATTGAAACCCTGCAGAACAAATTAAGAACCTGAGGGAAAGT  
CCGAGGTACCTGAAGAAAAAGCGGCCAGAAGATGTGACTGTACAAAATCAGCTACCACACCCAGCACAAAGG  
CCGCCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTCAGGAAGGGCCTGCAAGAGAAGGACAAGGTGTGGCTGTT  
GCGGGAGCAGAAGCGCAAGAAGAACTCCGCAAGCTGCTCAAGCGCCTGCAGAACACGACAGTGCAGCATGCC  
AGGCCTCACGTGCTTACCCACGACAACCAGCACTGGCAGACGGCGCCTTTCTGGACACTGGGGCCTTTCTGTGC  
CTGCACCAGCGCCAACAATAACACGTACTGGTGCATGAGGACCATCAATGAGACTCACAATTTCTCTTCTGTGA  
ATTTGCAACTGGCTTCTAGAGTACTTTGATCTCAACACAGACCCCTACCAGCTGATGAATGCAGTGAACACACT  
GGACAGGGATGTCTCAACCAGCTACAGTACAGCTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAA  
CCCCCGGACTCGAAACATGGACCTGGATGGAGGAAGCTATGAGCAATACAGGCAGTTTCAGCGTCAAGTGGCC  
AGAAATGAAGAGACCTTCTTCCAAATCACTGGGACAACCTGTGGGAAGGCTGGGAAGGTTAAGAAACAACAGAGGT  
GGACCTCCAAAAACATAGAGGCATCACCTGACTGCACAGGCAATGAAAAACCATGTGGGTGATTTCCAGCAGACC  
TGTGCTATTGGCCAGGAGGCTGAGAAAGCAAGCACGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCA  
GCAGGAGCAGAGATAACTTCAGGAAGTCCATTTTGGCCCTGCTTTTGTCTTGGATTATACCTCACCAGCTGCAC  
AAAATGCATTTTTCGTATCAAAAAGTCACCACTAACCTCCCCAGAAGCTCACAAGGAAAACGGAGAGAGCG  
AGCGAGAGAGATTTCTTGGAAATTTCTCCCAAGGGCGAAAGTCATTGGAATTTTAAATCATAGGGGAAAAGCA  
GTCTGTCTTAAATCCTTATTCTTTTGGTTTGCACAAAAGGAAGTAAGAAAGCAGGACAGAGGGCAACGTGG  
AGAGGCTGAAAACAGTGCAGAGACGTTTGACAATGAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCACTAT  
AAACCCTGGTTGCCTCTGAAGAACTGCCTTCAATGTATATATGTGACTATTTACATGTAATCAACATGGGAACT  
TTTAGGGGAACCTAATAAGAAATCCCAATTTTCAGGAGTGGTGGTGTCAATAAACGCTCTGTGGCCAGTGTAAAA  
GAAAAA

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**FIGURE 20**

MGPPSLVLCCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQV  
MNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHESTR  
FAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSDYSK  
DYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFNASQHITPSYNY  
APNPDKHWIMRYTGPMKPIHMEFTNMLQKRQLQTLMSVDDSMETIYNMLVETGELDNTYIVYT  
ADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPVNEAGCLNPHIVLNIDLAPTILDIAGLDIP  
ADMKGKSLKLLDTERPVRNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEENFLPKYQR  
VKDLCQRAEYQTACEQLGQKWQCVEDATGKLKHKCKGPMRLGGSRALSNLVPKYYGQGSEAC  
TCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSAIEVDGRVYHVGLGDAAQPRNLTKRHW  
PGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKSLQAWKDHKLH  
IDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRCLKHRGSSLHPFRKGLQEKD  
KVWLLREQKRKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLGPFCACTSANNNT  
YWCMTINETHNFLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQLHVQLMELRSCKGY  
KQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

**Important features:****Signal peptide:**

amino acids 1-17

**Sulfatases signature 1.**

amino acids 86-99

**Homologous region to sulfatase:**

amino acids 87-106, 133-146, 216-229, 291-320, 365-375

**N-glycosylation sites.**amino acids 65-69, 112-116, 132-136, 149-153, 171-175, 198-202,  
241-245, 561-565, 608-612, 717-721, 754-758, 764-768



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**FIGURE 21**

GGGCGCGGAGAGCTGCTAGGGCGGTTTCTCTGCCTCGGGCCTGTTGGGCAGGGCCGGCT  
AAGGTGCGCGTGCTCGCTGGTTCTAACCCTTCTGTTGGGCGTTTCTGCTGAGAGGCGGGA  
GGCGCTGAGAGTCTGTGCGGAGGTCCGTGGACAGACTGCTTTGCTCGTTGTTGCTCTTCG  
GAGGCGGCGATCCCCGAAGGCGAGCTGAAATACGGCTGCAGGCTACAATTTGCAGCCGAC  
GATTATGGAAGACGGAAGCGGGAGAGGTGGCCCACCCTCATGGAGCGCTTGTGCTCGGAT  
GGCTTCGCATTTCCCCAATACCCCATTAACCGTATCATCTGAAGAGGATCCACAGAGCT  
GTCTTACATGGTAATCTAGAGAACTGAAGTACCTTCTGCTCACGTATTATGACGCCAAT  
AAGAGAGACAGGAAGGAAAGGACCGCCCTACATTTGGCCTGTGCCACTGGCCAACCGGAA  
ATGGTACATCTCCTGGTGTCCAGAAGATGTGAGCTTAACCTCTGCGACCGTGAAGACAGG  
ACACCTCTGATCAAGGCTGTACAACCTGAGGCAGGAGGCTTGTGCAACTCTTCTGCTGCAA  
AATGGCGCCAATCCAAATATTACGGATTTCTTTGGAAGGACTGCTCTGCACTACGCTGTG  
TATAATGAAGATACATCCATGATAGAAAACTTCTTTCACATGGTACAAATATTGAAGAA  
TGCAGCAAGGTATAGGTCAACCAATGTTATTTTCAAACCTATCTGAAATGAATTTATTTTA  
ACATTGACACATGTAAGGGTCAATTTTTTCATATTTGGAAGCTCAACATTCCTTGAATGA  
AAATATTTTGAATGCCTTAACGTCTAAGATTTTACTTTAAATATTGGAACCTTTTAAAG  
AAGCATTATAGGGAACAGCCTTTTTTTCATGCACTTATGGTAAATAACTATAAAAACAAAT  
GAATTACAATAAATTTATAATTCATGACAACCTGAATTTGGGAAAGGTAATAGTTAAGTGT  
TTTTCCACTAAATTACTTTTT

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**FIGURE 22**

MERLCSDGFAFPQYPIKPYHLKRIHRAVLHGNLEKLYLLTTYDANKRDRKERTALHLACAT  
GQPEMVHLLVSRRCNELNLCREDRTPLIKAVQLRQEACATLLLQNGANPNITDFFGRTALHYA  
VYNEDTSMIEKLLSHGTNIEECSKV

**Important features of the protein:****N-glycosylation site.**

amino acids 113-117

**N-myristoylation site.**

amino acids 109-115

**Microbodies C-terminal targeting signal.**

amino acids 149-153

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**FIGURE 23**

GAGGCAGAAAGGCAGAAAGGAGAAAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTG  
CCATGTAGTGCACGCAGGACATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGT  
CACTTATTCTAAAGGCCCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAG  
GGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAAGAAATGAACTGAAGGAGTGTGT  
TTCCATCCTCCCACGGAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGC  
TGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGC  
CGCCCTGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCT  
GCCAGCAGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACT  
GAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCG  
TGCCGTTTCAAGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAGACAGTGA  
AACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGG  
AAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTTACTTTTTTATATA  
TGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGT  
CCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAATATGCCTGA  
AACACTACCCAATAATTCCTGCTATTAGCTGGCATTGCAAACTGGAAGAAGGAGATGAACT  
CCAATTGCAATACCAAGAGAAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTTGG  
TGCATTGAAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCCTCCCTTTCTCTGT  
ACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAA

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**FIGURE 24**

MDDSTEREQSRLTSCCLKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCCLTV  
VSFYQVAALQGD LASLRAELQGHHA EKLPAGAGAPKAGLEEAPAVTAGLKIFEP PAPGEGNSS  
QNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL EEEKENKILVKE  
TGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAK  
LEEGDELQLAIPRENAQISLDGDVTFFGALKLL

**Transmembrane domain:**

amino acids 47-72

**N-glycosylation site.**

amino acids 124-127, 242-245

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 33-36, 173-176

**N-myristoylation site.**

amino acids 96-101

**TNF family proteins.**

amino acids 172-206

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**FIGURE 25**

CTGCTTGGATACCTCCAGTCCCCAACTGTGTTCCAGGAGTTTTCTTGGCCGAAGCTGCCCCGA  
TGTTTTGAGCCTTTTTCTTCCCAGAGAAGAAGATGGACTGAAAGCTGCCAGTTGGGGACTTTTTTG  
TGATCACGGCGTTGCAGCGTTTTAAAGGAGGTGATGGGGCTTGCGCTGGCTTGTCTTCCCACC  
CAAGTGAAGAGTTGATGTTCACTGGTTATGCTTAGACAATGTGCAGTTTGTGTTAATTTAAAA  
TTTTGGGTGGGATAGGGGCATAGGCTTGTGAAGGGCAGTCCGGATCCGGAGGAACTCGTCTTT  
GTCCCTGGTAGGAGAGACACCCCCAGTCTATCCTCGATGCCGTGAGCCTTGGCCATCTTCACT  
TGCCGCCCCGAAGCTCGCACCCGTTTTCAGGAGCGTCATGTCTACCTGGACGAGCCCATCAAATC  
GGCCGCTCAGTGGCCCGCTGTGACACCAGCGCAGAATAATGCCACTTTTGATTGCAAAGTGCTA  
TCAAGGAACCACGCTCTCGTCTGGTTGATCACAAAGACGGGCAAGTTTTATCTTCAAGACACT  
AAAAGTAGTAATGGTACTTTTTATAAATAGCCAGAGATTGAGTCGAGGCTCTGAAGAAAGTCCA  
CCATGTGAAATTTCTTTCCGGTGACATTATCCAGTTTGGAGTAGACGTGACAGAGAATACACGG  
AAAGTTACCCATGGGTGTATTGTTTCCACAATAAACTTTTTCTACCAGATGGTATGGAAGCC  
CGGCTCCGCTCAGATGTCTATCCATGCACCATTACCAAGTCCTGTTGACAAAGTTGCTGCTAAC  
ACTCCAAGTATGTACTCTCAGGAAGTATTCCAGCTTTCTCAGTATCTACAGGAGGCCTTACAT  
CGGGAACAAATGTTGGAACAGAAGTTAGCCACGCTTCAGCGGCTACTAGCCATCACCCAAGAG  
GCTTCAGATACCAGTTGGCAGGCTTTAATAGATGAAGATAGACTCTTATCACGGTTAGAAGTT  
ATGGGAAACCAATTACAGGCATGCTCCAAAAATCAAACAGAAGATAGTTTACGAAAGGAACTT  
ATAGCATTACAAGAGGATAAACATAACTATGAGACAACAGCCAAAGAGTCCCTGAGGCGGGTT  
CTTCAGGAGAAAATTGAAGTGGTTAGAAAACCTTTCAGAAGTTGAGCGAAGTCTGAGTAATACT  
GAAGATGAATGTACCCATCTGAAAGAAATGAATGAAAGGACTCAGGAAGAATTAAGAGAATTA  
GCCAACAAATATAATGGAGCAGTTAATGAGATTAAAGATTTATCTGATAAATTAAGGTAGCA  
GAGGGAAAACAAGAGGAAATCCAACAGAAGGGACAGGCTGAGAAAAAAGAATTACAACATAAA  
ATAGATGAAATGGAAGAAAAAGAACAGGAGCTCCAGGCAAAAATAGAAGCTTTGCAAGCTGAT  
AATGATTTTACCAATGAAAGGCTAACAGCTTTACAAGTACGGTTAGAACATCTTCAGGAGAAA  
ACTCTTAAAGAAATGCAGCAGCTTGGCTGATCGTCAAGGGCATCTAACCAAAGCGGTAGAAGA  
AACAAAGCTTTCAAAGGTTTGTCTTCTGTTTTCTATGTTTTTTGACAGTTCTTTTGGATAA  
TGAAGGTTAGTGTATATTTTCAAGGTTATAGTATTTTAAACCATCAGTTTACTTCTTATAGCTC  
ACAAAATAGCAAGCCAGTAACAGTATCAGATAATATATAAAATAATCAGACTTCTGTTTTAAG  
AAGGGTATCGTAAGTGAATGTGTCTTTTTTAAAGTGGATGTATATTTATGGTTTTTTGAATGTT  
AGTACTTGATATAGGTTTCTTTAGGTATTAAAGATTTGTTGCAATCTCTGTCAATCCCAGCAT  
TAATTTTCAAGCTTTGATCTCAAATTTTAAATCAAACACAATGTAAGTCGTTTGTGATACAACTTA  
AGTGAAACATGCTTGCACTTCTATTTTGGGGGTACAGTACCTTTAAATCTCTTATGATGTT  
TAATATTTTCTTAATTTTTTGGCATCTCAGTTTGATTTAAACAAAATTAATGACTTTTGTGAAT  
GTAGAATCTTCTTATATTTTATGAGTAGTCCAGTAATTGCCCAAAGTAGTTTATTGTGTTAAT  
TCTGTTACAGTTGTCAGAGAAGAAAAGTGAGTTTAAAGCACCATATTGTCAAGTCACTTTTA  
TACATAGGGAAATTAGGCAAATAAATTTGGTGGCATGTGTTTATCATAGTAGAACTTTCATTA  
GACTATACCAGTATAAAATTTAAACTAGATTACAGTCCTTTTGGCCAATTAACAACTTGGAG  
TTACAAAAGTTTGAGATACTTAATTTTAGTACATTCTATTTTATTAAAGTAACTGGATTTCATT  
TGACTTTTTTAACCATGTAAGAGGATGGTGTATTTTCAAATATCTCGTGGTTTTCCATTCTGAA  
TTTTGTGCACGGCAGATGCCATATTTGGGGAAAAAATGCATAGAATATGCATCATTAAATATTG  
TTTTGGCAAACAGGCATTGAGTTTCAGAACAGTGAAGTATTTTATGATACATATGGCAATTTTT  
TTCACCTTATTAAAGTGAGATGAGAACAGACCTTAAATAGCTTTTACCTCACCATCCAAATA  
CCTATTCAGATTAGTTGGTTGAATAGCCAGCACTTTGAAGTAGAGCCTTAGG

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**FIGURE 26**

MEARLRSDVIHAPLPSPVDKVAANTPSMYSQELFQLSQYLQEALHREQMLEQKLATLQRLAI  
TQEASDTSWQALIDEDRLLSRLEVMGNQLQACSKNQTEDSLRKELIALQEDKHNYETTAKESL  
RRVLQEKIEVVRKLSEVERSLSNTEDECTHLKEMNERTQEELRELANKYNGAVNEIKDLSDKL  
KVAEGKQEEIQQKGQAEKKELQHKIDEMEEKEQELQAKIEALQADNDFTNERLTALQVRLEHL  
QEKTLEKCSSLADRRRASNQSGRRNKAFKRFVFCFSMFFDSSFG

**Important features of the protein:****N-glycosylation sites.**

amino acids 98-102, 271-275

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 138-142, 267-271

**Amidation site.**

amino acids 273-277

**Tropomyosins proteins.**

amino acids 169-217

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**FIGURE 27**

GAACCTGGCGCCGCGGAACTGATCGCGGCCTAGTCCCGACGCGTGTGTGCTAGTGAGCCGGA  
GCCGGCGACGGCGGCAGTGGCGGCCCGGCCTGCAGGAGCCCGACGGGGTCTCTGCCATGGGGG  
AGTGACGCGCCTGCACCCGCTGTTCCGCGGCAGCGGCGAGACATGAGGAGACCCCGCGACAGG  
GGCAGCGGCGGCGGCTCGTGAGCCCCGGG**GATG**GAGGAGAAATACGGCGGGGACGTGCTGGCCG  
GCCCCGGCGGCGGCGGCGGCCTTGGGCGGGTGGACGTACCCAGCGCTCGATTAAACAAAATATA  
TTGTGTTACTATGTTTCACTAAATTTTTGAAGGCTGTGGGACTTTTTCGAATCATATGATCTCC  
TAAAAGCTGTTTCACATTGTTTCAGTTCATTTTTATATTAAACTTGGGACTGCATTTTTTATGG  
TTTTGTTTCAAAAGCCATTTTCTTCTGGGAAAACATTACCAAACACCAAGTGGATCAAAATAT  
TTAAACATGCAGTTGCTGGGTGTATTATTTCACTCTTGTGGTTTTTTTGGCCTCACTCTTTGTG  
GACCACTAAGGACTTTGCTGCTATTTGAGCACAGTGATATTGTTGTCAATTTCACTACTCAGTG  
TTTTGTTTACCAGTTCTGGAGGAGGACCAGCAAAGACAAGGGGAGCTGCTTTTTTTCATTATTG  
CTGTGATCTGTTTATTGCTTTTTGACAATGATGATCTCATGGCTAAAATGGCTGAACACCCTG  
AAGGACATCATGACAGTGCTCTAACTCATATGCTTTACACAGCCATTGCCTTCTTAGGTGTGG  
CAGATCACAAAGGTGGAGTATTATTGCTAGTACTGGCTTTGTGTTGTAAAGTTGGTTTTTCATA  
CAGCTTCCAGAAAGCTCTCTGTGCGACGTTGGTGGAGCTAAACGTCTTCAAGCTTTATCTCATC  
TTGTTTCTGTGCTTCTCTTGTGCCCATGGGTCATTGTTCTTTCTGTGACAACTGAGAGTAAAG  
TGGAGTCTTGGTTTTTCTCTCATTATGCCTTTTGCAACGGTTATCTTTTTTGTGCATGATCCTGG  
ATTTCTACGTGGATTCCATTTGTTTCAGTCAAAATGGAAGTTTCCAAATGTGCTCGTTATGGAT  
CCTTTCCCATTTTTATTAGTGCTCTCCTTTTTTGGAATTTTTTGACACATCCAATAACAGACC  
AGCTTCGGGCTATGAACAAAGCAGCACACCAGGAGAGCACTGAACACGTCCTGTCTGGAGGAG  
TGGTAGTGAGTGCTATATTCTTCATTTTGTCTGCCAATATCTTATCATCTCCCTCTAAGAGAG  
GACAAAAGGTACCCTTATTGGATATTCTCCTGAAGGAACACCTCTTTATAACTTCATGGGTG  
ATGCTTTTTCAGCATAGCTCTCAATCGATCCCTAGGTTTATTAAGGAATCACTAAAACAAATTC  
TTGAGGAGAGTGACTCTAGGCAGATCTTTTACTTCTTGTGCTTGAATCTGCTTTTTTACCTTTG  
TGGAATTATTCTATGGCGTGCTGACCAATAGTCTGGGCCTGATCTCGGATGGATTCCACATGC  
TTTTTGACTGCTCTGCTTTAGTCATGGGACTTTTTGCTGCCCTGATGAGTAGGTGGAAAGCCA  
CTCGGATTTTCTCCTATGGGTACGGCCGAATAGAAATTCTGTCTGGATTATTAATGGACTTT  
TTCTAATAGTAATAGCGTTTTTGTGTTTATGGAGTCAGTGGCTAGATTGATTGATCCTCCAG  
AATTAGACACTCACATGTTAACACCAGTCTCAGTTGGAGGGCTGATAGTAAACCTTATTGGTA  
TCTGTGCCTTTAGCCATGCCCATAGCCATGCCCATGGAGCTTCTCAAGGAAGCTGTCACTCAT  
CTGATCACAGCCATTACACCATATGCATGGACACAGTGACCATGGGCATGGTCACAGCCACG  
GATCTGCGGGTGGAGGCATGAATGCTAACATGAGGGGTGTATTTCTACATGTTTTGGCAGATA  
CACTTGGCAGCATTGGTGTGATCGTATCCACAGTTCTTATAGAGCAGTTGGATGGTTCATCG  
CTGACCCACTCTGTTCTCTTCTACTGCTATATTAATATTTCTCAGTGTTGTTCCACTGATTA  
AAGATGCCTGCCAGGTTCTACTCCTGAGATTGCCACCAGAATATGAAAAAGAACTACATATTG  
CTTTAGAAAAGATACAGAAAATTGAAGGATTAATATCATACCGAGACCCTCATTTTTTGGCGTC  
ATTCTGCTAGTATTGTGGCAGGAACAATTCATATACAGGTGACATCTGATGTGCTAGAACAAA  
GAATAGTACAGCAGGTTACAGGAATACTTAAAGATGCTGGAGTAAACAATTTAACAATTCAG  
TGGAAAAGGAGGCATACTTTCAACATATGTCTGGCCTAAGTACTGGATTTCATGATGTTCTGG  
CTATGACAAAACAAATGGAATCCATGAAATACTGCAAAGATGGTACTTACATCATG**TGAG**ATA  
ACTCAAGAATTACCCCTGGAGAATAAACAATGAAGATTAAATGACTCAGTATTTGTAATATTG  
CCAGAAGGATAAAAATTACACATTAAGTGTACAGAAACAGAGTTCCTACTACTGGATCAAGG  
AATCTTTCTTGAAGGAAATTTAAATACAGAATGAAACATTAATGGTAAAAAAA

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**FIGURE 28**

MEEKYGGDVLAGPGGGGGLGPVDVPSARLTKYIVLLCFTKFLKAVGLFESYDLLKAVHIVQFI  
FILKLGTAFFMVLFFQKPFSSGKTITKHQWIKIFKHAVAGCIISLLWFFGLTLCGPLRTLLLFE  
HSDIVVISLLSVLFTSSGGGPAKTRGAFFIIIAVICLLLFNDNDLMAKMAEHPEGHHDSALTH  
MLYTAIAFLGVADHKGGVLLLVALLCCKVGFHTASRKLSVDVGGAKRLQALSHLVSVLLCPW  
VIVLSVTTESKVESWFSLIMPFATVIFVVMILDFYVDSICSVKMEVSKCARYGSFPFIFISALL  
FGNFWTHPITDQLRAMNKAHQESTEHVLSGGVVVSAIFFILSANILSSPSKRGQKGTIGYS  
PEGTPLYNFMGDAFQHSSQSIPRFIKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTN  
SLGLISDGFMFLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGFINGLFLIVIAFFVF  
MESVARLIDPPELDTHMLTPVSVGGLIVNLIGICAFSHAHSHAHGASQGSCHSSDHS SHHMH  
GHS DHGHGSHSGSAGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIADPLCSLSTA  
ILIFLSVVPLIKDACQVLLRLPPEYEKELHIALEKIQKIEGLISYRDPHFWRHSASIVAGTI  
HIQVTS DVLEQRIVQQVTGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMESMK  
YCKDGTIIM

**Important features of the protein:****Signal peptide:**

amino acids 1-46

**Transmembrane domains:**amino acids 59-77, 101-119, 150-167, 205-223, 239-258, 267-284,  
305-324, 343-360, 421-440, 452-469, 486-505, 522-539, 592-612,  
621-641**N-glycosylation site.**

amino acids 721-725

**Glycosaminoglycan attachment site.**

amino acids 143-147

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 225-229

**Tyrosine kinase phosphorylation sites.**

amino acids 750-758, 756-764

**N-myristoylation sites.**amino acids 14-20, 46-52, 102-108, 112-118, 144-150, 317-323,  
347-353, 369-375, 372-378, 437-443, 462-468, 529-535, 549-555,  
553-559, 579-585, 582-588, 583-589, 584-590, 605-611, 737-743**Multicopper oxidases protein:**

amino acids 561-569



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**FIGURE 29**

GGCACGAGGGCAGGATATTAGAA**ATG**GCTACTCCCCAGTCAATTTTCATCTTTGCAATCTGCA  
TTTTAATGATAACAGAATTAATTCTGGCCTCAAAAAGCTACTATGATATCTTAGGTGTGCCAA  
AATCGGCATCAGAGCGCCAAATCAAGAAGGCCTTTCACAAGTTGGCCATGAAGTACCACCCTG  
ACAAAAATAAGAGCCCGGATGCTGAAGCAAAATTCAGAGAGATTGCAGAAGCATATGAAACAC  
TCTCAGATGCTAATAGACGAAAAGAGTATGATACACTTGGACACAGTGCTTTTACTAGTGGTA  
AAGGACAAAGAGGTAGTGGAAGTTCTTTTGAGCAGTCATTTAACTTCAATTTTGATGACTTAT  
TTAAAGACTTTGGCTTTTTTGGTCAAAACCAAAACACTGGATCCAAGAAGCGTTTTGAAAATC  
ATTTCCAGACACGCCAGGATGGTGGTTCAGTAGACAAAGGCATCATTTCCAAGAATTTTCTT  
TTGGAGGTGGATTATTTGATGACATGTTTGAAGATATGGAGAAAATGTTTTCTTTTAGTGGTT  
TTGACTCTACCAATCAGCATAACAGTACAGACTGAAAATAGATTTTCATGGATCTAGCAAGCACT  
GCAGGACTGTCACTCAACGAAGAGGAAATATGGTTACTACATACACTGACTGTTTCAGGACAG**T**  
**AGT**TCTTATTCTATTCTCACTAAATCCAACCTGGTTGACTCTTCCTCATTATCTTTGATGCTAA  
ACAATTTTCTGTGAACATTTTTGACAAGTGCATGATTTCACTTTAAACAATTTGATATAGCTA  
TTAAATATATTTAAGGGTTTTTTTTTTTTTGACAAATTCAACATTCAACGAGTAGACAAAATGCT  
AATTATTTCCCTGATTAGGAAAGTTTCTTTAAAAAACACGTAATTTTGCCTAGTGCTTTTTTCT  
CTACCTGCCCTTGGGCTCACTAATATCACCAGTATTATTACCAAGAAAATATTGAGTTTACCT  
GATTAACTTTTAAAGTTAATTGTAGATTTAAATTGTGTGAACCTAATGATTTTTGCAGTGAA  
ACCTTTACTAATTCAAAGTTGCATGTTCTATGACATCTGTGACTTGCGTTGCAGAGTGACAT  
GAACTGTATAATTGAGTCATTCAGTAAAGGAGAACAGTATCTTGGTTAATTGCTACTGAAAG  
GTTGAGAAAGGAATGGTTTGATATTTACCACAGCGCTGTGCCTTTCTACAGTAGAACTGGGGT  
AAAGGAAATGGTTTTATTGCCCATAGTCATTTAGGCTGGAAAAAAGTTGAAAACCTAACGAAA  
TATTGCCAAGAGATTGTTATGTGTTTGGTTCCAGCCTAAAAATGATTTTGTAGTGTTGAAATC  
ATAGCTACTTACATAGCTTTTTTCATATTTCTTTCTTAGTTGTTGGCACTCTTAGGTCTTAGTA  
TGGATTTATGTGTTTGTGTGTGTGTAGTTTATCCTCTCTCATCTTTATCTAGAGATTGACT  
GATACCTCATTCTGTTTGTAAAACAGCCAGTAATTTCTGTGCAACCTTACTATGTGCAATAT  
TTTTAAATCCTGAGAAATGTGTGCTTTTGTTCGGATAGACTTATTTCTTTAGTTCTGCACT  
TTTCCACATTATACTCCATATGAGTATTAATCCTATGGATACATATTAAACAAGTGTCTCAT

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**FIGURE 30**

MATPQSIFIFAICILMITELILASKSYYDILGVPKSASERQIKKAFHKLAMKYHPDKNKSPDA  
EAKFREIAEAYETLS DANRRKEYDTLGHSAFTSGKGQRGSGSSFEQSFNFNFDDLKDFGFFG  
QNQNTGSKKRFENHFQTRQDGGSSRQRHHFQEFSFGGGLFDDMFEDMEKMFSFSGFDSTNQHT  
VQTENRFHGSSKHCRTVTQRRGNMVTITYTDCSGQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**Nt-dnaJ domain signature.**

amino acids 27-59, 66-90

**Glycosaminoglycan attachment site.**

amino acids 96-100

**N-myristoylation sites.**

amino acids 32-38, 99-105, 102-108, 126-132, 211-217

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**FIGURE 31**

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTGG  
GCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACAAT  
TCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCTGAG  
ATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCAAATG  
CAGACTTTTACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCTACGCA  
TTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTCTCTGTA  
CTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGAAACAGTG  
TACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCTGGATCCCC  
AGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATCACGGCCACT  
GTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTGGAGCATCCTG  
AAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGATCACCAAAGAT  
GGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTCCTTGTGGCCTAC  
TGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGGGGGTATTCCAGTG  
CACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGACATTCGTGAAGGCC  
ATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAAGGAGAGGCCATTCCC  
CTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGTGGTCGTGCCACTGTTC  
GTCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGGTGGTCCTCCCAGACACC  
TTGAAAATAACCAATTCACCCCAGAAGTTAATCAGCTGCAGAAGGGAGGAGGTGGATGCCTGT  
GCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGATCTCATAGGTTTGCGGAAGG  
GCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACCATGAGGGGACAAGTTGTGTT  
TCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGAGCCTGTTGTCTACAAGTCTAG  
AAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACTGACTGAGGCTTAGGGGATGTG  
ACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACCCTGGGAAAAGTGACTTCATCCCT  
TCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACCTACACACCTGCTAAACACACACAC  
ACAGAGTCTCTCTATATATACACACGTACACATAAATACACCCAGCACTTGCAAGGCTAGA  
GGGAAACTGGTGACACTCTACAGTCTGACTGATTCAGTGTCTTCTGGAGAGCAGGACATAAATG  
TATGATGAGAATGATCAAGGACTCTACACACTGGGTGGCTTGAGAGAGCCCACTTTCCCAGAAT  
AATCCTTGAGAGAAAAGGAATCATGGGAGCAATGGTGTTGAGTTCACTTCAAGCCCAATGCCG  
GTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGTAGGTGACCTGGAGGAAGGTCACAGCCACA  
CTGAAAATGGGATGTGCATGAACACGGAGGATCCATGAACTACTGTAAAGTGTTGACAGTGTG  
TGCACACTGCAGACAGCAGGTGAAATGTATGTGTGCAATGCGACGAGAATGCAGAAGTCAGTA  
ACATGTGCATGTTTGTGTGCTCCTTTTTTCTGTTGGTAAAGTACAGAATTCAGCAAATAAAA  
AGGGCCACCCTGGCCAAAAGCGGTAAAAA

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**FIGURE 32**

MQTFTMVLEEIWTSLEFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGET  
VYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSI  
LKHPFNRNSTILTRPGMEITKDG FHLVIELEDLGPQFEFLVAYWRREPGAEHVKMVRSGGIP  
VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLALFAFVGFM LILVVVPL  
FVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

**Important features:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 230-255

**N-glycosylation sites.**

amino acids 40-44, 134-138

**Tissue factor proteins.**

amino acids 92-120

**Integrins alpha chain proteins.**

amino acids 232-263

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**FIGURE 33**

GAGACACGCGAGCGGGGAGACCTCCAAGGCAGCGAGGCATCGGACATGTGTGTCAGCACATCTGG  
GGCGCACATCCGTCGAGCCCGAGGGGAGATTTGCCGGAACAATTCAAACCTGCGATATTGATCT  
TGGGGGTGACTGTCCCTGGCCGGCTGTCCGGTGGGAGTGCAGTGTGCACTCGCTCGGAAGTG  
TGTGCGAGTGTGTATGTGTGTGTGCCGTGTCCGGCTCCCCCTTCCCCCGTTTTCCCGTCGA  
GTGATGCACTTGGAATGAGAATCAGAGGATGGAAATAGTCTGGGAGGTGCTTTTTCTTCTTCA  
AGCCAATTTTCATCGTCTGCATATCAGCTCAACAGAATTCACCAAAAATCCATGAAGGCTGGTG  
GGCATAACAAGGAGGTGGTCCAGGGAAGCTTTGTTCCAGTTCCTTCTTTCTGGGGATTGGTGAA  
CTCAGCTTGGAATCTTTGCTCTGTGGGGAAACGGCAGTCGCCAGTCAACATAGAGACCAGTCA  
CATGATCTTCGACCCCTTTCTGACACCTCTTCGCATCAACACGGGGGGCAGGAAGGTCAGTGG  
GACCATGTACAACACTGGAAGACACGTATCCCTTCGCCTGGACAAGGAGCACTTGGTCAACAT  
ATCTGGAGGGCCCATGACATACAGCCACCGGCTGGAGGAGATCCGACTACACTTTGGGAGTGA  
GGACAGCCAAGGGTCGGAGCACCTCCTCAATGGACAGGCCTTCTCTGGGGAGGTGCAGCTCAT  
CCACTATAACCATGAGCTATATACGAATGTCACAGAAGCTGCAAAGAGTCCAAATGGATTGGT  
GGTAGTTTTCTATATTTATAAAAGTTTCTGATTCATCAAACCCATTTCTTAATCGAATGCTCAA  
CAGAGATACTATCACAAGAATAACATATAAAAAATGATGCATATTTACTACAGGGGCTTAATAT  
AGAGGAACATATCCAGAGACCTCTAGTTTCATCACTTACGATGGGTGATGACTATCCCACC  
CTGCTATGAGACAGCAAGTTGGATCATAATGAACAAACCTGTCTATATAACCAGGATGCAGAT  
GCATTCTTTGCGCCTGCTCAGCCAGAACCAGCCATCTCAGATCTTTCTGAGCATGAGTGACAA  
CTTCAGGCCTGTCCAGCCACTCAACAACCGCTGCATCCGCACCAATATCAACTTCAGTTTACA  
GGGGAAGGACTGTCCAAACAACCGAGCCCAGAAGCTTCAGTATAGAGTAAATGAATGGCTCCT  
CAAGTAGGGGAACAAAGCCAAGAAGATCCACCTCAGTGAAATGCTACAACCTGTGAATTGACG  
TAACCTAGAATGTCCCCCTTCTTGCTTCTCTCTCCTTCTTTCCCCCAAGCCTCATTCTTCTT  
GGGATTGGCCCTTTCTTCATGAAAAGTGTCTGCGAAACCATGGCAGAGGAATACATCTCTCAC  
ACATACTCACAAACACACACACAAGCACTTGACATACATACAAACACATGCAAAACATACCTA  
CACACACACACTCTCTTACAACCTCCATCATGGGAAGTCAAGTTTCAGAAACAAAAGTCTCAT  
TCATAAGAGGTCTTAGAAGAAAATAACCAGTTAACCTGATTTCAATTTTGATACCGTTTTCTT  
GAACTAATAAATCTACCCAATGAGACTTTTCAGCCTTTGTACATACAAAATTCTTCCAAAAGA  
GAGAGGAGAAAATACAGCTCTGATGGCATCAAACGGACTTTGCATCAAGTAATTTTCAGATAGT  
GTCCTAGGATCCTTTGAGGGTGTGGTAGCAGGTGAGCAGGACAAAGTTGACCAAGGACACTT  
ATTTCTAGATTATGATTCTTCTGTTTACTCAACAATTTACAAAGAAAAAAGGACAGACATTG  
AAGAGCTACACATTGTATATATATCACCACAGACTATAAGGAAATGGAATTATTTCCCTCTTT  
GTCACATATCTGTAGTAGGATTTGCCAAGATCAGAAATGATCCATTTGCTGTTTCTTGTTTTT  
CAAAGGTCATACATTGTGTTTGGTTATTGTTACCAGCTCAATAAATGTGTTTAAACGAGTTAAT  
TTCATTTTTCTGGCTTTGGTCTGTTCTCCTTCCCTACAGGCTAAGCCCTGGCTCCATGCAACT  
GCATTCTTTGATTTCACTTGTTCCTTCATCTACATGTTTTGTTTCAATTGTCAGCCAGTTTTTAC  
TGAGTTTGTGGCAATCAGGAATGCATTTGCTAAGCAAGTATGACTTTAATTCCACTCCATGGC  
TCAATCATTACATGAGGTGAGCTTCAGCCTGAGATAGCAGGCGACAGACTTCTTGCGTTTCA  
AACTGCCATGCCCCCTGTGATGCTCCCGTGAAGGAATGCACTTTGCCTTGTAAGTTCCTGG  
GAAAGGGGTATGTTTTCTCTCCAGGTGCAGCCAGATCTCACAAAGTACAAAACGAATGCCTTT  
CTTTTCTTGTTTATAATGGTCACTCACTGTGTTGGTTACTGTCAAGAAATCAATAAATGTGT  
TTAACAAGTTA

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**FIGURE 34**

MEIVWEVLFLQLQANFIVCISAQQNSPKIHEGWWAYKEVVQGSFVPVPSFWGLVNSAWNLC SVG  
KRQSPVNIETSHMIFDPFLTPLRINTGGRKVS GMTMYNTGRHVSLRLDKEHLVNI SGGPMTYSH  
RLEEIRLHFGSEDSQGSEHLLNGQAFSGEVQLIHYNHELYTNVTEAAKSPNGLVVVSIFIKVS  
DSSNPFLNRMLNRDTITRITYKNDAYLLQGLNIEELYPETSSFITYDGSMTIPPCYETASWII  
MNKPVYITRMQMHSRLRLSQNQPSQIFLSMSDNFRPVQPLNNRCIRTNINFSLQKDCPNNRA  
QKLQYRVNEWLLK

**Important features:****Signal peptide:**

amino acids 1-20

**Eukaryotic-type carbonic anhydrases proteins.**

amino acids 126-162, 220-269, 43-91

**N-glycosylation sites.**

amino acids 116-119, 168-171, 302-305

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**FIGURE 35**

GTCGGAACCCCTCAGGCCACCCTCGGGAGTCTGGGGTCCAGAGGGGTGTCCCTGTACCCCTTGAC  
ACAGGACCCTCACTCTGCAGGGATAAGCCAGCTGCGCCTGCAGCCTAGGGTGCCAAGGAGGCTGCTGA  
TTGTGGCCACAGCCTCATCTGAACGCCAGGAGACCAGGATACCGAGGCACCGGATCCCTCTCTGTG  
CCCTGGGGAGCCCCAGTGTGCCAGTCACCCAGGGCTGAGGTCTGCGTCCCTAGTGGTGCAAGGCC  
TGGTAGGACCACGGGGCAGGGAATGTGAGCGCCATCCGAGCTCACGGTGTCTGAGTCGCGGCTTCGT  
GACTTTGGCAGGGGCTCCGGACCAGTGACCCAGTCAAACCCAGAGGGTCTTGGGCGGCAGCGACGA  
AGGAGGTATTAGGCTCCAGGCCAGGTGGGGCCGAGCGCCCCAGCCATCCACCATGGTGGTGGCACA  
CCCCACCGCCACTGCCACCACGCCCCTGCACTGTACGGCCACCGTTGTGATGACCACGGCCA  
CCATGGACCTGCGGGACTGGCTGTTCTCTGCTACGGGCTCATCGCCTTCCTGACGGAGGTTCATCGAC  
AGCACCACTGCCCCCTCGGTGTGCCGCTGCGACAACGGCTTCATCTACTGCAACGACCGGGGACTCAC  
ATCCATCCCCGCAGATATCCCTGATGACGCCACCACCCTCTACCTGCAGAACAACAGATCAACAACG  
CCGGCATCCCCAGGACCTCAAGACCAAGGTCAACGTGCAGGTTCATCTACCTATACGAGAATGACCTG  
GATGAGTTCCCATCAACCTGCCCCGCTCCCTCCGGGAGCTGCACCTGCAGGACAACAATGTGCGCAC  
CATTGCCAGGGACTCGCTGGCCCGCATCCCGCTGCTGGAGAAGCTGCACCTGGATGACAACCTCCGTGT  
CCACCGTCAGCATTGAGGAGGACGCTTCGCCGACAGCAAACAGCTCAAGCTGCTCTTCTGAGCCGG  
AACCACCTGAGCAGCATCCCCCTCGGGGCTGCCGCACACGCTGGAGGAGCTGCGGCTGGATGACAACCG  
CATCTCCACCATCCCGCTGCATGCCTTCAAGGGCTCAACAGCCTGCGGCGCCTGGTGCTGGACGGTA  
ACCTGCTGGCCAACAGCGCATCGCCGACGACACCTTCAGCCGCTACAGAACCTCACAGAGCTCTCG  
CTGGTGCGCAATTGCTGGCCGCGCCACCCCTCAACCTGCCAGCGCCACCTGCAGAAGCTCTACCT  
GCAGGACAATGCCATCAGCCACATCCCCTACAACACGCTGGCCAAGATGCGTGAGCTGGAGCGGCTGG  
ACCTGTCCAACAACAACCTGACCACGCTGCCCCGCGGCTGTTGACGACCTGGGGAACCTGGCCAG  
CTGCTGCTCAGGAACAACCTTGGTTTTGTGGCTGCAACCTCATGTGGCTGCGGGACTGGGTGAAGGC  
ACGGGCGGCGCTGGTCAACGTGCGGGGCTCATGTGCCAGGGCCCTGAGAAGGTCCGGGGCATGGCCA  
TCAAGGACATTACCAGCGAGATGGACGAGTGTGTTTGTAGACGGGGCCGAGGGCGGCGTGGCCAATGCG  
GCTGCCAAGACCACGGCCAGCAACCACGCCTCTGCCACCACGCCCCAGGGTTCCTGTGTTACCCCTCAA  
GGCCAAAAGGCCAGGGCTGCGCCTCCCCGACTCCAACATTGACTACCCCATGGCCACGGGTGATGGCG  
CCAAGACCCTGGCCATCCACGTGAAGGCCCTGACGGCAGACTCCATCCGCATCACGTGGAAGGCCACG  
CTCCCCGCCTCTCTTTCCGGCTCAGTTGGCTGCGCCTGGGGCCACAGCCCAGCCGTGGGCTCCATCAC  
GGAGACCTTGGTGCAGGGGGACAAGACAGAGTACCTGCTGACAGCCCTGGAGCCCAAGTCCACCTACA  
TCATCTGCATGGTCACCATGGAGACCAGCAATGCCTATGTAGCTGATGAGACACCCGTGTGTGCCAAG  
GCAGAGACACCGCAGCTATGGCCCTACCACCACACTCAACCAGGAGCAGAACGCTGGCCCCATGGC  
GAGCTTGCCCCCTGGCGGGCATCATCGGCGGGGCACTGGCTCTGGTCTTCCTCTTCTGGTCTGGGG  
CCATCTGCTGGTACGTGCACCAGGCTGGCGAGCTGCTGACCCGGGAGAGGGCCTACAACCGGGGCAGC  
AGGAAAAAGGATGACTATATGGAGTCAGGGACCAAGAAGGATAACTCCATCCTGGAAATCCGCGGCCC  
TGGGCTGCAGATGCTGCCCATCAACCCGTACCGCGCCAAAGAGGAGTACGTGGTCCACACTATCTTCC  
CCTCCAACGGCAGCAGCCTCTGCAAGGCCACACACACCATTTGGCTACGGCACCACGCGGGGCTACCGG  
GACGGCGGCATCCCCGACATAGACTACTCCTACACATGATGCCCCGCCACCCGGGCTGCCCCGCCTCA  
GCCCCAGCTGCCCTGGCGTGGCCATGTGGCTTTGCCAGCCTGCTGCAATCCAAGAGAGCAAGGAAGA  
GAAATTCCATGGGTGACTTTCTCCGAGAAAGCAAAGTTTGGGGAGGGCTGACGATTTTGTAGAACA  
CAACAGTGACAATTTTTTTTTTAAAGAATAGAAGGCAGGAGGGGGAATTTCGACATTGTTGAAGACATAA  
TTTATACCAAGTTATGCCAGTTGGGGAGGGAAGGACTAAAAATAATATTGCAGGCAGGGCTGGGTGG  
GTTTTTTTTTTTTCCCCCTGAACTGGAAGGATACTACCTGTACAACATCTGTGGACACCTCATGCTCT  
GTTCAAGGCCATCACAAAGGAACCGCCAGGGAGAAGCAGCCGGCTCTCAAAGCTCCCACGCAGCTCTC  
CCGCCACTGGCCACTCGCTGGCGACCCGATGGAAGTTTTCAGGCTCCTCACAAAGGAGAGAGGGAAG  
AAAAGATCTTTTGGCCTGGAGATATGGTCTGAAATCTCTCCCTGGCTTATTCCATACCATTTCCCT  
TGCAGATTTGCAGAAACATGGCATCTTTCCTGCACTTCTTTGAACAATCATGTAGTCGATTAAAAAAA  
AAAACAACTTTTTTTTTTCTAGGCTGAAGCCCTCTTCAGTTCCATGCACCACGCTCCGTAGAAGCCCC  
GGCGGAAGCCGTAGCTTTCCCTGCCACCTGGAGGTGCATCTGTCTGCCTGTCTATCCCTGTGCGGGTG  
TCTCTAAGTACAGATGGGTAGATAGAGCCACATGCACGGTCCTTACCGTTCTTCTTGGGTGAGTTCTT  
ACCATTTCTGAACAATAGAATTGTGAAAGTGTTAAAAA

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**FIGURE 36**

MVVAHPTATATTTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRCNDG  
FIYCNDRGLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDEFPINLP  
RSLRELHLQDNNVRTIARDSLARIPLEKLHLDNSVSTVSIEEDAFAFSKQLKLLFLSRNHL  
SSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIADDTFSRLQNLTE  
LSLVRNSLAAPPLNLP SAHLQKLYLQDNAISHIPYNTLAKMRELERLDLSNNNLTTLP RGLFD  
DLGNLAQLLLLRNNPWFCGCNLMWLRDWVKARAAVVNV RGLMCQGPEKVRGMAIKDITSEMDEC  
FETGPQGGVANAAAKTTASNHASATTPQGSFLT LKAKRPGLRLPDSNIDYPMATGDGAKTLAI  
HVKALTADSIRITWKATLPASSFRLSWLR LGHSPAVGSITETLVQGDKTEYLLTALEPKSTYI  
ICMVTMETS NAYVADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIGGAVALVFLF  
LVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMESGTTKDNSILEIRGPGLQMLPINPYRAK  
EEYVVHTIFPSNGSSLCKATHTIGYGTTRGYRDGGIPDIDYSYT

**Important features of the protein:****Transmembrane domain:**

amino acids 552-573

**N-glycosylation sites.**

amino acids 249-252, 305-308, 642-645

**Leucine zipper pattern.**

amino acids 182-203, 299-320

**Phospholipase A2 aspartic acid active site.**

amino acids 57-67



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**FIGURE 37**

[illegible]

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**FIGURE 38**

MAEPGSHHLSARVRRRTERRIPRLWRLLLWAGTAFQVTQGTGPELHACKESEYHYEYTACDS  
TGSRRWRVAVPHTPGLCTSLSDPVKGTECSFSCNAGEFLDMKDQSCKPCAEGRYSLGTGIRFDE  
WDELPHGFASLSANMELDDSAESTGNCTSSKWVPRGDYIASNTDECTATLMYAVNLKQSGTV  
NFEYYPDSSIIIEFFVQNDQCQPNADDSRWMKTTEKGWEFHSVELNRGNNVLYWRTTAFSVW  
TKVPKPVLVRNIAITGVAYTSECFPCPKPGTYADKQSSSFCKLCPANSYSNKGETSCHQCDDPK  
YSEKSSSSCNVRPACTDKDYFYTHTACDANGETQLMYKWAKPKICSEDLEGAVKLPAAGVSKTH  
CPPCNPFGFKTNNSTCQPCPYGSYSNGSDCTRCPAGTEPAVGFEYKWWNTLPTNMETTTLVSGI  
NFEYKGMTGWEVAGDHIYTAAGASDNDFMILTLLVVPGRPPQSVMAADTENKEVARITFVFETL  
CSVNCELYFMVGVNSRTNTPVETWKGSGKQSYTYIIIEENTTTSTFWAFQRTTFHEASRKYTN  
DVAKIYSINVTNVMNGVASYCRPCALEASDVGSSCTSCPAGYYIDRDSGTCHSCPPNTILKAH  
QPYGVQACVPCGPGTKNNKIHSCLYNDCTFSRNTPTRTFNYNFSALANTVTLAGGPSFTSKGL  
KYFHHFTLSLCGNQGRKMSVCTDNVTDLRIPEGESGFSKSITAYVCQAVIIPPEVTGYKAGVS  
SQPVSLADRLIGVTTDMTLDGITS PAELFHLES LGIPDVIFFYRSNDVTQSCSSGRSTTIRVR  
CSPQKTVPGLSLLPGTCS DGTCDGCNFHFLWESAAACPLCSVADYHAI VSSCVAGIQXTTYVX  
REPKLCSGGISLPEQRTICKTIDFWLKVGISAGTCTAILLTVLTCYFWKKNQKLEYKYSKLV  
MNATLKDCDLPAADSCAIMEGEDVEDDLIFTSKKS LFGKIKSFTSKRTPDGFDSVPLKTSSGG  
PDMDL

**Important features of the protein:****N-glycosylation sites:**

amino acids 153-156, 390-393, 391-394, 404-407, 544-547, 576-579,  
672-675, 717-720, 947-950

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

amino acids 15-18, 563-566, 709-712

**Casein kinase II phosphorylation sites:**

amino acids 42-45, 59-62, 81-84, 146-149, 168-171, 282-285, 331-  
334, 340-343, 431-434, 449-452, 465-468, 523-526, 557-560, 761-  
764, 780-783, 835-838, 860-863, 893-896, 949-952

**Tyrosine kinase phosphorylation sites:**

amino acids 50-56, 109-116

**N-myristoylation sites:**

amino acids 77-82, 88-93, 152-157, 268-273, 288-293, 320-325,  
400-405, 405-410, 414-419, 463-468, 599-604, 616-621, 634-639,  
644-649, 839-844, 874-879, 912-917, 916-921

**Amidation site:**

amino acids 707-710

**Cell attachment sequence:**

amino acids 162-164

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**FIGURE 39**

GGGAAGGGGTTCTGGGCTGCCGCAGGCACACAGGCCAGAGCTTCGTGGATACCTGCAGGGCCC  
AAAGGTCCCTCCCTGTTTTGAAGAGTGAGTGATGGCTATGAGGTAGCGGCCAGGCTGATCACC  
CCTGCGTTGGCTGGAGGCAGAATTCTGTAAATCCTCGCCAAGTCTTTCTCCAGGGCCACTGGTT  
AGCTCATCTCAGCCTCCTCTGGGAGCATCAACACCAACATGGCACAGGGGACTGCAGTGGTGT  
GCTTTGGACCTGTGTACCCACCCAAGGCTAAAGGCAGAGCCAGGTGACTTTGCGGGGGTCTCT  
TCTCTAGGATTATCTGTACTTCCCCTCTGTCTCTTTTACTACGGGAGATCGAGCTAGCTATA  
ACCCACCTTCTTTTCATGAGAACCACACTAAATTGCAAAAATTATCCCAGTGCTGGAGGAGGGC  
AGCAGGTTGAGATTATGTTGGCAGGAAGAATGTTGGCATTGATTGGCACGCAGGGGACGAGAG  
CTGCTTTGTGCTTTAAAGGAGCCAAGTTACACCCTGTTTAACCCTGCCTTCAAAGGGACGACT  
CTGTAAGATTCTCTGCTACTTATTCAAGTTGACACGATGCCCTTCACACTCCACCTGAGGTCC  
CGCCTTCCCTCTGCCATAAGGAGTTTGATTCTACAAAAGAAACCAACATCAGAAATACATCC  
AGCATGGCTGGAGAGCTCCGACCAGCCAGCCTGGTGGTCTGCCCAGGTCCCTTGCTCCAGCT  
TTTGAAAGATTCTGCCAGGTCAACACTGGTCTCTACCCCTGCTGGGCCAGAGTGAGCCAGAA  
AAGTGGATGCTGCCCCCTCAAGGTGCTATCTCAGAGACCAGGATGGGCCATCCCCAGTTCTGG  
AAATACGAGTTCGGTGCCTGCACCGGTAGCCTGGCTTCGCTGGAGCAGTACTCGGAGCAGCTG  
AAGGACATGGTGGCCTTCTTCCCTGGGCTGCAGCTTCTCCCTGGAGGAGGCCTTGAGAAAGCG  
GGGCTCCCCAGAAGAGACCCAGCAGGTACAGCCAGGCGGGTGCATACAAGACAACAGTGCCT  
TGTGTTACCCATGCTGGCTTCTGCTGCCCTCTGGTGGTACGATGAGGCCCATTTCCCAAGGAC  
AAGCTGGAAGGGCTGGTGCGGGCCTGCTGCTCCCTCGGAGGTGAGCAGGGGCAACCTGTTTAC  
ATGGGCGACCCAGAAGTGTGGGAATCAAAGAGCTTTCCAAACCTGCCTACGGGGATGCCATG  
GTGTGTCCCCCAGGGGAGGTTCCAGTGTTCTGGCCTTCTCCGCTGACCAGTCTCGGAGCTGTC  
AGCAGCTGTGAGACCCCACTGGCTTTTGCCAGCATCCCAGGCTGCACAGTTATGACTGACCTG  
AAGGATGCAAAGGCTCCACCTGGTTGTCTACCCCAAGAGAGAATTCCAGAGGTCCATCACATT  
TCCCAAGATCCTCTGCACTACAGCATCGCGTCAGTCTCTGCTTCTCAGAAGATCAGAGAACTA  
GAGTCTATGATCGGCATAGACCCAGGGAACCGGGGGATTGGGCACCTGCTCTGTAAAGATGAG  
CTGCTGAAGGCCTCTCTCTCGCTGTCCCATGCCCGCTCAGTGCTCATCACCCTGGGTTCCTCC  
ACACATTTCAATCATGAGCCTCCAGAAGAGACAGATGGCCACCAGGAGCTGTTGCTCTGGTT  
GCCTTCCTGCAGGCCTTGAGAAAGGAGGTGCGCCATAATCGTTGACCAGAGAGCCTGGAACCTG  
CACCAGAAGATTGTTGAAGATGCTGTTGAGCAAGGTGTTCTGAAGACGCAGATCCCGATATTA  
ACTTACCAAGGTGGATCAGTGGAAGCTGCTCAGGCATTCTGTGCAAAAATGGGGACCCGCAG  
ACACCTAGATTTGACCACCTGGTGGCCATAGAGCGTGCCGGAAGAGCTGCTGATGGCAATTAC  
TACAATGCAAGGAAGATGAACATCAAGCACTTGGTTGACCCCATTTGACGATCTTTTTCTTGCT  
GCGAAGAAGATTCCTGGAATCTCATCAACTGGAGTCGGTGATGGAGGCAACGAGCTTGGGATG  
GGTAAAGTCAAGGAGGCTGTGAGGAGGCACATACGGCACGGGGATGTCATCGCCTGCGACGTG  
GAGGCTGACTTTGCCGTCATTGCTGGTGTCTTAAGTGGGGAGGCTATGCCCTGGCCTGCGCA  
CTCTACATCCTGTACTCATGTGCTGTCCACAGTCAGTACCTGAGGAAAGCAGTCGGACCCCTCC  
AGGGCACCTGGAGATCAGGCCTGGACTCAGGCCCTCCCGTCCGTCATTAAAGGAAGAAAAAATG  
CTGGGCATCTTGGTGCAGCACAAAGTCCGGAGTGGCGTCTCGGGCATCGTGGGCATGGAGGTG  
GATGGGCTGCCCTTCCACAACACCCACGCCGAGATGATCCAGAAGCTGGTGGACGTCACCACG  
GCACAGGTGTAAACCGTCCATGTTCCGTGTGAGCAGAGTCCCTACCAACGGGCAGGTCTGCATC  
CGGGGAGAATGCAGCTGCTTCTGGCGACAATCCTGCTAGTAAACACTGGTCTTCGGTGAGCAA  
CGAACACTCGCCTGGCCTGGGAAACTGCATGCCCACTTTCTGGGAGGGGTTAGTGCAGGTGCC  
GTGGACAAAGGACAACATTTCTCTGGGGCTTTTTAACTTTTATTCTAAGACTCTAAAGGCGT  
TGATTTCAACCCTCCTTCACTCTGGCTTCTTCAGGCAACCCACGTGGTCTCCTATGAGAATCT  
TCTCGACAGTTACTTATGGGGACACTTGTGAACAATTAAGTCCAGGGCAGAGCATGAGAACA  
AACATTTCCAGGCCATGTAGGATAGGATACTCCAGACTCCAGTCATCCTCCCCCATCCATGGT  
TTCTGTTACTCATGGTTTCAGTTACTCATAGCCAACTGCAGACCGAAAAATACTAAATGAAAAA  
TTTCAGAAATAAACAACCTCTTAAGTTTAAAAA

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**FIGURE 40**

MPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAGELRPASLVVLPRSLAPAFERFCQVNTGPL  
PLLGQSEPEKWMPLPPQGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFLGCSF  
SLEEALKEAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCPLVVTMRPIPKDKLEGLVRACCSL  
GGEQGQPVHMGDPELLGIKELSKPAYGDAMVCPGGEVPVFWPSPLTSLGAVSSCETPLAFASI  
PGCTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQKIRELESMIGIDPGNRG  
IGHLLCKDELLKASLSLSHARSVLITTGFPTHFNHEPPEETDGPPGAVALVAFLQALEKEVAI  
IVDQRAWNLHQKIVEDAVEQGVLTQIPILTYQGGSVAAQAFCKNGDPQTPRFDHLVAIER  
AGRAADGNYYNARKMNIHLVDPIDDLFLAAKKIPGISSTGVGDGGNELGMGKVKEAVRRHIR  
HGDVIACDVEADFAVIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQAWTQAL  
PSVIKEEKMLGILVQHKVRSVSGIVGMEVDGLPFHNTHAEMIQKLVDVTTAQV

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 358-378, 517-539

**N-glycosylation site.**

amino acids 28-32

**Tyrosine kinase phosphorylation site.**

amino acids 444-452

**N-myristoylation site.**

amino acids 98-104, 102-108, 123-129, 149-155, 181-187, 190-196,  
238-244, 308-314, 399-405, 413-419, 448-454, 477-483, 482-488,  
487-493

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 233-244, 531-542

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**FIGURE 41**

CTTTCCTGTTTTATCCGCAGCCCTTTTCTTCTTTGAGTTAGTAAAGATTTATTCTGTAACCTG  
ACACTCATCTGGCCCTTTGCAGTTTGCCAGCCATATTCCCATGTGATTTCCCACTGGATCCAG  
GCCCCATCCGGCTGGCAGGAGGGGGCTCTGACGTACAGGTTGGAAATCAGAAGTCTGTGAGA  
GCGCGGGAGTGCATGGCAGCTCTGGGTCCCAGACCTGGCCCGACCCCTCTGCTTCACCTECAG  
CTCTGCTGCTCCTCTACTCTTGGGTGAGATCCCTTTGGAGCCACAGCGAGGAACCCTGTGGT  
CCTCAGGCAGGTGTACCTTGAGTCAGCCAGGAGCCCTCTTTTCCTGTGTCAAAGCCTGCCCTC  
GGGCTCTGCTCACCTCTGGTGACCCTCCAAGATGCCCCTGCCCTCAGTTTCCCCTCATGATCT  
GGCCTCTGCCCCCTTCTCTAGCCACAGCCTCTAGTACACTTTAGCAATACCACCAGACTAGTT  
AGAGTTCCCCACTCACCAAGCAAGACCATGCAGTTTCATGCCTCTGTGCCTTCGCTCATGCTGT  
TTCTTCCGACTGGAATGCCTTCCCCTGCTCCTCCTGCCTTGTCTGCCTGGCAAGTTCATCTCT  
CACGATCCCCCTCAAAGGCCCCCTCCTCCAGGAAGGCAACCCCTGTGCCCCCTCCCCTCCAGGCT  
ACCTCTGCACTTTGTCAATGCTTCTCTTGTGGCACTTATCACACTGTATTTTACTTGTTTACA  
TGTTTGTCTCCCCTTCTAGACTGTGAATCCTTAAGGGCATGGACTGTATCTTATGCATCTCTG  
TATTTCTGCGCCTAGCACGGTGCCTAGCACACAGTAGGCGCTCAATAAATGTTGAATGAATGA  
ATGATTT

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## **FIGURE 42**

MQFHASVPSLMLFLPTGMPSAPPALSAWQVHLSRSPQRPPPPGRQPLCPSPPGYLCTLSMLL  
LWHLSHCILLVYMFVSPSRL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Microbodies C-terminal targeting signal.**

amino acids 81-83

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**FIGURE 43**

GTTTCCAACAAGGATGATATGAAGACTTCCCTGAAGAAAGTTGTGAAGGGACCTCCTACGAGA  
**TG**ATGATGCAGTGTGTGTCCCGCATGTTGGCCCACCCCCTGCATGTCATCTCAATGCGCTGCA  
TGGTCCAGTTTGTGGGACGGGAGGCCAAGTACAGTGGTGTGCTGAGCTCCATTGGGAAGATTT  
TCAAAGAGGAAGGGCTGCTGGGATTCTTCGTTGGATTAATCCCTCACCTCCTGGGCGATGTGG  
TTTTCTTGTGGGGCTGTAACCTGCTGGCCCACTTCATCAATGCCTACCTGGTGGATGACAGCT  
TCAGCCAGGCCCTGGCCATCCGGAGCTATACCAAGTTCGTGATGGGGATTGCAGTGAGCATGC  
TGACCTACCCCTTCCTGCTAGTTGGCGACCTCATGGCTGTGAACAACCTGCGGGCTGCAAGCTG  
GGCTCCCCCTTACTCCCCAGTGTTCAAATCCTGGATTCACTGCTGGAAGTACCTGAGTGTGC  
AGGGCCAGCTCTTCCGAGGCTCCAGCCTGCTTTTCCGCCGGGTGTCATCAGGATCATGCTTTG  
CCCTGGAG**TAA**CCTGAATCATCTAAAAAACACGGTCTCAACCTGGCCACTGTGGGTGAGGCCT  
GACCACCTTGGGACACCTGCAAGACGACTCCAACCCAACAACAACCAGATGTGCTCCAGCCCA  
GCCGGGCTTCAGTTCATATTTGCCATGTGTCTGTCCAGATGTGGGGTTGAGCGGGGGTGGGG  
CTGCACCCAGTGGATTGGGTACCCGGCAGACCTAGGGAAGGTGAGGCGAGGTGGGGAGTTGG  
CAGAATCCCCATACCTCGCAGATTTGCTGAGTCTGTCTTGTGCAGAGGGCCAGAGAATGGCTT  
ATGGGGGCCCAGGTTGGATGGGGAAAGGCTAATGGGGTCAGACCCACCCCGTCTACCCCTCC  
AGTCAGCCCAGCGCCCATCCTGCAGCTCAGCTGGGAGCATCATTCTCCTGCTTTGTACATAGG  
GTGTGGTCCCCTGGCACGTGGCCACCATCATGTCTAGGCCTATGCTAGGAGGCAAATGGCCAG  
GCTCTGCCTGTGTTTTTCTCAACTACTTTTCTGATATGAGGGCAGCACCTGCCTCTGAATG  
GGAAATCATGCAACTACTCAGAATGTGTCCTCCTCATCTAATGCTCATCTGTTTAATGGTGAT  
GCCTCGCGTACAGGATCTGGTTACCTGTGCAGTTGTGAATACCCAGAGGTTGGGCAGATCAGT  
GTCTCTAGTCCTACCCAGTTTTAAAGTTCATGGTAAGATTTGACCTCATCTCCCGCAAATAAA  
TGTATTGGTGATTTGGAAAAAAAAAAAAAAAAA

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**FIGURE 44**

MMMQCVSRMLAHPLHVISMRCMVQFVGREAKYSGVLSSIGKIFKEEGLLGFFVGLIPHLIGDV  
VFLWGCNLLAHFINAYLVDDSFQALAIRSYTKFVMGIAVSMLTYPFLLVGDLMAVNNCGLQA  
GLPPYSPVFKSWIHCWKYLSVQQLFRGSSLLFRRVSSGSCFALE

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 51-72, 97-114

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 160-163

**N-myristoylation sites.**

amino acids 34-39, 100-105, 123-128, 165-170



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**FIGURE 45**

GCTCACTCTTTGGGTCCACACTGCCTTTATGAGCTGTAACACTCACTGGGAATGTCTGCAGCT  
TCACTCCTGAAGCCAGCGAGACCACGAACCCACCAGGAGGAACAACTCCAGACGCGCAG  
CCTTAAGAGCTGTAACACTCACCGCAAGGTCTGCAGCTTCACTCCTGAGCCAGCCAGACCAC  
GAACCCACCAGAAGGAAGAACTCCAAACACATCCGAACATCAGAAGGAGCAAACCTCGTGACA  
CGCCACCTTTAAGAACCGTGACACTCAACGCTAGGGTCCGCGGCTTCATTCTTGAAGTCAGTG  
AGACCAAGAACCCACCAATTCCGGACACGGCAAAGTAACATCCTAGACCATGGCTTTAGAGATC  
CACATGTCAGACCCCATGTGCCTCATCGAGAACTTTAATGAGCAGCTGAAGGTTAATCAGGAA  
GCTTTGGAGATCCTGTCTGCCATTACGCAACCTGTAGTTGTGGTAGCGATTGTGGGCCTCTAT  
CGCACTGGCAAATCCTACCTGATGAACAAGCTGGCTGGGAAGAACAAGGGCTTCTCTGTTGCA  
TCTACGGTGCAGTCTCACACCAAGGGAATTTGGATATGGTGTGTGCCTCATCCCAACTGGCCA  
AATCACACATTAGTTCTGCTTGACACCGAGGGCCTGGGAGATGTAGAGAAGGCTGACAACAAG  
AATGATATCCAGATCTTTGCACTGGCACTCTTACTGAGCAGCACCTTTGTGTACAATACTGTG  
AACAAAATTGATCAGGGTGCTATCGACCTACTGCACAATGTGACAGAACTGACAGATCTGCTC  
AAGGCAAGAACTCACCTGACCTTGACAGGGTTGAAGATCCTGCTGACTCTGCGAGCTTCTTC  
CCAGACTTAGTGTGGACTCTGAGAGATTTCTGCTTAGGCCTGGAAATAGATGGGCAACTTGTC  
ACACCAGATGAATACCTGGAGAATTCCCTAAGGCCAAAGCAAGGTAGTGATCAAAGAGTTCAA  
AATTTCAATTTGCCCCGTCTGTGTATACAGAAGTTCTTTCCAAAAAGAAATGCTTTATCTTT  
GACTTACCTGCTCACCAAAAAAGCTTGCCCAACTTGAAACACTGCCTGATGATGAGCTAGAG  
CCTGAATTTGTGCAACAAGTGACAGAATTCTGTTCCCTACATCTTTAGCCATTCTATGACCAAG  
ACTCTTCCAGGTGGCATCATGGTCAATGGATCTCGTCTAAAGAACCTGGTGCTGACCTATGTC  
AATGCCATCAGCAGTGGGGATCTGCCTTGATAGAGAATGCAGTCCTGGCCTTGCTCAGAGA  
GAGAACTCAGCTGCAGTGCAAAAGGCCATTGCCCACTATGACCAGCAAATGGGCCAGAAAGTG  
CAGCTGCCCATGGAAACCTCCAGGAGCTGCTGGACCTGCACAGGACCAGTGAGAGGGAGGCC  
ATTGAAGTCTTCATGAAAACTCTTTCAAGGATGTAGACCAAAGTTTCCAGAAAGAATTGGAG  
ACTCTACTAGATGCAAAACAGAATGACATTTGTAAACGGAACCTGGAAGCATCCTCGGATTAT  
TGCTCGGCTTTACTTAAGGATATTTTTGGTCTCTAGAAGAAGCAGTGAAGCAGGGAATTTAT  
TCTAAGCCAGGAGGCCATAATCTCTTCATTGAGAAAACAGAAAGTGAAGGCAAAGTACTAT  
CGGGAGCCTCGGAAAGGAATACAGGCTGAAGAAGTTCTGCAGAAATATTTAAAGTCCAAGGAG  
TCTGTGAGTCATGCAATATTACAGACTGACCAGGCTCTCACAGAGACGGAAAAAAGAAGAAA  
GAGGCACAAGTGAAAGCAGAAGCTGAAAAGGCTGAAGCGCAAAGGTTGGCGGCGATTCAAAGG  
CAGAACGAGCAAATGATGCAGGAGAGGGAGAGACTCCATCAGGAACAAGTGAGACAAATGGAG  
ATAGCCAAACAAAATTGGCTGGCAGAGCAACAGAAAATGCAGGAACAACAGATGCAGGAACAG  
GCTGCACAGCTCAGCACAAACATTCCAAGCTCAAAATAGAAGCCTTCTCAGTGAGCTCCAGCAC  
GCCCAGAGGGCTGTTAATAACGATGATCCATGTGTTTTACTCTTAAAGTGCTAAATATGGGAGT  
TTCCTTTTTTTACTCTTTGTCACTGATGACACAACAGAAAAGAACTGTAGACCTTGGGACAA  
TCAACATTTAAATAAACTTTATAATTATTAAA

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**FIGURE 46**

MALEIHMSDPMCLIEINFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAGKNK  
GFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALALLLSSTF  
VYNTVKNIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFFPDLVWTLRDFCLGLEI  
DGQLVTPDEYLENSLRPKQGSQDQRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQKKLAQLETLP  
DDELEPEFVQQVTEFCFSYIFSHSMKTLPGGIMVNGSRLKKNLVLTYVNAISSGDLPCIENAV  
ALAQRENSAAVQKAIHYDQMQQKQVQLPMETLQELLDLHRTSERAIEVFMKNSFKDQVDSF  
QKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAVKQGIYSKPGGHNLFIQKTEEL  
KAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQALTETEKKKKEAQVKAEAEKAEQRL  
AAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEEQQMQEQMQEQAAQLSTTFQAQNRSL  
SELQHAQRAVNNDPCVLL

**Important features of the protein:****Transmembrane domains:**

amino acids 31-49, 114-131

**N-glycosylation sites.**

amino acids 90-94, 144-148, 287-291, 563-567

**N-myristoylation sites.**

amino acids 45-51, 283-289

**Prenyl group binding site.**

amino acids 583-588

**ATP/GTP-binding site motif A (P-loop).**

amino acids 45-53

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**FIGURE 47**

CACTCATTTCATTCCAAAGGGTCTCTCAAGGCAATGGTAATGTGCAAGGAGGTGATACCTAAAT  
GAATGACCAAAAAGAACATGCTTCTGCTTTTGTGTGTCTCCTACATTTTAGACATTTGTTTGT  
TCTCTTGGTAGCCTTTAAATTCCTTGAAGCCCAGGACCATGTCTCACTTACCTTTGTGTTTCC  
ACTAAGTAGTCTACCTCCTGGAATTGGCAGATACTCAGTGAAAGCCTGTGAAATAAGTGATGT  
CTATTTCTAGCATATTATTCTGAGATTTAATGATAGATTTAGTGATTGAATGAGATTTCCATT  
TTCAAATACAGCAAAAGCATAACTATTTTCATTTCATTTCATATTCATTCAACTTCATTCTCAA  
ATTAGGTCTGAGTTAACTAATAATTACCTTTGAAATGTGTGGGTATTGAGGCAATCAGGT  
GGTGACATTGAGCTCTCAGCCAGAGTTTGTCTTCTGGAATTGATTTCAGTTCCATTGCATTGATT  
TTTGTCTCTCAGAAGCCAAGGTTTCCCATGAAAAATCATTCCCCTTGAATTGGGCTGTGATTC  
TTGCTGCGTTTAAGTAAAGGAAGCCTCTTGGTTCTAGTTCTGCAAACTTACACACTGAACTGG  
GACAAGTTTTTGTGTTAGAGTAATGGCTGGGAAAAGAGGAACCTTTTATTTTATTGAGAAGTCA  
AAAACAAAGGCCTCCAGCCACCTGGAGATGTTTTGTTGCAGACACCAGCCTGGCTCTGTCTT  
TATGCCTAACAAATTGAGCATCCAGTCTTCTTTGTGCTGGGACCATTGCTCAGCTCTGCAAGGG  
GAAAAGAGGGAGAAAGCCAGAGCTGCCAGGCTTCTTGCCTGCGGGCCGGGGAGGGTTCCTGG  
GAAGCAGGTGCTCTCTGGCTTCTTGGTACGTGAGGCTCTCGGAGCTGCCTCTCCTCTGACCCT  
CAGGTCTCACCAGTTTGCTCCAGGAGTATATTGAAAACATACCCAGTGCTCTCTCAAGCAC  
CCACTGCTTAGAGGGCCCAGATTTCTTTTCCTTCTTTCCCTTGCAGAGCTGGAGACTGCATCG  
GGCATCTGGTGTGTTAACTAAACAGGAAAAGTACTAAAGGTCCACAGTGCTCATTGTGTAGA  
CTAGCTGCCCTCCGATGGGTGCTCTGATTATCAGTGAGTTCCAGTGCAGGGCCTGTCACTAAAC  
AGGCCTCACTTCCTCCTTGGGGGCTTTCCCATGGGAGGTGTGGCTTTTTACTCTACATGGAAA  
TGACTCTCTGCAGCCACAGAACACAGTCATTTTCTGAATTATCCCAGTCTCTCATGCGCCCTG  
GATTCCTCCAGATGCCTTATATCTCTTGTGCAAAGTTGTCTAAAATTTGGTTCCTCAGCTTCCA  
AGCCTTGCCCTTTTGGCCTTCCTGGAAGTATTTTTGTTGATGAGTCGTCTGTCAATTATTCTCTA  
AAATGATTTGCTTTTTGTTTCTTTTCATTTCCTATTTCCACCCACATATACACACATGCTTCTT  
**AACTTAGGGGATTACATGCCAATAAATCTATTGTTGAAAATGCACTAATACTATCGCAAAGAC**  
GAAAATTCACAGGCTGAACCGTTGTAAGTCCATATGCTCCTCACTTACATGTGTGATGGAGT  
TATGCCCAAATAAGTCCATCGTCAAGTTGAAAAATCAAATCAAGCCATCTTAGGTTGAGGAC  
CATTTGTTTGTACCTCCAAAGATGTCATATCTTTAAACATACTCCCTAGCTTTTCTTTTACT  
TTTTATTTTGAAGTAATTATAGAATCACAGAAAGTTGCAAAAAA

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## **FIGURE 48**

MGALIISGSSAGPVTQASLPPWGLSHGRCGFLLYMENTLCSHRTQSFSELSQSLMRPGFLQM  
PYISCAKLSKIWFPAKPCLLAFLEVFLMSRLSLFSKMICFLFLSFLFPPHIYTHAS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 88-107

**Casein kinase II phosphorylation site.**

amino acids 47-50

**N-myristoylation site.**

amino acids 24-29

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**FIGURE 49**

GGCTTCTACAGTCCACAACACCCACCAGCCCCAGGCCAGCAGAATGAGCCAGTGAGTGCCGGGGCTCCAGTT  
TGGCTGTTGCTATGACAACGTGGCCACTGCAGCCGGTCTCTTGGGGAAGGCTGTGTGGGCCAGCCAGCCATGC  
CTACCCCGTGCGGTGCTGCTGCCAGTGCCCATGGCTCTTGTGCAGACTGGGCTGCCCGCTGGTACTTCTGTTGC  
CTCTGTGGGCCAATGTAACCGCTTCTGGTATGGCGGTGCCATGGCAATGCCAATAACTTTGCTCGGAGCAAGA  
GTGCATGAGCAGCTGCCAGGGATCTCTCCATGGCCCCGTCGTCCCCAGCCTGGGGCTTCTGGAAGGAGCACCCA  
CACGGATGGTGGCGGCAGCAGTCTGCAGGCGAGCAGGAACCCAGCCAGCACAGGACAGGGGCGCGGTGCAGAG  
AAAGCCCTGGCCTTCTGGTGGTCTCTGGCGGCAAGACCAACAGCCTGGGCCAGGGGAGGCCCCCACACCCAGGC  
CTTTGGAGAATGGCCATGGGGGAGGAGCTTGGGTCCAGGGCCCCCTGGACTGGGTGGAGATGCCGGATCACCAGC  
GCCACCCCTCCACAGTCTCTCTACAGATCTCACTTCCACCTCTCCAGGATTAGCTTGGCAGGTGTGGAGCCCT  
CGTTGGTGCAGGCAGCCCTGGGGCAGTTGGTGGGCTCTCTGCTCAGACGACACTGCCCCGGAATCCAGGCTG  
CCTGGCAGAAAGATGGCCAGCCCATCTCTCTGACAGGCACAGGCTGCAGTTCGACGGATCCCTGATCATCCACC  
CCCTGCAGGCAGAGGACGCGGGCACCTACAGCTGTGGCAGCACCCGGCCAGGCCGCGACTCCAGAAAGATCCAAC  
TCCGCATTATAGGGGGTGACATGGCCGTGCTGTCTGAGGCTGAGCTGAGCCGCTTCCCTCAGCCAGGGACCCAG  
CTCAGGACTTTGGCCAAGCGGGGGCTGCTGGGCCCTGGGGGCCATCCCTCTTACACCCACAGCCTGCAACA  
GGCTGCGTTTGGACCAGAACCAGCCCCGGGTGGTGGATGCCAGTCCAGGCCAGCGGATCCGGATGACCTGCCGTG  
CCGAAGGCTTCCCGCCCCAGCCATCGAGTGGCAGAGAGATGGGCAGCCTGTCTCTTCTCCAGACACCAGCTGC  
AGCCTGATGGCTCCCTGGTCATTAGCCGAGTGGCTGTAGAAGATGGCGGCTTCTACACCTGTGTGCTTTCAATG  
GGCAGGACCGAGACCAGCGATGGGTCCAGCTCAGAGTTCTGGGGGAGCTGACAATCTCAGGACTGCCCCCTACTG  
TGACAGTGCCAGAGGGTGATACGGCCAGGCTATTGTGTGTGGTAGCAGGAGAAAGTGTGAACATCAGGTGGTCCA  
GGAACGGGCTACCTGTGCAGGCTGATGGCCACCGTGTCCACCAGTCCCAGATGGCAGCTGCTCATTACAACT  
TGCGGGCCAGGGATGAGGGCTCTACATGTGCAGTGCCTACCAGGGGAGCCAGGCAGTCAGCCGAGCACCAGG  
TGAAGGTGGTCTCACCAGCACCCACCGCCAGCCAGGGACCCTGGCAGGGACTGCGTCGACCAGCCAGAGCTGG  
CCAACCTGTGATTTGATCTCTGCAGGCCCAGCTTTGTGGCAATGAGTATTACTCCAGCTTCTGCTGTGCCAGCTGTT  
CACGTTTCCAGCCTCAGCTCAGCCCATCTGGCAGTAGGGATGAAGGCTAGTTCAGCCCCAGTCCAAAATAGTT  
CATAGGGCTAGGGAGAAAGGAAGATGGACTCTTGGCTTCTCTCTGGCTGGCAAAGGGAGTTATCTTCTGGAA  
TACATTAGCTCTTTCAAAAACCCACCCAGTGTTAGCCTCAACGGCAGCCAGTTACCAGCTTCTCTCTGTAGCCT  
TCAGCAGTGTGTGTCATCTCTGACATAACACAGGCTGCTGTTTTCAAGAAGAGCAATCTGTTTGGATAAGAAAA  
CCTTTACTTTACAGCTTCCCTTTATAATTTGTACACAGGAATAGTTAAATGCATTTGTTTGTGTTTTTTGAG  
ACGGAGTTTTCACTCTGTGTCAGGCTGGAGGGCAATGGCGCGATCTCAGCTACTGCAACCTCCGTCTCCTGG  
GTTCTTGATTCTCCTGTGTCAGCCTTCTGAGTAGCTGGGATTACAGATGCCTATCACCATGCCTGGGTAATTTTT  
GTATTTTTAGTTGAGATGGGGTTTTCGCCATGTTGGCCAGGCTGGTCTCGAAGTCTGACCTCAGATGATCTGCCC  
GCCTCAGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCGCCAGCCATCAATGCATTTTTTTTTTATTTT  
TTTTTTGAGACAGAGTTTCGCACTTCTTGCCAGGCTGGAGTACAATGGTGGATCTTGGCTCACTGCAACCTCC  
ACCTCCTGGGTTCAAGCGCTTCTCCAGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGTATGTGCCACCATGCCT  
GGCTAATTTTTGTATTTTTGGTGGAGACGGGGTTTTCCATGTTGGTCAGACTGGTCTTGAAGTCCCAGCCTCAGG  
TAATCCGCCCCGCTCCGCTCCCAAATGCTGGGATTAGAGGTGTGAGCCACTGTGCCCAGCCCATCAATGTGTT  
TTAAAGCTAGCTGTGAGGGTTCCACTTAATTTAAAGCTGGGCAGGGAGATGTGTAATGATTTCAAAGTTAACACC  
TGTTTTGTTTTCTAAAGGGCATGCCAAGTCTGTGTATCAGGGAAGTATTCTGTGCTAAAATCAGCGATGGTTCA  
TTGCTCTAGTCTCTCTCACCCCTTCTAGGCAGTGTCATCAGTCAGCTCTAAATCTGGTGCAGAGGGTTAACAGCATA  
ACCCTTGTGTCGCAAAATGGAATAGATGTTAAGACCTCAAATAGGGATTGGGATGAAACAGCTGCAGTTAGCACT  
GTTATCTGAGCATGAAAGAACTGGAACGCTCCTTACGTGAGATGTTGGACCTGAAAGCCCTCCTGAGGCCAAC  
ATGCAATCTGGCTGTGACGGTTCTCTGACACCTGTGTAAAGCTGACCAGCCTGCTCTGTACAGTGACAATGAG  
GAGCCCTCTCTTCTTAAGTAGGAATCTGTGAAGCAAAATGTTTGTGTCGCAAGACAAATCAGACTGTGAGTCA  
TTAAAAACAGCATTAGCAGGATGAGGATAGCAATGGGGAAGGGTTGTGGGCAATGCAGTAACAGGGAAATGGCTT  
CAGAAATGGTTTGAGTTGGAAGACAACATTTCTCATCTCTCAGGACTTCTAATTCCTTGATGCTAAAAGAAGAGG  
CATGGATTCTATGAGCTTCAAGTCCCTTTCCACTTAACCTTCTACAAATCTTTCAGAGGACTGCCTAGTAGCA  
AAGGTTATTCCTGGACACAGGAAAGACGGGCATTACAGGGACCAAAGCTCTGAAAGGTGACTTTTATTACCAACA  
CACTGGCTGGAAAAGGGACAAACCACATCACGGGTGAGTGATACTTCTCAGTCTTCTTACTCATTCAACAAAGG  
AAATGTGGGCTGGGGCAGAGGTCTTTTTTCAATTAATACTGGAAAAATATTGAAGAGCATCCATGTTCACTTATG  
CTGGTTTTGCTATAGAAATTGGAAATAAAGGCCACTTTTTTG

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**FIGURE 50**

MGPVVPSLGLLEGAPTRMVAAAVLQASRNPASTGQGPRCRES PGLLVVSGGKTNSLGQGRPPT  
PRPLENGHGGRSLGPGPLDWVEMPDHQRHPSTAPPTDLTSHLSRISLAGVEPSLVQAALGQLV  
RLSCSDDTAPESQAAWQKDGQPISSDRHRLQFDGSLIIHPLQAEDAGTYSCGSTRPGRDSQKI  
QLRIIGGDMAVLSEAELSRFPQPRDPAQDFGQAGAAGPLGAIPSSHPPQANRLRLDQNPQPRV  
DASPGQRIRMTCTRAEGFPPPAIEWQRDQGPVSSPRHQLQPDGSLVISRVAVEDGGFYTCVAFN  
GQDRDQRWVQLRVLGELTISGLPPTVTVPEDGTARLLCVVAGESVNIRWSRNLPLVQADGHRV  
HQSPDGTLLIYNLRARDEGSYMCSAYQGSQAVSRSTEVKVVSPAPTAQPRDPGRDCVDQPELA  
NCDLILQAQLCGNEYYSFCCASC SRFQPHAQPIWQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**Tyrosine kinase phosphorylation site.**

amino acids 392-400

**N-myristoylation sites.**

amino acids 9-15, 50-56, 112-118, 146-152, 173-179, 195-201,  
220-226, 229-235, 280-286, 306-312, 336-342, 397-403.

**Myelin P0 protein.**

amino acids 153-182

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**FIGURE 51**

CAGGCAGAAGCGAACAAAGACCCAGCAAGAGAAGGCAGAGGCTAAGACCCATCCCGTATCTGC  
TCTCCTGAAATAATTCTGGAGTCATGCCTGAAATGCCAGAGGACATGGAGCAGGAGGAAGTTA  
ACATCCCTAATAGGAGGGTTCTGGTTACTGGTGCCACTGGGCTTCTTGGCAGAGCTGTACACA  
AAGAATTTTCAGCAGAATAATTGGCATGCAGTTGGCTGTGGTTTCAGAAGAGCAAGACCAAAAT  
TTGAACAGGTTAATCTGTTGGATTCTAATGCAGTTCATCACATCATTCATGATTTTCAGCCCC  
ATGTTATAGTACATTGTGCAGCAGAGAGAAGACCAGATGTTGTAGAAAATCAGCCAGATGCTG  
CCTCTCAACTTAATGTGGATGCTTCTGGGAATTTAGCAAAGGAAGCAGCTGCTGTTGGAGCAT  
TTCTCATCTACATTAGCTCAGATTATGTATTTGATGGAACAAATCCACCTTACAGAGAGGAAG  
ACATAACAGCTCCCCATAATTTGTATGGCAAACAAAATTAGATGGAGAAAAGGCTGTCCTGG  
AGAACAATCTAGGAGCTGCTGTTTTGAGGATTCTATTCTGTATGGGGAAGTTGAAAAGCTCG  
AAGAAAGTGCTGTGACTGTTATGTTTGATAAAGTGCAAGTTCAGCAACAAGTCAGCAAACATGG  
ATCACTGGCAGCAGAGGTTCCCCACACATGTCAAAGATGTGGCCACTGTGTGCCGGCAGCTAG  
CAGAGAAGAGAATGCTGGATCCATCAATTAAGGGAACCTTTCAGTGGTCTGGCAATGAACAGA  
TGACTAAGTATGAAATGGCATGTGCAATTGCAGATGCCTTCAACCTCCCCAGCAGTCACTTAA  
GACCTATTACTGACAGCCCTGTCTAGGAGCACAACGTCCGAGAAATGCTCAGCTTGACTGCT  
CCAAATTGGAGACCTTGGGCATTGGCCAACGAACACCATTTCGAATTGGAATCAAAGAATCAC  
TTTGGCCTTTCCTCATTGACAAGAGATGGAGACAAACGGTCTTTCATTAGTTTATTTGTGTTG  
GGTTCTTTTTTTTTTTTAAATGAAAAGTATAGTATGTGGCACTTTTTTAAAGAACAAAGGAAATA  
GTTTTGTATGAGTACTTTAATTGTGACTCTTAGGATCTTTCAGGTAAATGATGCTCTTGCACT  
AGTGAAATTGTCTAAAGAACTAAAGGGCAGTCATGCCCTGTTTGCAAGTAAATTTCTTTTTTA  
TCATTTTGTGTTGCTGGCTAAACTTGGAGTTTGTAGTATAGTAAATTATGATCCTTAAATATT  
TGAGAGTCAGGATGAAGCAGATCTGCTGTAGACTTTTCAGATGAAATTGTTTCATTCTCGTAAC  
CTCCATATTTTCAGGATTTTTGAAGCTGTTGACCTTTTCATGTTGATTATTTTAAATTGTGTG  
AAATAGTATAAAAATCATTGGTGTTTATTATTTGCTTTGCCTGAGCTCAGATCAAAATGTTTG  
AAGAAAGGAACCTTTATTTTTTGCAAGTTACGTACAGTTTTTATGCTTGAGATATTTCAACATGT  
TATGTATATTGGAACCTTCTACAGCTTGATGCCTCCTGCTTTTATAGCAGTTTATGGGGAGCAC  
TTGAAAGAGCGTGTGTACATGTATTTTTTTCTAGGCAAACATTGAATGCAAACGTGTATTTT  
TTTAATATAAATATATAACTGTCCTTTTTCATCCCATGTTGCCGCTAAGTGATATTTTCATATGT  
GTGGTTATACTCATAATAATGGGCCTTGTAAGTCTTTTCACCATTTCATGAATAATAATAAATA  
TGTAAGTGTGGCATGTAATGCTTAGTTTTCTGTATTTACTTCTTTTTTTTAAATGTAAGGACC  
AACTTCTAACTAATTGTTCTTTTGTGCTTTAATTTTTTAAAAATTACATTCTTCTGATGTA  
ACATGTGATACATACAAAAGAATATAGTTTAAATATGTATTGAAATAAAACACAATAAAATT

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**FIGURE 52**

MPEMPEDMEQEEVNI PNRRVLVTGATGLLGRAVHKEFQQNNWHAVGCGFRRARPKFEQVNLLD  
SNAVHHIIHDFQPHVIVHCAAERRPDVVENQPDAAASQLNVDASGNLAKEAAAVGAFLIYISSD  
YVFDGTNPPYREEDI PAPLNLYGKTKLDGEKAVLENNLGA AVLRIPILYGEVEKLEESAVTVM  
FDKVQFSNKSANMDHWQQRFPTHVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQMTKYEMAC  
AIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKLET LGIGQRTPPFRIGIKESLWPFLIDK  
RWRQTVFH

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 105-127

**N-glycosylation site.**

amino acids 197-201

**N-myristoylation site.**

amino acids 303-309

**Short-chain dehydrogenases/reductases family proteins.**

amino acids 18-30



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**FIGURE 53**

TGGGCTCCCTCCAGCACTGCTGTTGCCTGCTGCCTAAGATGGGTGACACTTGGGCCCAGCTTCCCTGGCCCTGGGG  
CACCCACCCAGCAATGCTGCTGATCTCCCTCCTCTTGGCAGCCGGGTTGATGCACTCGGATGCCGGCACCAGCT  
GCCCCGTCCCTTTGCACATGCCGTAACCAGGTGGTGGATTGTAGCAGCCAGCGGCTATTCTCCGTGCCCCCAGACC  
TGCCAATGGACACCCGAAACCTCAGCCTGGCCCAACCGCATCACAGCAGTGCCGCTGGCTACCTCACATGCT  
ACATGGAGCTCCAGGTGCTGGATTTGCACAACAACTCCTTAATGGAGCTGCCCCGGGGCCTCTTCTCCATGCCA  
AGCGCTTGGCACACTTGGACCTGAGCTACAACAATTTAGCCATGTGCCAGCCGACATGTTCCAGGAGGCCCATG  
GGCTAGTCCACATCGACCTGAGCCACAACCCCTGGCTGCGGAGGGTGCATCCCCAGGCCTTTTCAAGGCCTCATGC  
AGCTCCGAGACCTGGACCTCAGTTATGGGGGCTGGCCTTCTCAGCCTGGAGGCTCTTGAGGGCCTACCGGGGC  
TGGTGACCTGCAGATCGGTGGCAATCCCTGGGTGTGTGGCTGCACCATGGAACCCCTGCTGAAGTGGCTGCCGAA  
ACCGGATCCAGCGCTGTACAGCAGATTCTCAGTGGCTGAGTGCCGGGGCCCTCCTGAAGTCGAGGGCGCCCCGC  
TCTTCTCACTCACTGAGGAGAGCTTCAAGGCCTGCCACCTGACCCTGACCCTGGATGATTACCTATTTCATTGCGT  
TCGTGGGCTTCTGTGTTCTCCATTGCTTCTGTGGCCACCAACTTCTCCTGGGCATCACTGCCAACTGCTGCCACC  
GCTGGAGCAAGGCCAGTGAAGAGGAAGAGATCTGACATGCCTGCCTCTCATCCCTCCATGCTGCTGACCGCCACA  
GCTGCTGGCCACCAGACGCCCTCCCTGATTGCTCACTCTGGTTCCATGGTGACCTGGCTGCCTCAGTCATGGTTC  
AAGCAAGGTGGGACACTCATTTTGTATGAGCATCTGCTTTGGGCCAGGCGGCACGCTAGGAATTGGGAACATCA  
AGTGAATGACTGACTGCCCTGCCCTCAAGGCATTTCCCTCTGGTCAAGGAGAGAGATCCAAAACTATTCCCTTT  
AAGACTATATGTCAGGACTCTGAGCACGTCAATTATGGAGGCCAGAGGAGGAGCCATCATCTGTATCTAGCAATG  
TCCATGAGAATTATAAGATTAGAGTGATTTGTGAAGTGGGTGCATCAGGAAATATCTACTTTGTGAGGTAGGCAAA  
GAAGGGTGTCTGCACATGGCAGAGGCCAGAAATGCATAGTGTGCTGTGTTGAGAAGAGTGAACAGTTCCTGGTC  
ACTTACTTGTATAGAGGGGGTGTGGCACAGAACTCAAACCTACCCCTCACCTCCTGACACCAAACTGTCAGCTC  
TCAGCAATGCCAGCTGCCTACAGGGAGTAAAGAACACCTCTATGACAGCCCTGGCCTCCTTCCACGAGCAGC  
TACCAGGTGAGACCACCTCCAGTGACTGCCCCATATGACCAATGTCACCAGTTGGTGAGGTCCCAGGCAGCA  
GGCTGAGGATGGACACTTTCAATGCCCTTGTCTCTGCTCTCACTCAAGTTTGTCTCAGAAGAGAGAGGCAGGA  
GGCCACAGCAACTGGGGCAGCAAGAGTCCCTGGCAGCTTGGGATCCTAATCATGTGACTGTTCTTGCCACAGTGCTC  
ATGCCACAGGGTCTCACCAGGAAAGTGCAGTGTGGGCCACAGACCCACAGCCTGGCAGCACCCAGAGCTAAAAGG  
GGACAAAGGCAGCACAGTTATGACCATATGAGGCTTTGCATTTTCTTCTAAGCAACTTACCCACGTTAAGCATGA  
GGGTGAGAGAGCTATTAAATACTAAGCCCTTGGCAGTGTGAGGTACTTTGAAAAGCTCTCTGCACAAACCATTC  
CTTTGACACACACACACAAATCTTTGAGGTGAACGCTGTTGTTCCCATTTTACGGATGAGGCAACTAAGGCT  
CAGAGAGGTTAAAGTCACATGCCACTATGAGCAAGATAAAGTCTGTGCTCTTCTACTGCCCCATCCAAGTTGGG  
GAACATCACCATTCCCTCTAGAGTTATATAAATTCAAATTCAACTAGAGCTGACAAAGTTCCTCATAAGGTCCAG  
GCACTCCTCTGGGCACTTTTATATCTATTGACTCACTTCTTCAATTCTCACAGCAAACTGCCTGGTGGTTTTT  
ATTATCCCCATTTGACAGATGAATTAATCGTAGAGAGTTGAGTGACTTACCAAGGTTGTCTGGATAAGCTAG  
AAGGAAGGCGGTAGGCAGCTCCATTACGGGAACTGCATGATCAATCAGTCAGTCAAAAAATCAAGTAACCTTACGAG  
CAAAGCACAAATTATCATCATCGTGGTCTTCTTCATCAGTTTCGTGAGCAGCATCATTATCTTCCCTCTATTGTT  
CAGCACCGGATAGTTGATGAGTATTTTTGCATCATTCTCCTTGACTTTTACATCCCTGTGAGGAGGTAAATCA  
AACATCAGTAATCCTGTTTTACAGATGGGGAAGGCTCTCAAGGTTGGATATGACTTGCTATGTGGCAAGGTTG  
GGGCTCAACCCCTAACACAGTTCTCTTCCAGTGCTTCTCAAGTGCTTGGGGAAGAGAATGCCCTCAGAAGGCTGG  
GAGTGGGGCCCTGGAATTGAGCATCCATGATGCTGTAGTGAATAAGCTAAATAGAAGGCAGCCAAACCCATCT  
GCTGTACAGATTGAATGCTACGGTAGGGCAAATTGCAGGCTCTGAAACAGAGACTACACAGGTAACACCTG  
AATAGGAGACTCCTGCTTTACAATGTGTAGATAAAACATCAGCAATGGTGGCCATGGTGGCAGTCATGTGAAAAG  
TAAGATCTTTGGGAATCAAGAAAGGAAGCTGTGTTAACCCTCCTGCTCAAGCCCTGCTGCGTGTGTTGCAAGAG  
ATACTAAGAGAGCAAGAAAGCTATAGGTGAGAACCTCTGCAGTTTAGGAGAAGAACATCAAGGCACAGTCCACA  
TGCTGATAAGTCTGGCCAGGAGGAGAATTAACAGGGGCTTTCCACACCTCCCTTGCCCCAAGCTCCAGCGGTA  
TTCTATCAGCCCATCCTCCTGGAAAGCCTGAAAGGAATGAAGGAGGCTAATAAGTCACTTCCAGGAAGGCATCC  
CTCACTCGTGCTTCCCTGAGCTAGTCAACCAAAAGAGTCTTCAGAACTTTGCTAGACCTGAAGTACTTGAACCT  
GTGTCCCCTGAATCTTCTTACAACATCTGGGACAAATCCCTGGTCTGTGACATCCGAAGCAGAACTGTGCCCT  
GCTCTCTCCTTCTGTGATGACCAAGGATGGTGAACCTCAAGTTGTTCTCTACAAGCCAGGCCAGCAACCTAAATAC  
TTGGAGAGGAACTTTTAGAACTATAATCCTGACAAAATAGAAAAGTTTCCCATAGGGGCATACCATAATACTAT  
AATAACCTCCAGGAACATTGTTTGGCAAAATGAGTTAATATATTTAAGATATATGCTTTTTTGCATAGGAC  
TAGAACCAGAAAAGACACAAATGCCCCCTGACATCAATGTCTTCTAGTGGGACAATTTGGTCTCCATTAAAT  
GCCAAACCTTTCTGAACAGGATACATGGCTTTTAAAGGACAGATGTTTCTCCTGCTGCTAGAAGTTCCTCAGTTT  
ACTAGAGCACAATGAGGAAAGTATTCAACCTCCCTACTGCCAAGGAATCCCTGCTTCTCCCCACCGCCATCAT  
CTTGTCCAAGCTATCAGAAGCAACCTTCTAGAGATAATCTAACAATCCTGATTAGAATTGCTCCCATATCCCTGG  
TGACCACAGGCTTCATTCAAATGTCCAACTGGTTAACATGTATGTGATGGGGTATCTCTGCATCTGTATGTCT  
GTCCTGCGAGGTTCTTGTATATTGGCTGTCCGCTGACTTGGGACAGATCTCTCTAGAAGTTGGGTTCAAGTTCTCT  
GACATAGTCCACTCAGCTAGGCTGAGTGGCTAAATATGCATAAATAAGCATGCCTAAATAGGCATATATAGGT  
TGGTGCAAAAGTAATTGCGGTTTTTGGCATTAAAAATGATGGCAAAAATCCCAATTACTTTTGGCTCAATCTAAT  
ATTACATTGCTTGATAGATTAAGATGGAATCCACACAGGTTTAGGGTAGGACTGGATGCTCAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

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**FIGURE 54**

MLLISLLLLAAGLMHSDAGTSCPVLCTCRNQVVDCCSSQRLFSVPPDLPM DTRNLSLAHN RITAV  
PPGYLTCYME LQVLDLHNNSLMELPRGLFLHAKRLAHL DLSYNNFSHV PADMFQEAHGLVHID  
LSHNPWLRRVHPQAFQGLMQLRDL DLSYGGLAFLSLEALEGLPGLVTLQIGGNPWVCGCTMEP  
LLKWLRNRIQRCTADSQLAECRGPPEVEGAPLFSLTEESFKACHLTLTDDYLFIAFVG FVVS  
IASVATNFLLGITANCCHRWSKASEEEEEI

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation sites.**

amino acids 52-55, 81-84, 107-110

**Tyrosine kinase phosphorylation site.**

amino acids 148-154

**N-myristoylation sites.**

amino acids 11-15, 263-268

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 175-185

**Leucine zipper pattern.**

amino acids 77-98

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**FIGURE 55**

GGCTGCGCCCAGGCCGGCGGGCCCCAGCAGCTGCGAACC GCCGGCGCACCACCTGTTTCCGCGC  
CCGGGGACTTCCCCGGCGGGGCTCAGAAAGTGTGGGGTGGTTCGCTTGGCTTCCCCTGGCGTCA  
GCGACCCAGGGTAACCTCCTCCACTGCTGCGTGCCGTGCAGGCCTGCCTGTGTGAGAGCCACG  
TGTGCCGCGCTCTGGGCACAGCCTTGGAAGTGCAGGACCGCGACGGCAGCAGAGCAGAAACCT  
TACAGAAACATGAAGCCCTCAACCATCTGCTACTCAGTTATTCGGGGCTGACGGCGGCTTCTA  
GAACATCCAGGTGTTCTGCAGATGCGGAGAACTCATCCTGTAGTCACCAGATGGAGTCCCAAAC  
AGCCAAGCAGATGTAAGGCCTGTGCTGTGGCTCTGAGGCCCTGAATACAGAAGGGTCACTTTC  
TTAGTGGCCAAAGAGCAGTTGTTGACATTGATGTCTAATTATTGAACACGACCAGTCATTTTA  
CTGAGCTGCAGTGAGGAAACACTGACCATAGAAGATCAAGCCAAATGAGGGATTGCAAATTTT  
CTGATTCTTTTGAATTAGGATTCCAGATGGGGGCTCATTTTCTACAGCCCCCAACATTCCTAT  
AGCCGTTATCACTGCCATCACCCTGCCACCAGCATCTTCTTGCAGATTCCACCCCTGCTCCC  
CAGAGACTTCCTGCTTTGAAAGTGAGCAGAAAGGAAGCTCTCAGAAAAATCTCTAGTGGTGGC  
TGCCGTGCTCCAGACAATCGGAATCCTGCCTTCACCACCAATGGGCTGGCTTTTTTCTAAAGGT  
TTTGTGGCGGGAGTGAGTTTCTCAGGATTTCTTTATCCTCTTGTGGATTTTTCATCAGTGG  
GAAACAAGAGGACAGAAAGCCAAACTTTGTGATTATTTTGGCCGATGACATGGGGTGGGGTGA  
CCTGGGAGCAAACCTGGGCAGAAACAAAGGACACTGCCAACCTTGATAAGATGGCTTCGGAGGG  
AATGAGGTTTGTGGATTTCCATGCAGCTGCCTCCACCTGCTCACCTCCCGGGCTTCCTTGCT  
CACCGGCCGGCTTGGCCTTCGCAATGGAGTCACACGCAACTTTGCAGTCACTTCTGTGGGAGG  
CCTTCCGCTCAACGAGACCACCTTGGCAGAGGTGCTGCAGCAGGCGGGTTACGTCACTGGGAT  
AATAGGCAAATGGCATCTTGGACACCACGGCTCTTATCACCCCAACTTCCTGGGTTTTGATTA  
CTACTTTGGAATCCCATATAGCCATGATATGGGCTGTACTGATACTCCAGGCTACAACCACCC  
TCCTTGTCACGCGTGTCCACAGGGTGATGGACCATCAAGGAACCTTCAAAGAGACTGTTACAC  
TGACGTGGCCCTCCCTCTTTATGAAAACCTCAACATTGTGGAGCAGCCGGTGAACCTGAGCAG  
CCTTGCCCAGAAAGTATGCTGAGAAAGCAACCCAGTTTCATCCAGCGTGCAAGCACCAGCGGGAG  
GCCCTTCCTGCTCTATGTGGCTCTGGCCACATGCACGTGCCCTTACCTGTGACTCAGCTACC  
AGCAGCGCCACGGGGCAGAAAGCCTGTATGGTGCAGGGCTCTGGGAGATGGACAGTCTGGTGGG  
CCAGATCAAGGACAAAGTTGACCACACAGTGAAGGAAAACACATTCCTCTGGTTTTACAGGAGA  
CAATGGCCCGTGGGCTCAGAAAGTGTGAGCTAGCGGGCAGTGTGGGTCCCTTCACTGGATTTTG  
GCAAACCTCGTCAAGGGGGAAAGTCCAGCCAAGCAGACGACCTGGGAAGGAGGGCACCGGGTCCC  
AGCACTGGCTTACTGGCCTGGCAGAGTTCCAGTTAATGTCAACAGCACTGCCTTGTTAAGCGT  
GCTGGACATTTTCCAACCTGTGGTAGCCCTGGCCCAGGCCAGCTTACCTCAAGGACGGCGCTT  
TGATGGTGTGGACGTCTCCGAGGTGCTCTTTGGCCGGTCACAGCCTGGGCACAGGGTGCTGTT  
CCACCCCAACAGCGGGGCAGCTGGAGAGTTTGGAGCCCTGCAGACTGTCCGCCTGGAGCGTTA  
CAAGGCCTTCTACATTACCGGTGGAGCCAGGGCGTGTGATGGGAGCATGGTGCCTGAGCTGCA  
GCATAAGTTTCTCTGATTTTCAACCTGGAAGACGATACCGCAGAAGCTGTGCCCTAGAAAG  
AGGTGGTGCAGGAGTACCAGGCTGTGCTGCCCAGGTCAGAAAGGTTCTTGACAGACGTCCTCCA  
AGACATTGCCAACGACAACATCTCCAGCGCAGATTACACTCAGGACCCTTCAGTAACTCCCTG  
CTGTAATCCCTACCAAATTGCCTGCCGCTGTCAAGCCGCATTAACAGACCAATTTTTATTCCAQ  
GAGGAGGAGTACCTGGAAATTAGGCAAGTTTGTCTCCAAATTTTCAATTTTACCCTCTTTACAA  
ACACACGCTTTAGTTTAGTCTTGGAGTTTAGTTTGGAGTTAGCCTTGATATCCCTTCTGTA  
TCCTGTCCCCCTCCACGCCGACCCGAGAGCAGCTGAGCTGCGCTGGCTCTGGGCAGGGAGTG  
TGCTTAAATGGGAAGCACACGGGCTTTGGAGTCAGGCACAGGTGCCAGCTCCAGCTTTTGAAC  
TTGGGCAATTGTTTAACTAACCTGCAAGTTGATTTTGAGGGTTAAATAAAGGCATACATGAA  
AATGCCTGGCAACTTTAAAAA

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**FIGURE 56**

MGWFLKVLLAGVSFSGFLYPLVDFCISGKTRGQKPNFVII LADDMGWGDLGANWAETKDTAN  
LDKMASEGMRFVDFHAAASTCSPSRASLLTGRLGLRNGVTRNFAVTSVGGLPLNETTLAEVLQ  
QAGYVTGIIIGKWHLGHHGSYHPNFRGFDYYFGIPYSHDMGCTDTPGYNHPPCPACPQGDGPSR  
NLQRDCYTDVALPLYENLNIVEQPVNLSSLAQKYAEKATQFIQRASTSGRPFLLYVALAHMHV  
PLPVTQLPAAPRGRSLYGAGLWEMDSL VGQIKDKVDHTVKENTFLWFTGDNGPWAQKCELAGS  
VGPFTGFWQTRQGGSPAKQTTWEGGHRVPALAYWPGRVPVNVSTALLSVLDIFPTVVALAQA  
SLPQGRRFDGVDVSEVLFGRSQPGHRVLFHPNSGAAGEFGALQTVRLERYKAFYITGGARACD  
GSMVPELQHKFPLIFNLEDDTAEAVPLERGGAEYQAVLPEVRKVLADVLQDIANDNISSADYT  
QDPSVTPCCNPYQIACRCQAA

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 353-373

**N-glycosylation sites.**

amino acids 117-120, 215-218, 356-359, 397-500

**N-myristoylation sites.**

amino acids 12-17, 33-38, 52-57, 97-102, 101-106, 113-118, 158-163, 328-333, 388-393, 418-423, 435-440, 436-441

**Amidation site.**

amino acids 382-385

**Sulfatases signature 2.**

amino acids 129-138

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**FIGURE 57**

TGGACAAGACACCTCCAGGAGCCCAGCTCACAGCCACCGGTACCTTCTTCCAGGACAAGCTGG  
GGGCCTCCATGGGCGCCTGAGGGCCAGGCGCCAGGGCCGTGGGCACGAGT**ATGGT**GAGACACC  
AGCCCCTGCAGTACTACGAGCCACAGCTGTGCCTCTCCTGCCTCACGGGCATCTACGGCTGCC  
GTTGGAAGCGCTACCAGCGCTCCCATGATGATACCACACCGGGCACAGCGCCATTCCCTGCATG  
TGGGGGCTGTGGCAGCAGTCACCATGCTCTCCTGGATCGTGGCAGGACAGTTTCGCCCCGTGCAG  
AGCGGACCTCCTCCCAGGTGACCATCTCTGTACCTTCTTCACCGTGGTGTTCGCCCTCTACC  
TGGCCCCCTCTACCATCTCCTCTCCCTGCATCATGGAGAAGAAAGACCTCGGCCCCAAGCCTG  
CTCTCATTGGCCACCGCGGGGGCCCCATGCTGGCTCCAGAGCACACGCTCATGTCTTCCGGA  
AGGCCCTCGAGCAGAAGCTGTACGGGCTCCAGGCTGACATTACCATCAGCCTGGACGGCGTGC  
CCTTCCTCATGCATGACACCACCTGCGGGCGCACCACCAACGTGGAGGAGGAGTTCCCGGAGC  
TGGCCCGCAGGCCTGCCTCCATGCTTAAGTGGACCACCTGCAGAGACTCAACGCTGGCCAGT  
GGTTCCTGAAGACTGACCCCTTCTGGACAGCCAGCTCCCTGTCACCTCCGACCACAGAGAGG  
CCCAGAACCAGTCCATCTGCAGCCTGGCAGAGCTCCTGGAGCTGGCCAAGGGCAATGCCACAC  
TGCTGCTCAACCTGCGTGACCCGCCCCGGGAGCACCCCTACCGCAGCAGTTTTATCAACGTGA  
CTCTGGAGGCCGTGCTGCACTCCGGCTTCCCCCAGCACCAAGTTCATGTGGCTGCCTAGCAGGC  
AGAGGCCCTGGTGCGGAAGGTGGCTCCCGGCTTCCAACAGACATCAGGCTCCAAGGAGGCAG  
TCGCCAGCCTGCGGAGAGGCCACATCCAGCGGTGAACCTGCGCTACACTCAGGTGTCCCGCC  
AGGAGCTCAGGGACTACGCGTCTGGAACCTGAGTGTGAACCTCTACACAGTCAACGCACCGT  
GGCTCTTCTCCCTGCTGTGGTGTGCGGGGGTCCCATCCGTACCTCTGACAACTCCACACCC  
TGTCCCAGGTGCCTTCCCCCTCTGGATCATGCCCCCGGACGAGTACTGTCTCATGTGGGTCA  
CTGCCGACCTGGTCTCCTTCACCTCATCGTGGGCATCTTCGTGCTCCAGAAGTGGCGCCTGG  
GTGGCATAACGGAGCTACAACCCTGAGCAGATCATGCTGAGTGCTGCGGTGCGCCGGACAGCC  
GGGACGTCAGCATCATGAAGGAGAAGCTTATTTTCTCAGAGATCAGCGATGGTGTAGAGGTCT  
CCGATGTGCTCTCCGTATGTTTCAGACAACAGTTATGACACATATGCCAACAGCACCGCCACCC  
CTGTGGGGCCCCGAGGGGGTGGCAGCCACACCAAGACCCTCATAGAGCGGAGTGGGCGT**TAGC**  
TGAAGACATGTCTGTCCCACCTGTACCTGACACAGAAGCTGGGGAGCCTAGGAGAGCTGGTGG  
AAGTGTGTCTGAACTCGGAGTGCTCTGGGAGCGGGCTCCACAGCCTCCTTGTGGGCTCCAGCC  
CCTTGTGACCCGACGCTCTCTTGAGGGGGACTCCCTGTCTCCTGAGGCCAGCTGGGCCAGG  
ACTCCATCCTTTCAGATGCCCTGACGGCCTGGGGCTCCTTCTGGGAAGTATGGGGCTAGGG  
CTTGGTCCCCCTCTTCTGAGGCCCTCTCCTGTATCCCGACCTGGAAGCTTTGATGGGTCTAGG  
GCCATGCCATAACCCCTGTGGCAATGGAGTGTGTGGATGCTCACCTGTGCCATCTGTCTCCT  
GTCTGTGCCAGGAGGCACCTGAGTTCTCTGCTGTTATCCTGCCCCAAGGGCCTGGGCCGAGCC  
TCTACCTGAAGCAACTCTGCTCTTCTGTCAGTCTCAAAGCACAAAGGAGGTTTCAGCCCAGGAG  
GAAGCCAGCTGCAATGTGGAGACACGTCCTCCTCCCAACCCACCTCATGCCACCGCCAACCC  
CCTGCCCCAGGAGCGGGCCTGAGCCACGTCCCTAGGAGCAGCTGGAGATGGCCAAAAGAGTG  
AGCTCAGGACTACTGGATCCCATGCCCAGGTGTCCAGCAGACCTCAAGGCAGAAGGGTCACCT  
AACCCAGGAGTCCACAGACTGATGTGACCTCAGGTTCACACATCAGTGGCCACAGGGCAGGGC  
CCACCTGGTAGAAGTGTTCTGGATATGGCCAGGGTGGGTGTGTGGCTAAGTGGGCCTGAACAG  
AGGGAACCTAGGGCCCTTGGCCAATGTGATTAAAGCTGCCATCTTGAAA

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**FIGURE 58**

MVRHQPLQYYEPQLCLSLTGIYGCRWKRYQRSHDDTTPGTAPFLHVGAVAAVTMLSWIVAGQ  
FARAERTSSQVTILCTFFTTFVFALYLAPLTISSPCIMEKKDLGPKPALIGHRGAPMLAPEHTL  
MSFRKALEQKLYGLQADITISLDGVPFLMHD TTLRRTTNVEEEFPELARRPASMLNWTTLQRL  
NAGQWFLKTDPFWTASSLSPSDHREAQNQSICSLAELLELAKGNATLLLNLRDPPREHPYRSS  
FINVTLEAVLHSGFPQHQMVLPSRQRPLVRKVAPGFQQTSGSKEAVASLRRGHIQRLNLRYT  
QVSRQELRDYASWNLSVNLYTVNAPWLFSLWCAGVPSVTSDNSHTLSQVPSPLWIMPPDEYC  
LMWVTADLVSF TLI VGI FVLQKWRLLGGIRSYNPEQIMLSAAVRRTSRDVSIMKEKLIFSEISD  
GVEVSDVLSVCSDNSYDTYANSTATPVGPRGGGSHTKTLIERSGR

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 47-61, 77-93, 335-350, 380-399

**N-glycosylation sites.**

amino acids 182-186, 217-221, 233-237, 255-259, 329-333, 462-466

**Tyrosine kinase phosphorylation site.**

amino acids 130-139

**N-myristoylation sites.**

amino acids 21-27, 48-54, 294-300, 404-410, 442-448, 473-479

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**FIGURE 59**

CCTGAGCAAACACAGCAGCCCGAGTGTTCCCAAGGCCAAAATGCTGAGAACGTCCACTCCTAA  
TCTGTGTGGTGGTCTGCATTGCCGGGGCCCCCTGGCTCTCTTCTGGCATTCTCTGCCTCTGCCT  
CATATTCTTGTTAGGCCAGGTGGGCTTGCTGCAGGGACACCCCCAGTGCCTGGATTACGGGGC  
CCCTTTCCAGCCCCCTCTGCACCTTGAGTTTTGCTCTGACTATGAGTCCTTCGGCTGCTGTGA  
TCAGCACAAGGACCGCCGCATCGCTGCCCGGTACTGGGACATCATGGAATATTTTGATCTGAA  
GAGACATGAGCTGTGTGGAGATTACATTAAAGACATCCTTTGCCAGGAGTGCTCGCCCTACGC  
AGCCACCTCTACGACGCCGAAAACACCCAGACGCCTCTCCGGAATCTCCGGGGCCTCTGCTC  
TGATTACTGCTCTGCCTTCCATTCTAACTGTCACTCAGCCATTTCCCTGCTGACCAATGACCG  
CGGCCTCCAGGAGTCTCATGGAAGGGACGGTACCCGCTTCTGCCACCTCCTGGACCTTCCTGA  
CAAGGACTATTGCTTCCCTAATGTCCTGAGGAACGACTATCTCAACCGCCACCTGGGCATGGT  
GGCCCAAGATCCTCAGGGCTGCCTGCAGCTCTGCCTGAGCGAGGTGGCCAACGGGCTGAGGAA  
CCCCGTCTCCATGGTCCATGCTGGGGACGGCACCCATCGCTTCTTTGTTGCCGAGCAGGTAGG  
AGTGGTGTGGGTCTACCTCCCTGATGGGAGTCGCCTGGAGCAACCTTCCTGGACCTCAAGAA  
CATCGTGTGACCACCCCATGGATCGGGGATGAGAGAGGCTTCTTGGGGTTGGCTTTTACCC  
CAAATTCGCCACAATCGCAAGTTCTATATTTATTATTCGTGCCTGGACAAGAAGAAGGTAGA  
AAAGATCCGAATTAGTGAGATGAAGTTTTCTCGGGCTGATCCTAACAAAGCTGACCTGAAATC  
AGAGAGGGTCATCTTGAGATTGAAGAACCAGCCTCAAACCATAATGGCGGACAACCTTCTTTT  
TGGCCTGGATGGCTATATGTACATATTCAGTGGGGACGGGGGACAGGCTGGAGATCCCTTTGG  
CCTGTTTGAAATGCTCAGAACAAAAGTTCCCTGCTGGGAAAAGTTTTAAGGATCGATGTGAA  
CAGGGCAGGCTCACATGGCAAGCGGTACCGAGTCCCCTCGGACAATCCATTTGTTTCTGAGCC  
AGGGGCCCCACCCCGCCATCTATGCCTATGGGATCAGGAACATGTGGCGTTGTGCTGTGGACCG  
AGGGGACCCCATCACGCGCCAGGGCCGAGGCCGGATATTCTGTGGGGACGTGGGGCCAGAACAG  
GTTTGAAGAGGTTGACCTCATTTTGAAAGGTGGAACTATGGCTGGAGAGCAAAGGAAGGGTT  
TGCATGTTATGACAAAAAAGTTTGTCAATGCCTCTTTGGATGATGTTCTGCCAATCTATGC  
TTATGGCCATGCAGTGGGGAAGTCAGTCACTGGAGGTTATGTCTATCGTGGTTGTGAATCCCC  
AAATCTCAATGGCCTGTATATCTTTGGAGACTTCATGAGTGGTCGACTTATGGCTTTGCAGGA  
AGATAGAAAAACAAGAAATGGAAGAAGCAGGATCTTTGCCTGGGCAGCACCCAGTCCTGTGC  
CTTCCCAGGGCTGATCAGCACCCATAGCAAGTTCATCATCTCCTTTGCTGAAGATGAAGCAGG  
GGAGCTGTATTTCTGGCGACCTCTTACCCAAGTGCCTATGCACCACGTGGATCTATTTACAA  
GTTTGTGACCCCTCAAGGCGAGCACCCCCAGGCAAGTGCAAATACAAGCCAGTGCCCGTGAG  
AACCAAGAGTAAGCGGATCCCGTTCAGACCACTCGCCAAGACAGTCTTGGAAGTTGCTAAAGGA  
ACAATCAGAGAAAGCTGCTAGAAAATCTTCCAGTGCAACCTTAGCTTCTGGCCCAGCCCAGGG  
TTTGTCTGAGAAAGGCTCCTCCAAGAAGCTGGCTTCTCCTACAAGCAGCAAGAATACATTGCG  
AGGGCCTGGTACAAAGAAGAAAGCCAGAGTGGGGCCCCACGTCCGCCAGGGCAAGAGGAGGAA  
GAGCCTGAAAAGCCACAGTGGCAGGATGAGGCCATCAGCAGAGCAGAAGCGAGCTGGCAGAAG  
TCTCCCTTGACCTATTGGTCAAGGTGGCCGACAGGGTGACGTGAGAGAGGAGAGCCACCTCAT  
CAAATGAAAGTCACTGCTGAATAAAGACCTTAGAAGTCTGGGAAGCCAGGGTAGAGGTGGGGC  
AGGGCGGTTTTCTCTCCCTGGGAAATCTTGCTGTCTACTGAATAAATAAATGCACCTTCTCT  
GTATGCAGTGCTTCTGTGGGAGACCATATCCAGATTGCTGGTGCACCTGGGTTATGGTAAGC  
ACTAGTCCATGAGCCTGCTTGAATCACACTGGATGTCTCCGTTTTGTCTTGTAATGCCTAC  
AACCTGAGGTAATAAATCAACATTTGCTCA

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**FIGURE 60**

MLRTSTPNLCGGLHCRAPWLSSGILCLCLIFLLGQVGLLQGHQPCLDYGPPFQPPLHLEFCSD  
YESFGCCDQHKDRRIAARYWDIMEYFDLKRHELCDYIKDILCQECSPYAAHLYDAENTQTPL  
RNLPGLCSDYCSAFHSNCHSAISLLTNDRLQESHGRDGTFRFCHLLDLPDKDYCFPNVLRNDY  
LNRHLGMVAQDPQGCLQLCLSEVANGLRNPVSMVHAGDGTFRFFVAEQVGVVWVYLPDGSRL  
QPFLDLKNIVLTTPWIGDERGFLGLAFHPKFRHNRKFYIYYSCLDKKKVEKIRISEMKVSRAD  
PNKADLKSERVILEIEEPASNHNGGQLLFGLDGYMYIFTGDGGQAGDPFGLFGNAQNKSSLLG  
KVLRIDVNRAGSHGKRYRVPSDNPVFSEPGAHPAIYAYGIRNMWRCVDRGDPITRQGRGRIF  
CGDVGQNRFEEDLILKGGNYGWRAKEGFACYDKKLCHNASLDDVLPYAYGHAVGKSVTGGY  
VYRGCEPNLNGLYIFGDFMSGRLMALQEDRKNKKWKKQDLCLGSTTSCAFPGLISTHSHKFII  
SFAEDEAGELYFLATSYPSAYAPRGSYKFVDPSSRAPPGKCKYKVPVVRTKSKRIPFRPLAK  
TVLDLLKEQSEKAARKSSSATLASGPAQGLSEKGSSKKLASPTSSKNTLRGPGTKKKARVGPH  
VRQGKRRKSLKSHSGMRPSAEQKRAGRSLP

**Important features of the protein:****Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 17-36

**N-glycosylation sites.**

amino acids 372-376, 480-484

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 645-649, 699-703

**Tyrosine kinase phosphorylation site.**

amino acids 81-89

**N-myristoylation sites.**amino acids 11-17, 37-43, 156-162, 165-171, 357-363, 365-371,  
368-374, 408-414, 459-465, 548-554, 557-563**Amidation sites.**

amino acids 391-395, 696-700

**Cell attachment sequence.**

amino acids 428-431

**Leucine zipper pattern.**

amino acids 25-47



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**FIGURE 61**

CTCCATTAAACCACCACCAGCTCCCCAAGCCACCCCTTCAGCCATGAAAGTTCCTGCTCCTGGT  
CTTGGCAGCCCTCGGATTCCTGACCCAGGTGATCCCAGCCAGTGCAGGTGGGTCAAAATGTGT  
GAGTAACACCCCAGGATACTGCAGGACATGTTGCCACTGGGGGGAGACAGCATTGTTTCATGTG  
CAACGCTTCCAGAAAATGCTGCATCAGCTACTCCTTCCTGCCGAAGCCTGACCTACCACAGCT  
CATCGGTAACCACTGGCAATCAAGGAGAAGAAACACACAAAGGAAAGACAAGAAGCAACAAAC  
GACCGTAACATCATAATAACCACTGCTATCGCCTCCACCAACTCAGAGAAATATCATTTCCAC  
AGTTCCAATTCCTCCTACATTGCTGAGTACTAGCCAAGGCTCCTCTTTATGGGGCAGATATCT  
ATAGCCAACCCCAAACCTTCTGTCTTCTATCATTCTGTCAATTCATCTAGTAACATAATTTGGAG  
TTTGTATCTATCTTACGAGAACATCATCATGCAGATTTCGTCCACAGGGGATCTGTCAGTTTG  
GGTCTCCAAATGAAAAATGTCAAGACAGAATTGGACATGCAAAAGATTGACTGGGAGAACAC  
ACCTCTGATGGACAAAGGTGAGACAGAGCAGCCACAGGCAGGGAGAGCCTTCAGACTGCAACG  
CTGGCCTGATACGTGTCAAAGGAGAGAGGGATAGAGGAGGATTGAATAGAAGGAGACTAAGAC  
TGCAGCTCTAAGAAAGTCTCAGCCAAACAGATGGGGAGGCCCAAAGCAAGGCTTGCCCCTCAG  
AGGAGCTCACGCAGGGCAGGAATAGCCAGGTTCTCATATCCCAGGGGTTTCAGACTTGGCTGAG  
AACAGCCCCTGGAGAACATGGGGTGACTGCTACCATAGGTCTGGAAGTATGAGGCTGTCCACC  
AACTATCCCCTTGAAGCAAGTTCTCTTGAAAGGAAATCTAAACAGTGCACCCCCATGGCTGCC  
ACGGAGTATAAGGAGGGAGAGAAAGGAGCTGAAAGTCTAGGTTTGGCCAGCTAGGTAGACTGA  
CTTGTGAGGTATTTATTTATTCATTTGAGTAACAAAGCAGACAGAATACATAGCCACCATTGG  
TAGTACACCCCAAAGCAAGGATGGCATGATGCTGGTGACTCAAACGTGCCTACTCATGGTGT  
CAAATTGGCATAATCCTCTTGGAAGCTGTGTGGAAATAAGCACAGAGAAGCAGAACTCTAAT  
TGCTTAATCCACTAAACATTACTTCTGGGAATTGGCTCATCATAAATTATCCAAGAGAAAGCA  
CAAAGTTATGGGCACAAAGGTTTTCCATATAATATTATTTAAAATGCTGAGAAAATGAAAAA  
TCTAAATGGTGAAATATATACTAATGCCATCTATAAATACAAACAAATAGAATGTTTATAGAA  
TAATGGAACATAATAACATTATTCAAATTTGCATTTATGCTATAGTTGTCAAATTTGTCTCCT  
TATATGATACAAAACCTCATGAAAATTATGACTTTTTTGTGGTTGGAAAGCAGAATTATGCA  
TAAATTTCTCTTACAGTTCGATGCCCATTAGTTTTATATAACATTTATTTGACACGTACTGA  
CTTCTATCTGAGAAGAACAACCAAAACACTCAGGCCTAAATAATTAAAAACGGTCCTA<sup>\*</sup>AAAA  
CTAGCAAACCAGATAAGAAAAGATGT<sup>\*</sup>TAATGCCCATTCCTTAACCTTATGTCTTAGACCAAAAT  
TAATTCTAGATGGTTTTTAAATGACAGTGTAAGTAAAGTATTAAAGATTGTGTGGTCAAA  
TATTCAATTTAAGAGCAAGGAAATTCCTATAAATATAACAATAGAGGCAGAACTCATGTAAGA  
ATAAATTGATTAGGTGGTATTAAATATTAAGTTCTTATGTATGTCAAAGATATCATTTTGAA  
ATTCATCCATCTTATTGGGTATTGCAGGAGTTCATTCCTTTTTGTTTATAAATACTCTCCGT  
CATATGAATAGTATTCAATTTGTATACTGGTTTGTTGATGGACATTTGGGTGTTCCAGTTTA  
TGGCTATTACAAATAAAGCTTCTATGAACATTTATGTACA

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## **FIGURE 62**

MKFLLLVLAALGFLTQVIPASAGGSKCVSNTPGYCRTCCHWGETALFMCNASRKCCISYSFLP  
KPDLPQLIGNHWQSRRRNTQRKDKKQQTTVTS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 1-22

**N-glycosylation site.**

amino acids 50-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 79-82

**N-myristoylation site.**

amino acids 23-28

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**FIGURE 63**

GCGGAGCGCCTGGGAGAGGAGAAGGAGCCGACCTGCCGAGATGGAGGCGACCGGCACCTGGGC  
GCTGCTGCTGGCGCTGGCGCTGCTCCTGCTGCTGACGCTGGCGCTGTCCGGGACCAGGGCCCG  
AGGCCACCTGCCCCCGGGGCCACGCCGCTACCACTGCTGGGAAACCTCCTGCAGCTACGGCC  
CGGGGCGCTGTATTACGGGCTCATGCGGCTGAGTAAGAAGTACGGACCGGTGTTACCATCTA  
CCTGGGACCTGGCGGCCTGTGGTGGTCCTGGTTGGGCAGGAGGCTGTGCGGGAGGCCCTGGG  
AGGTCAGGCTGAGGAGTTCAGCGGCCGGGGAACCGTAGCGATGCTGGAAGGGACTTTTGATGG  
CCATGGGGTTTTCTTCTCCAACGGGGAGCGGTGGAGGCAGCTGAGGAAGTTTACCATGCTTGC  
TCTGCGGGACCTGGGCATGGGGAAGCGAGAAGGCGAGGAGCTGATCCAGGCGGAGGCCCGGTG  
TCTGGTGGAGACATTCCAGGGGACAGAAGGACGCCCATTCGATCCCTCCCTGCTGCTGGCCCA  
GGCCACCTCCAACGTAGTCTGCTCCCTCCTCTTTGGCCTCCGCTTCTCCTATGAGGATAAGGA  
GTTCCAGGCCGTGGTCCGGGCAGCTGGTGGTACCCTGCTGGGAGTCAGCTCCCAGGGGGGTCA  
GACCTACGAGATGTTCTCCTGGTTCCTGCGGCCCTGCCAGGCCCCCAAGCAGCTCCTCCA  
CCACGTACGACCTTGGCTGCCTTCACAGTCCGGCAGGTGCAGCAGCACCAGGGGAACCTGGA  
TGCTTCGGGCCCCGCACGTGACCTTGTCGATGCCTTCCTGCTGAAGATGGCACAGGAGGAACA  
AAACCCAGGCACAGAATTACCAACAAGAACATGCTGATGACAGTCATTTATTTGCTGTTTGC  
TGGGACGATGACGGTCAGCACCACGGTCGGCTATACCCTCCTGCTCCTGATGAAATACCCTCA  
TGTCCAAAAGTGGGTACGTGAGGAGCTGAATCGGGAGCTGGGGGCTGGCCAGGCACCAAGCCT  
AGGGGACCGTACCCGCTCCTTACACCGACGCGGTTCTGCATGAGGCGCAGCGGTGCTGGC  
GCTGGTGGCCATGGGAATACCCCGCACCTCATGCGGACCACCCGCTTCCGAGGGTACACCCT  
GCCCCAGGGCACGGAGGTCTTCCCCCTCCTTGGCTCCATCCTGCATGACCCCAACATCTTCAA  
GCACCCAGAAGAGTTCAACCCAGACCGTTTCCCTGGATGCAGATGGACGGTTCAGGAAGCATGA  
GGCGTTCCCTGCCCTTCTCCTTAGGGAAGCGTGTCTGCCTTGGAGAGGGCCTGGCAAAAGCGGA  
GCTCTTCTCTTCTTACCACCATCCTACAAGCCTTCTCCCTGGAGAGCCCGTGCCCGCCGGA  
CACCTTGAGCCTCAAGCCCACCGTCAGTGGCCTTTTCAACATTCCCCCAGCCTTCCAGCTGCA  
AGTCCGTCCCCTGACCTTCACTCCACCACGCAGACCAGATGAAGGAAGGCAACTTGGAAGTG  
GTGGGTGCCCAGGACGGTGCCTCCAGCCTCAACAGTGGGCATGGACAGGGTTAATGTCTCCAG  
AGTGTAACACTGCAGGCAGCCACATTTACACGCTGCAGTTGTTTTCCGGAGTCTGTCCCACGG  
CCCACACGCTCACTTGACTCATGCTGCTAAGATGCACAACCGCACACCCATAACAACATAAA  
GGGCCACAAAGCAACTGCTGGGTAGCTTTCCACAGACATAAATATAGTCCATCTGCAATCAC  
AAGCACATAGCCAGGTAACCCACCAACTCCCCTGGATCTGCAGCCACACGTGGGAGTCTGGC  
TGTCACCTTCACAAGCCACAGAAACGGCCACACATGTTACAGCTCACACGCCCTCTCCATTC  
ATCGAACTTCTCAGTGTCCCTGTCCCTGGTGCCTGGCACAGGGAACAGCATGCCCCCTCCGGG  
GTCATGCCACCCAGAGACTGTGCTGTCTATGGCCCCAACTCATGCTCCCTCTCTTGGCTACA  
CCACTCTCCCAGCCTGTGACCACCGATGTCCACACACCCCCAACCCTTGTCACACAGCTAC  
CCACGTACAACATCGTCCTGGCTCCCCAGAGTATCTTCCCACTGAGACACGCCGCCCCCACAG  
AGGCACAGTCCCCAGCCACCTCTGCAACTGCAGCCCTCAGTCACCCCTTTTAAAGCACCTGA  
TTCTACCAAATGCAAACACATCTGGGTCTGCGATTATGCACAGAGACTTTGGACATACGAGGA  
CCCTCAGACCGGAGGAACACCTGCCCAACCCCAACACGTGCTTATGTAACCACGTGGAAAGCG  
GCCCCTGCTGCCCTCCACACACATACACACTCACTGATCTACAGCCCCTGTTTCGGCGTCA  
GAGTCCCCACTAGACCCAGTGGAAGGGGTTAGAGACCAAGTAGGGGCCAGTTTCCAATTCACC  
CTGTCAGGGAGTGAGCCGGATCTGACGTTCTTGTGACTTAAGGGTCCGGCTTGGGAATTA  
GTTTGTCTTCTGGCCTTTAGCCTAAAAA

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**FIGURE 64**

MEATGTWALLLALALLLLTLALSGTRARGHLPPGPTPLPLLGNLLQLRPGALYSGLMRLSKK  
YGPVFTIYLGWPWPVVVLVGQEAVERALGGQAEFEFSGRGTVMLEGTFDGHGVFFSNGERWRQ  
LRKFTMLALRDLGGMKREGEELIQAEARCLVETFQGTEGRPFDPSSLQAQATSNVCSLLFGL  
RFSYEDKEFQAVVRAAGTLLGVSSQGGQTYEMFSWFLRPLPGPHKQLLHHVSTLAAFTVRQV  
QQHQGNLDASGPARDLVDAFLLKMAQEEQNPGTEFTNKNMLMTVIYLLFAGTMTVSTTVGYTL  
LLMKYPHVQKWVREELNRELGAGQAPSLGDRTRLPYTDAVLHEAQRLALVPMGIPRTLMRT  
TRFRGYTLPQGTEVFPLLGSILHDPNIFKHPEEFNPDRFLDADGRFRKHEAFLPFSLGKRVCL  
GEGLAELFLFFTILQAFSLESPPDPTLSLKPTVSGLEFNIPPAFQLQVRPTDLHSTTQTR

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 294-313

**Glycosaminoglycan attachment site.**

amino acids 99-103

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 128-132

**N-myristoylation sites.**amino acids 51-57, 109-115, 115-121, 188-194, 207-213, 257-263,  
284-290, 339-345, 370-376, 444-450**Amidation sites.**

amino acids 140-144, 435-439

**Leucine zipper pattern.**

amino acids 32-54, 39-61

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 433-443

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**FIGURE 65**

CGGACGCGTGGGGCCGTATGCGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCCC  
CCAGCCCCCTGCTCCTTTGGACTCTACTTCTGTTTGCAGCCCCATTTGGCCTGCTGGGGGAGA  
AGACCCGCCAGGTGTCTCTGGAGGTCATCCCTAACTGGCTGGGCCCCCTGCAGAACCTGCTTC  
ATATACGGGCAGTGGGCACCAATTCCACACTGCACTATGTGTGGAGCAGCCTGGGGCCTCTGG  
CAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCTGAGCATCAACTGGAGCCTCCTGC  
TATCCCCTGAGCCCGATGGGGGCCTGATGGTGCTCCCTAAGGACAGCATTAGTTTTCTTCTG  
CCCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGC  
CTTTGGGAAGACCATATCCTCCATACTCCTTGCCGATTTCTCTTGGAACAACATCACTGATT  
CATTGGATCCTGCCACCCTGAGTGCCACATTTCAAGGCCACCCCATGAACGACCCTACCAGGA  
CTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCTTTTCCAGGTCCAGCCGACCAGCCC  
AACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCTGATTGGAGCCT  
CTCCCCGGGGAAACCGTTCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGACT  
GCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGG  
ACCAGCTACTGTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCC  
AGAAGCCGGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTTCCCCTCTTCATCCTGCCTTAG  
CATACTCTCTTCCCCAGTCACCCATTGTCCGAGCCTTCTTTGGGTCCCAGAATAACTTCTGTG  
CCTTCAATCTGACGTTTCGGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT  
GGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCCCACTAGTCCTGGGCA  
TCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGGTTCTGCTGC  
TGCACCACAAGAAGTACTCAGAGTACCAGTCCATAAATTAAGGCCCGCTCTCTGGAGGGAAGG  
ACATTACTGAACCTGTCTTGCTGTGCCTCGAAACTCTGGAGGTTGGAGCATCAAGTTCCAGCC  
GGCCCCCTTCACTCCCCCATCTTGCTTTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCCTGG  
AGACCCCCAGGTGGGGCTTCCTTCATACTTTGTTGGGGGACTTTGGAGGCGGGCAGGGGACAG  
GGCTATTGATAAGGTCCCCTTGGTGTTGCCTTCTTGCACTCTCCACACATTTCCCTTGATGGG  
ACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGA  
TTTATTTTTTTTTCACAGGGAAAAAAAAAAAA

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**FIGURE 66**

MRGSVECTWGWGHCAPSPLLLWTLLLFAAPFGLLGEKTRQVSLEVIPNWLGPLQNLLHIRAVG  
TNSTLHYVWSSLGPLAVVMVATNTPHSTLSINWSLLLSPEPDGGLMVLPKDSIQFSSALVFTR  
LLEFDSTNVSDTAAPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHMNDPTRTFANGS  
LAFRVQAFSRSSRPAQPPRLLHTADTCQLEVALIGASPRGNRSLFGLEVATLGQGPDCPSMQE  
QHSIDDEYAPAVFQLDQLLWGSLSGFAQWRPVAYSQKPGGRESALPCQASPLHPALAYSLPQ  
SPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGFPPVDGLSPLVLGIMAVAL  
GAPGLMLLGGGLVLLLHHKKYSEYQSIN

**N-glycosylation sites:**

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234,  
333-337

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 397-401

**Casein kinase II phosphorylation sites:**

amino acids 151-155, 249-253, 255-259

**N-myristoylation sites:**

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

**Leucine zipper pattern.**

amino acids 371-393

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**FIGURE 67**

[illegible]

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**FIGURE 68**

MFPLRALWLWVWALLGVAGSCPEPCACVDKYAHQFADCAKELREVPEGLPANVTTLSSLANKI  
TVLRRGAFADVTQVTSWLAHNEVRTVEPGALAVLSQLKNLDLSHNFISFPWSDLRNLSALQ  
LLKMNHNRGLGSLPRDALGALPDLRSLRINNRLRTLAPGTFDALSALSHLQLYHNPFHCGCGL  
VWLQAWAASTRVSLPEPDSIACASPPALQGVVYRLPALPCAPPSVHLSAEPPEAPGTPLRA  
GLAFVLHCIADGHPTPRLQWQLQIPGGTVVLEPPVLSGEDDGVGAEEGEGEGDGDLLTQTQAA  
TPTPAPAWPAPPATPRFLALANGSLLVPLLSAKEAGVYTCRAHNELGANSTSIRVAVAATGPP  
KHAPGAGGEPDQGAPTSEKSTAKGRGNSVLPSKPEGKIKGQGLAKVSILGETETETEPEEDTSE  
GEEAEDQILADPAEEQRCGNGDPSRYVSNHAFNQSAELKPHVFELGVIALDVAEREARVQLTP  
LAARWGPGPGGAGGAPRPGRRPLRLLYLCPAGGGAQVQWSRVEEGVNAYWFRGLRPGTNYSVC  
LALAGEACHVQVVFSTKKELPSLLVIVAVSVFLLVLATVPLLGAACCHLLAKHPGKPYRLILR  
PQAPDPMEKRIAADFDPRASYLESEKSYPAGEAGGEEPEDVQGEGLDEDAEQGDPSGDLQRE  
ESLAACSLVESQSKANQEEFEAGSEYSDRLPLGAEAVNIAQEINGNYRQTAG

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 587-610

**N-glycosylation sites.**

amino acids 52-55, 121-124, 337-340, 364-367, 474-477, 563-566

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 397-400

**Casein kinase II phosphorylation sites.**amino acids 19-23, 202-205, 289-292, 246-249, 411-414, 431-434,  
433-436, 440-443, 544-547, 583-586, 650-653, 700-703**N-myristoylation sites.**amino acids 15-20, 48-53, 165-170, 296-301, 351-356, 362-367,  
390-395, 419-424, 514-519, 536-541, 557-562, 561-566, 610-615,  
661-666, 716-721**Amidation site.**

amino acids 522-525

**Prokaryotic membrane lipoprotein lipid attachment sites.**

amino acids 10-20, 603-613



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**FIGURE 69**

GGCGGCGGGAGCAGCGAAGGGGGCGGCAGGGATCCTCCAGGCTGCCGGCTGGGAAGGCGTGGG  
CGACCCGGTGTGTGGCGCGCCCAGAGCCCCGCGTTTCAGCCCTAGGGAAGGAAGCCAGTTGAG  
GGAAGTTCTCCATGAATGTACGTCACA**ATG**ATGATGACCGACCAAATCCCTCTGGAACCTGCCA  
CCATTGCTGAACGGAGAGGTAGCCATGATGCCCCACTTGGTGAATGGAGATGCAGCTCAGCAT  
GTTATTCTCGTTCAAGTTAATCCAGGTGAGACTTTCACAATAAGAGCAGAGGATGGAACACTT  
CAGTGCATTCAAGGACCTGCTGAAGTTCCCATGATGTCACCCAATGGATCCATTCTCTCCCAT  
CATGTGCCTCCAGGTTATATCTCACAGGTGATTGAAGATAGTACTGGAGTCCGCCGGGTGGTG  
GTCACACCCCAGTCTCCTGAGTGTTATCCCCAAGCTACCCCTCAGCCATGTCTCCAACCCAT  
CATCTCCCTCCCTATCTGACTCACCATCCACATTTTATTTCATAACTCACACACGGCTTACTAC  
CCACCTGTTACCGGACCTGGAGATATGCCGCCTCAGTTTTTCCCCAGCATCATCTTCCCCAC  
ACAATATATGGTGAGCAAGAAATTATACCATTTTATGGAATGTCAAGCTACATCACCCGAGAA  
GACCAGTACAGCAAGCCTCCGCACAAAAAAGTGAAGACCGCCAGATCGATCGCCAGAACC  
CTCAACAGCCCTCCTTCTTCTATCTACAAAAGCAGCTGCACAACAGTATACAATGGCTATGGG  
AAGGGCCATAGTGGTGGAAGTGGCGGAGGCGGCAGCGGTAGTGGTCCCGGAATTAAGAAAAA  
GAGCGACGAGCAAGAAGCAGCCCAAAGTGAATGATTGAGACTTGCAAGAATATGAGTTGGAA  
GTAAAGAGGGTGCAAGACATTCTTTCGGGAATAGAGAAACCACAGGTTTCTAATATTCAGGCA  
AGAGCAGTTGTGTTGTCTGGGCTCCCCCTGTTGGACTTTCCTGTGGACCCACAGTGGTCTT  
TCCTTCCCTTACAGTTACGAGGTGGCCTTATCAGACAAAGGACGAGATGGAAAAATACAAGATA  
ATTTACAGTGGAGAAGAATTAGAATGTAACCTGAAAGATCTTAGACCAGCAACAGATTATCAT  
GTGAGGGTGTATGCCATGTACAATTCGTAAGGGATCCTGCTCCGAGCCTGTTAGCTTCACC  
ACCCACAGCTGTGCACCCGAGTGTCTTTCCCCCTAAGCTGGCACATAGGAGCAAAAGTTCA  
CTAACCTGTCAGTGGAAAGGCACCAATTGACAACGGTTCAAAAATCACCAACTACCTTTTAGAG  
TGGGATGAGGGAAAAAGAAATAGTGGTTTCAGACAGTGCTTCTTCGGGAGCCAGAAGCACTGC  
AAGTTGACAAAGCTTTGTCCGGCAATGGGGTACACATTCAGGCTGGCCGCTCGAAACGACATT  
GGCACCAGTGGTTATAGCCAAGAGGTGGTGTGCTACACATTAGGAAATATCCCTCAGATGCCT  
TCTGCACCAAGGCTGGTTCGAGCTGGCATCACATGGGTACGTTGCAGTGGAGTAAGCCAGAA  
GGCTGTTACCCGAGGAAGTGATCACCTACACCTTGGAATTCAGGAGGATGAAAATGATAAC  
CTTTTCCACCCAAAATACACTGGAGAGGATTTAACCTGTACTGTGAAAAATCTCAAAAGAAGC  
ACACAGTATAAATTCAGGCTGACTGCTTCTAATACGGAAGGAAAAAGCTGTCCAAGCGAAGTT  
CTTGTTTGTACGACGAGTCCTGACAGGCCTGGACCTCCTACCAGACCGCTTGTCAAAGGCCCA  
GTTACATCTCATGGCTTTAGTGTCAAATGGGATCCCCCTAAGGACAATGGTGGTTCAGAAATC  
CTCAAGTACTTGCTAGAGATTACTGATGGAATTTCTGAAGGTGAAGTTTTTGGCAATTGTTTT  
ATTCAAATCCA**ATAG**CAAGCTCTGTTTTCTAATATAGTAAATGTCTTTATAGTAATAGTGAGT  
AATCATTAATTCTAAAGATAGAATTATTATTACAATAAAACAACTTTAGTCACATATTGGCAG  
TTTTTCTATTTCAAACACAGCACCAGAGATCAGAGTCTACTTGAACTTACATTTGTGTTATT  
TAACAATTTTTCTGTATCTTTTTTCATTGGTGTTTTGTGTTTATCTTTTGTGTTTTGTTTCT  
TTGGTTTGGTTTGTGTTTTGTTTTGTTTTGAGATACGATCTCTGTACACAGGCTGGAGGGC  
AGTGGCACAGACATGGCCCATGTCAGTCTCAGACTCCTGGGCTTAAGTGACTCTTCTGCCACA  
GAAGATGAGGAAGAATACATTTTTTCATAGTGATGGGGTCTCACTATGTTATCTAGGCTGGTCT  
CAAACCTCTGGCCTCAAGCAACCCTCCACCTTGGCCTCCCAAAGTGCTGGGACTATAGACATG  
AATCACCACACTCAGCTTCCATGTCTTTTTATGAACTAGGGTTCCTAATTAATCAGATAAATT  
TGGTATTTTCATCTCCTAACTTGCCATATGTTTTCTGGAAATTCCTATAAGCAGCCGAGAGTG  
GTGGCTCACGCTGTAGTCCCAGCACTTTGGGAGGCTGAGGTGGGTGGTCAGGAGATCAAGACC  
ATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGTGTGGTG  
GCAGGCACCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGAAGAATTGCTTGAACCCAGCAG  
GCGGAGGTTGCAGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGTGACAGAGTGAGACTC  
TGCTCTCAAAAAAAAAAAAA

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**FIGURE 70**

MMMTDQIPILELPPLLNGEVAMMPHLVNGDAAQHVILVQVNPGETFTIRAEDGTLQCIQGPAEV  
PMMSPNGSIPPIHVPPGYISQVIEDSTGVRRVVVTTPQSPECYPPSYPSAMSPTHHLPPYLTHH  
PHFIHNSHTAYYPPVTGPGDMPPQFFPQHHLPHTIYGEQEIIIPFYGMSSYITREDQYSKPPHK  
KLKDRQIDRQNRNLNSPPSSIIYKSSCTTVYNGYGKGHSGSGSGSGSGPGIKKTERRARSSPK  
SNDSDLQEYELEVKRVQDILSGIEKPQVSNIQARAVVLSWAPPVGLSCGPHSGLSFPYSYEVA  
LSDKGRDGGYKIIYSGEELEC�LKDLPATDYHVRVYAMNSVKGSCSEPVSFTHSCAPECP  
FPPKLAHRSSSLTLQWKAPIDNGSKITNYLLEWDEGKRNSGFRQCFFGSQKHCKLTKLCPAM  
GYTFRLAARNDIGTSGYSQEVVCYTLGNIPQMPSAPRLVRAGITWVTLQWSKPEGCSPEEVIT  
YTLEIQEDENDNLFHPKYTGEDLTCTVKNLKRSTQYKFRLTASNTEGKSCPSEVLVCTTSPDR  
PGPPTRPLVKGPVTSHGFSVKWDPPKDNGGSEILKYLLEITDGNSEGEVFGNCFIQIQ

**Important features of the protein:****N-glycosylation sites.**

amino acids 69-73, 254-258, 401-405

**Glycosaminoglycan attachment sites.**

amino acids 229-233, 234-238, 236-240

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 416-420, 535-539

**Tyrosine kinase phosphorylation site.**

amino acids 319-326

**N-myristoylation sites.**amino acids 52-58, 227-233, 228-234, 230-236, 231-237, 232-238,  
235-241, 239-245, 402-408, 610-616**Amidation site.**

amino acids 414-418

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 290-301

**ATP/GTP-binding site motif A (P-loop).**

amino acids 546-554

**CUB domain proteins profile.**

amino acids 294-301

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**FIGURE 71**

AAGTCATTCAAGTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTT  
GCTGTAACCTGCTGCTCAGTCCACCATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAAACCAGGAAGCCGAA  
GACCTGTTCTATCAAAGTTCACCTTGCTTCTTGGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATG  
AATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCCCAATGTATCCACTACAAGAA  
ATTGAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTCAGTGTCTCAGAAGACAAG  
AGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAAACCCAGATAAT  
CCACAAGAATGCTTATTACTTGAACCAGGTTTGAATGAAATAATGGCAACAGTTTAGACTACAATGAGAGGCTC  
TGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTTGAAA  
AATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGACTATGAAGTAAATGGGGTA  
GATGGCTATGACTACAGCCGCGGCCAGTTGATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATAT  
GAACATCTTCATGCCTATGTGAGGGCAAAGTTGATGAATGCCTATCCTTCTATATCAGTCCAATTGGATGCCTC  
CCTGCTCATTGCTTGGTGATATGTGGGGTAGATTTTTGGACAATCTGTACTCTTTGACAGTTCCCTTTGGACAG  
AAACCAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAGAATATTCAAGGAGGCCGAG  
AAGTTCTTTGTATCTGTTGGTCTTCTTAATATGACTCAAGGATTCTGGGAAAATTCATGCTAACGGACCCAGGA  
AATGTTTCAGAAAGCAGTCTGCCATCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACA  
AAGGTGACAATGGACGACTTCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGCTGCA  
CAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGAAAATCATGTCACTTTCTGCA  
GCCACACCTAAGCATTTAAAATCCATTGGTCTTCTGTCAACCCGATTTTCAAGAAGACAATGAAACAGAAATAAAC  
TTCCTGCTCAAACAAGCACTCACGATTGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGGTGGATG  
GTCTTTAAAGGGGAAATTTCCCAAAGACCAGTGGATGAAAAGTGGTGGGAGATGAAGCGAGAGATAGTTGGGGTG  
GTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCCGCATCTCTGTTCCATGTTTCTGATGATTACTCATT  
ATTGATATTACACAAGGACCCTTTACCAATCCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGC  
CCTCTGCACAAATGTGACATCTCAAACCTACAGAAGCTGGACAGAACTGTTGTAAAGAAATACCTCAAATGTT  
GAACCTCTCCTAGTATTAGTATTACTCATTCCATGCCTAGGTTTGTATTTGATTTCTTTGTTCTAAAAAGAAA  
ATTTTATGGCCTCAAATGTCTCATTACAAACCAAAACATTTAATTTGTGGTCAGACAGGAACCTAGACCATAC  
AACAATTGGGTGGGCCACCTCTTTCTCCCTATCATACTACAGCCCTCTCTTCTGGTAATTGGAAGGAAAGAG  
CGGTTTAGGGTGGAAATATATCTGTTAATATGCATTCTTTCTTATCTGCCAGAAGCAAATTTAGCCAAGTCAAAG  
AGAAGAAACCATAGATCATAGATGTAATATATGTACATCTGGAACCCCTCAAAGGCCCTGAACCCCTTTTTTT  
TGTGTAGCAATATGCTGAGGCTTGAAAATCAGAACCCCTGAGCCCTAGCATTGAAAATGTTGTAGGAGCAAGAA  
CATGAATGTAAGCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAAGATTTCTTT  
TGTGGGATGGAGTACCGACTGGAGTCCATATGCAGACCCAAAGCATCAAAGTGAGGATAAGCCTAAATCAGCTC  
TTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATATGCTATGAGGC  
AGTACTTTTTTAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAA  
GAATCTCCTTTAATTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCTAGAACTGAAGTTGAAAAGG  
CCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATAC  
AGCCAACACTTGGACCTCCTAACAGCCCCCTGTTCCATATGGCTGATTGTTTTTGGAGTTGTGATGGGAGTGA  
TAGTGGTTGGCATTGTCACTCCTGATCTTCACTGGGATCAGAGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAG  
AAAATCCTTATGGCTCCATCGATATTAGCAAAGGAGAAAAATAATCCAGGATTCCAAAACACTGATGATGTTTCAGA  
CCTCCTTTTAGAAAAATCTATGTTTTCTCTTGGAGTGATTTTGTGTATGTAATGTTAATTTATGGTATAG  
AAAATATAAGATGATAAAGATATCATTAAATGTCAAACCTATGACTCTGTTCAAGAAAAAATTTGTCCAAAGACA  
ACATGGCCAAAGGAGAGAGCATCTTCATTGACATTGCTTTTCAAGTATTTATTTCTGTCTCTGGATTTGACTTCTGTT  
CTGTTTCTTAATAAGGATTTTGTATTAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTTCAAGGGA  
TAATCTAAATGTAATGTCTGTTGAATTTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTGGATCT  
TGTATGGAATATGGATGGATCACTTGTAAAGACAGTGCCTGGGAACCTGGTGTAGCTGCAAGGATTGAGAATGGCA  
TGCATTAGCTCACTTTCAATTAATCCATTGTCAAGGATGACATGCTTTCTTCACAGTAACTCAGTTCAAGTACTA  
TGGTGATTTGCCACAGTGTATGTTTGAATCGATCATGCTTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATC  
CAGGGAACAGGTAGAGGACATTGCTTTTTCACTTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAAAACCTA  
GAGCCAGGGGCTCCGTGAACCTCCCAGAGCATGCCTGATAGAACTCATTTCTACTGTTCTCTAACTGTGGAGT  
GAATGGAAATCCAACCTGTATGTTCAACCTCTGAAGTGGGTACCCAGTCTCTTAAATCTTTTGTATTTGCTCACA  
GTGTTTGAGCAGTGTGAGCACAAAGCAGACACTCAATAAATGCTAGATTTACAAAA

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**FIGURE 72**

MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMN  
NAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTI  
YSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNE  
MARANHYEDYGDYWRGDYEVNGVDGYDYSRGLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY  
PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFQKPNIDVTDAMVDQAWDAQRI FKEAEKFF  
VSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGGH  
IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLK  
QALTIVGTLFPFTYMLEKWRWMVFKGEIPKDQWMKKWEMKREIVGVVEPVPHDETYCDPASLF  
HVSDDYSFIRYYTRTLYQFQFQEQEALCQAAKHEGPLHKCDISNSTEAGQKLL

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 53-57, 90-94, 103-107, 322-326, 432-438, 546-550

**N-myristoylation sites.**

amino acids 260-266, 286-292, 395-401

**Cell attachment sequence.**

amino acids 204-207

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 371-381

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**FIGURE 73**

CCCACGCGTCCGAGCGGGGTGGACAAAGTGGCGTGTGTGCTGCGACCCCGAGGGAAGATGAACG  
GGACGCGGAAGTGGTGTACCCTGGTGGACGTGCACCCAGAGGACCAGGCGGCGGGCAGGA  
AGACCTATGCCATGGTGTCCAGCCACTCAGCTGGTCATTCTCTGGCTTCAGAACTGGTGGAGT  
CCCATGATGGACATGAGGAGATCATTAAAGGTGTACTTGAAGGGGAGGTCTGGAGACAAGATGA  
TTCACGAGAAGAATATTAACCAGCTGAAGAGTGAGGTCCAGTACATCCAGGAGGCCAGGAAGT  
GCCTACAGAAAGCTCCGGGAGGATATAAGTAGCAAGCTTGACAGGAACCTAGGAGATTCTCTCC  
ATCGACAGGAGATACAGGTGGTGTAGAAAAGCCAAATGGCTTTAGTCAGAGTCCCACAGCCC  
TGTACAGCAGCCACCTGAGGTGGACACCTGTATAAATGAGGATGTTGAGAGCTTGAGGAAGA  
CGGTGCAGGACTTGCTGGCCAAGCTTCAGGAGGCCAAGCGGCAACACCAGTCAGACTGTGTGG  
CTTTTGAGGTCACACTCAGCCGGTACCAGAGGGAAGCAGAACAAAGTAATGTGGCCCTTCAGA  
GAGAGGAGGACAGATGTCCAGAGTGATTGGAGAATGTCCTGGGGGAATGAAGTTCCTTCCACA  
AACACAGCTCAGTTCTTAGCAACAACTGTTTGTCTTTCTACTTGCTCCATCTGCAGCCTACG  
CTGCCCTGGCCTCCTGCAGACAGATAGTGGGGTTACCTGGCAAGGCCTGGTGAGAGCCAGTGA  
ACCTAAGCTTTGACTGGGTGGCCTTGTCTTTCTGGGGAGGAGGGAATGTACATTCAGGGAGTA  
GCCTTTTGCGGAAAAATTCTCTAGGGCTACAGACAGTCATGTGTGACTTCTCTCTGCTGTGAA  
AACTCCAGAGTCTCTTTAGGGATTTTCCCTAAGGTGTACCACCAGGCACACCTCAGTCTTCT  
TGACCCAGAGCCTGAAAAGTGTCTTCACTGGGTTCACCAGTCCCAGCAAAATCCTCTTTGTA  
TTTATTTTGCTAAGTTATTGGTGGTGTGCTTACATCTCATGATTGATATAATACCAAAGTTC  
TATAGCCTTCTCTTGCAATTTTGGATTTGCTTGAAACCGGGAAAGTGTCCCATTAGGCTT  
GTTAATGTCAGAGTGACACTATTATGAATCTTTCTCTCCCTTTCCTCTGCCTGTTTCTTCTCT  
CTTTCTCCTTCAAAGTGTCTCTGCAGCTAAGGAAGGTGAGTCTACTTTCCCTGAGGCTTTGGG  
GTCAGAGTATATGTTGTTTGGAGAAAGAGGGCAATCAGGACTCTTCTGGGACCCAGATGAGTT  
CTTCACTAGCCCTTCTGAACCCCTTGCTCCATAATTGGTCTTTTATCCTGGCTCTGAATGACC  
CTGCAGGTCATCATGGTTTTCTTTTTTTATTGTTTTTTTTTTTTTCTGAGACAGAGTCTCACT  
CTGTCACCCAGGCTGGAGTGCAGTGGCGCGATCTCAGCTCACTGCAACCTCTGCCTCCCGGAT  
TTAAGCGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGTGTGCCACCACGCCTG  
GCTGATTTTTGTATTTTGTAGTAGAGATGGGGTTTACCATACTGGCTAGGCTGGTCTCGAATT  
CCTGACCTCAGGTGATCCACCCACCTCGGCTTCCCAAAGTGCTAGGATTATAGGCTTGAGCTA  
CTGCGCCCCGGCCCATGGTGTCTTTCTTTAGGGCTCTTCCCTACAGCCTTGAGAAGTAGATAGGC  
ATCAGAGTATGGTACTATAGGAATCAGAAAAATTCAAACAAATGTGGATTAAAGTGTTTAGGC  
TCTATGTGGCTCACGCAGCCAGAATCCTTAAGTCTGTGTGTTTCTGTGTCTCAAGACTGGGCT  
CACATTCTGGCTTTGTCCATAACAATGCTCTGGGATTTTCAAGGAGTTCCTCATTTGTAAAAT  
GAGGGGGTCAGAGCAGGTGATATCCATGTTTCTTCCCTTCTGATATTGTTGTCTGTGGCATA  
TTCTTTGTATGGCGAATTTAATAAATTATATTAATGTGTCA

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**FIGURE 74**

MNGTRNWCTLVDVHPEDQAAAGRKTYAMVSSHSAGHSLASELVESHGHEEIIKVYLKGRSGD  
KMIHEKNINQLKSEVQYIQEARNCLQKLREDISSKLDRLGDSLHRQEIQVVLEKPNGFSQSP  
TALYSSPPEVDTCINEDVESLRKTVQDLLAKLQEAKRQHQSDCVAFEVTLSTRYQREAEQSNVA  
LQREEDRCPE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-39

**N-glycosylation site.**

amino acids 2-6

**Amidation site.**

amino acids 21-25

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**FIGURE 75**

GCTTGCACACATGGCTCCGGAGGCTCCGGTTGCCCATCCGAGCCCCTGCCAGGCTCTAACGTTCCCAACTGACAA  
CACCAGTAACTAAATATAGGAGCAGATGGTGGGGACGGGCTGTGCGAGCGGCTCCTTTGCAGAGGTCTCCGGACT  
GCAGATAAGGCTCAGGCCCTTTTGTGAGAAGCAGACCAGCCTGGGGGCTGGCGGCAGGACACCTGTGTCTGCATG  
CTGAAGAAGATGGGTGAGGCCGTGGCCAGAGTAGCAAGGAAGGTCAACGAGACGGTGGAGAGCGGCTCTGACACT  
CTGGACCTGGCCGAGTGCAAGCTGGTCTCCTTTCCATTGGCATCTACAAGTCTGCGGAATGTCTCTGGCCAG  
ATCCACCTCATCACCTGGCTAACAACGAGCTTAAAGTCCCTCACCAGCAAGTTCATGACCACATTAGTCAGCTC  
CGAGAGCTCCACCTGGAGGGGAACCTTCTACACCGCTCCCCAGCGAGGTGAGTGCCTGCAGCACCTCAAGGCC  
ATTGACCTGTCCCGAACCAGTTCAGGACTTCCCTGAGCAGCTTACCGCCTGCCGGCGCTGGAGACCATCAAC  
CTGGAGGAGAACGAGATCGTAGATGTGCCCGTGGAGAAGCTGGCCGCCATGCCAGCCTTGCGCAGCATCAACCTC  
CGCTTCAACCCACTCAACGCCGAGGTGCGCGTGATCGCCCCGCCGCTCATCAAGTTTGACATGCTCATGTCTCCG  
GAAGGCGCAAGAGCCCCCTACCTTAGGCCACCCTCCTCATGCCACCCAGCAAGGGACAGAGGCCACAGGCCTG  
GAACCCTGGAAGGGAGGGAGGCCCATGGGAGGCCAAGCCTGGGGGCTGGGGGCGGCTGGGGCCGAGCAGCAGTGG  
TGGGTGGGGTGCAGCTGGTCTGGATAGATAGCTTACAGCAGTAGTGGGCTCTGGAATGCCAAGGGAAGAGGCAA  
GGTGGGGCCTGCAGCCTGGACTCGGCACTCACAGCTGCTGTGCAAACTCAGGCAGATCTCCTGCCCTCTCTGAGC  
CTTGTCACCTTGAAAAAACAGGACCCTTTCCCTCCTTTGGGCTCCCTGGAGGTTTTAAAGCAGTACGTGCCTCCA  
AGTTACCTCCAGATCAGCAGGCACAGGTGGGCATTGCCAGGTATTTTCTGAGCCCCCTGCGGGTTTGAGGCCTTGT  
TTTTAGTGCTGAGAGCCAGTTGCTGCCCTGAGAAGAGAAGACAACCTCCATCTATTTATTGCTTCTGAGAACTG  
ACCTGGATGCGGCCCTCTGCAGGGCCAGTCTTCAGTCTGTGGTCCCTGGACTGGTGGGAACCTGAAGTAGGAG  
TCCTGGGAGAGCTGTGGTGGGAATATGGGCTGGCACTGCTGCAGGGCAAGAACATTCATGTAGGAGCCCGAGGAC  
CANCANGCTGGGAATGGGAGCAAGTCACGTGAGCTGTGTCATTCCCCACAGTTAACAAATTGGCGGGGTGGGAA  
GTCCTGAGTGCTCCGTCCCTCTAGCATCACTCTGAGCTGCGGGAGAGGTGGCCAGAGAACAGCAGAGTCAGTT  
ACACCTGCAGCTCTTGTCTAAAGTGATTAGATGGCCACCCTCACCAGTGTCCAGTCCAGCAGCAGCCTGGCTGCC  
TTGTCTATGGCCTCCTGGGGGAGAAGGCGATGTGGACCACGGGATTTGTAGCCAGCCAGCTCCCAGGCCAACGCC  
CAAAGCCCTGATGACCTGGTTCTTCTGAGGCCCTCAACCTGGCATCTTAGGGTATGGTCAGGCAACAGGGTGACC  
AGCTGTCTGGTTTCCAGGACATGGAACCTTCAATGCTAAACTGGGACATTACCCAGCAAGTGGGGATGGTTG  
GTCCCCTACCAGGAGAGGGCCTGGGGCTCTTGCTTCCCGAGAAGCCTGTGGCTTGAAGAACCTTGACTGCTTGG  
TCCTCAGGTATCTACCTCCACCTTCTCCTCATCTGTGGAGCAAGCCAACTCAGTGCCCCAGACCCACCTGATC  
TGCATCTTTGTTTGTCTCCAGAGACACCTGAGGCCCCAGAGCTTGAGGCAAGCCAGGCCGTCCAAATCCTGTGTG  
CCGTGGACGAGTGGCCACTTTACTACTCCTAAGGCTAAGATGTTGAGAGCTCAGACCACTGCTCAGAGCAGTAAT  
CCCTGCTCAGAACTGCTCCAGTTCCCTCGTCCCTGCCAGGTCTCTTGTCTCTTGGGAAGGAAGTATAGGTCGG  
GCCATTGTTGGGCCATCACTGAGCGCTCAGTATCTCAAGAGACTCTGTTTATTCTGCTCGTATCCCAAGGCCTGG  
TTGGTCAAACCTCTGGGCAAAGGGTTTTTCAGGATGAGGAGGTCAAGACAGGATGTCCAGAGCTACCGAGTTCATCT  
GTGGGTGTTGGGGCAAGTGGGGGCTGAAGTCTGTGAGGCTGCGCTGGCCCCACCTGCCTTGTGCCCTGGAGT  
GGGGTTTTCTCCTGTTGAAGAAGAGGCATCCTTCTCTGATGTGCACAAACACAATGTATGACCAGAGCCTTGCAA  
CTCAAAGTGTGGTCTGTGGACCAGCAGCGGCAGTGACACCTGGGAGCTTGTAGGAATGCAGAGTCTAGGCCTCA  
CCCTATACCTCCCGACTCAGACCCTGCATTTTAGCAAGACCCCCAGCTGATTCTATAAGCACTTTAGAGTTTGA  
GAAGCAAGGACCTAGGCTGGGGATGTCTCCGAGCAGAGGGTGAAGTTTCTCAGTCTCTCCCTGCCACTTCC  
AGGGATCTGAGCCTGTGTTGAGCCTCCTCCCTAACCCACCCTGGGAGACACTTGGCCTGTTAGATTGTTCCAGAG  
TCTGCATGGCACTCCTGAAGAAGGGAGTGTGACCTGCAGTACCAGGAGATGAGGGTAGGTGTGCCAGCCCTC  
CAGACCCGGCCTTCTGGTTAACCCCTGCATGCCAAGCTGCCTGCTGCCCCAGGTCTCACCTCAGGCCTTTGAA  
GGGGCAGCTTCTGGAAGTTGTTTTCTCCTCTGCTTGGAGAGTTTGGCCTTGTCTGTCTTGGAAAGTGTGGGCAGC  
CACAGATGCCCCCAATCAGAGCTCACAGTGAGTGAGCCCCTAAGCTTCAGTCTGCAATAAAGAATGCATTGGTT  
TCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 76**

MLKKMGEAVARVARKVNETVESGSDTLDLAECKLVSFPIGIYKVLNRNVSGQIHLITLANNELK  
SLTSKFMTTFSQLRELHLEGNFLHRLPSEVSALQHLKAIDLSRNQFQDFPEQLTALPALETIN  
LEENEIVDVPVEKLAAMPALRSINLRFNPLNAEVRVIAPPLIKFDMLMSPEGARAPLP

**Important features of the protein:**

**N-glycosylation sites.**

amino acids 17-21, 47-51



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**FIGURE 77**

CACCAACAAGCAATCGTTCATGAGAAAGCCGTGCACCCGCTGCAGTTGGGCCATGTGGTCCGCATCGTATTCCAC  
TAGGTCCCCATTGTACACCAAGTACTGTCCCGGCGTCTCCAGCAGATGCCTGCAGCCTTCCACCTTCTCAAGCAG  
GGTGGTGTGAGTGCCTGCTTTCTTCCCTCGCTGGACCGGAGCCGTGCGGGGAGGCACCCCGGGGGTGGAGAA  
AAAGCCGGCCTGGCCTCGGAGGTGGTCTCGGCCCCCGCCCCACCGACTCCCTCCTCCCTCCAGAGGCGGCGGC  
GGCTCCGGCGGCAGCAGCGGCAGGCAGCAACGTAAGCGGGATGCTCTCCAGGCTGCTTTTCTGCTCGGTACAGCA  
ATGGCTGAGCTGGTACATCTCGCTCTCCAGGTAGGAGATCTCGCGGGCCGTCTCTATGAACTGCCGGTAGTTCTG  
GTAGACGTTGCGCTTCAGGTTCTGCGCCGTCTCCTCCGCCAGCGCCTGGATGCGCTGCCGGTGTCTTGGAGGTC  
CCGGTCCCCATCCGACTGCTGCGAGAGCTGCTTACGTACAGCCGCGCCTCAAACCCCCCTGACTCCAGCTGCCG  
ACGAGGCGGGCTCGCCCCACTGTCCGACATCGCCATCGCCATTTCTCTCCGGGTCTCACGCACTCACTGTCACTA  
TCGGCGCCGAGCCGCGCGGCTGTCTAGACCCACCCAAGGCCAACCGAGCTCCTGGGCTGAGGAAGCAGGAATG  
GGAACGAGACGAGTACGCCTGCGCCGGGTCTGAGCGTCAGACACTGCGCCTGCGCAAGTGGGCCGAGCGCAGACA  
TTGCGCCTGCGCAGCAATGCCATCGGTTAAAGCGCATGCGCAAGATGAGCTATTGCGGAAGTGAGGGGAGGGAGA  
GGCCGAGAGAAATTTCCGTACTGCGCATGAACCGAGCGTGACGTTGAGGTTTGAATAACCGGCAAAGAGTAAAG  
GCTGAAACTAGCTTCTGAAAGCTTCGTAGGGCCGAGCCCTGTGAGCCAGGTTCTGCGCCCACTAGGAGGTGT  
CATGCTGACTGCTTTTAAAGCCCTAGAATCCTTGGCTTCGGCGTTTGGGGTAAGCTCCGTTCTCGTTCTCAA  
GCGCGTTTCCGCGAATCTCGCGGGATTGACGGGCGTCTCGAGAGCCGGCATCTCCTAGGAGCTAGTCTGGTC  
CTCGGCTAGGCGGCTTGGGGTCGCGGCGTAACCTGGGGAGCCAGCCTGACGCCGCGGACCCCGCCTGTGATCCTG  
GCAACGATGGATGATGACTTGATGTTGGCACTGCGGCTTCAGGAGGAGTGGAACCTGCAAGGAGGCGGAGCGCGAT  
CATGCCCAGGAGTCCCTGTGCTAGTGGACGCGTCTGGGAGTTGGTGGACCCACACCGGACTTGCAGGCACTG  
TTTGTTCAGTTTAAAGCAATTTCTTGGGGCCAGCTGGAGGCGTCGAGGTGAAGTGAGCGTGCGAATGACC  
CTGTGTGCTGGGATATGCAGCTATGAAGGGAAGGTGGAATGTGTTCCATCCGTCTCAGCGAACCCTTTTGAAG  
TTGAGGCCAAGAAAGGATCTTGTAGAGACCTCCTGCATGAAATGATACATGCCTATTTATTTGTCACTAATAAC  
GACAAAGACCGAGAAGGGCATGGTCCAGAAATTTGTAAACATATGCATCGCATCAACAGCCTGACTGGAGCCAAAT  
ATAACGGTATACCACTATTTTACGATGAGGTGGATGAGTATCGGCGACACTGGTGGCGCTGCAATGGGCCGTGC  
CAGCACAGGCCACCGTATTACGGCTATGTCAAACGAGCTACTAACAGGGAACCTCTGCTCATGACTATTGGTGG  
GCTGAGCACCAGAAAACCTGTGGAGGCCTTACATAAAAAATCAAGGAACAGAGAATTACTCAAAAAAGGCAAA  
GGAAAGGCAAACTAGGAAAGGAACAGTATTGGCCGAGAGAATAAAGGTACCTTCGTGTATATTCTTCTGATT  
TTTATGTGACCATAGCTATGATGTAAAGACAATACTGTCTTCAGAGAACTGGTATTAAGATAAACTTAAGGATC  
GTTTCTGGTGTAGAAGCTTCAAGTGTAGCTTAAGGAAAAATCCCCTGTCCATGAAATGATGGTAGGAAAC  
AGACTTTGCTCTGTACAGAAGTAAGTAAAGTAGGAATAGTTTCCATGGATATTTTTATTTTATTAACTTTTT  
CAGTTTCTTTTATTTCAAAGAAACAAATTCATCTCTGATAATATTTGAGGTAAAGTTCCTTTCCCTATCTTGA  
CTCACTGAGTTATTAGGAAACAGAAGGCAAAAGATTGTCAAATAAAAAACAATAATTCAAGTAACAATGCCCGG  
AATATACGTCCTAACTACACCCCTTCTATCAGCTGGATTCTATCCAAGTGACTCTATTGATGTATGTATGTTCA  
TTCAAAGAATGGGAAAAGGATATGACATATATTTGCCAGTACTTCATCTTCAAGATTTACCCTTTTCTGTGAAG  
TTCAGAGTTACTGAAGATGCTTCTTCCCTTGGGAAGTTGTTGACCCAAGAACATAGGTTATATTTCCCAAATCTT  
TAATTATTGAGTGAAAGAGCTATAGATGAATTGATATGGAAGACCGTATCTTCATTTTCTGTAGTAGAAGGAAA  
GATAAGAATGAGGCAGCAGATTTTCCCTCCTGGAATTACACATAAAGGACACTAAGCAATTTTCAAGGTAAATGT  
TGCCTTGTGTTGGTCTTTGGCATGATAAGATTCTTTATTTAAATATGAGAGAATTTTTTTTTATCCTTTATATT  
CTCTCAATATCAGAACCTCTGAATTCTGAAGATTGCCCTCCTCCCATTAATAGGATTGTATGGATGTAAGATGGA  
ATAAAATACTAGTCTTCAATTTGAGAAAAGTACATTAGTTTAAATGTTTGTACTGTATTTCTTTTGTAGTTGA  
GGCACTTACATAACAATCTTCTTTGCTTTTTTGGCAGATAAACCCAACAGAGGTGAGGCCAGCTAGTAATCCCT  
TTTAGTGGGAAAGGATATGTTCTAGGAGAAACAAGCAATTTACCTTCACCTGGGAACTGATCACTTCACATGCC  
ATTAATAAAACCAAGATCTTTTAAATCAAAACCATTCAGCAAATGCTGTAAGACCTAATTTCTAAAATCAAGGTG  
AAATTTGAACAGAATGGTTCAAGTAAAAATCTCATCTGGTCTCCCTGCTGTAGTAACAGTCACCAAAATGTT  
CTAAGCAACTACTTTCTAGAGTATCATTTGCCAACCAAAAGGCTTTTCAGAGGTGTGAATGGATCTCCAAGGATA  
AGTGTAAAGTTGGCAACATCCCTAAAACTCAGTCTCTTCTAGTTCTCAGAGAAGGGTTTCATCTTCTAAGATA  
TCCCTAAGAAATTTCTTCAAAAGTAACGGATCAGCATCTGTGATGCCATCCCAGGATGTGAGTGGGTCTGAAGAT  
ACATTTCCCAAATAAACGACCTAGGCTAGAAGATAAAAAAAA

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**FIGURE 78**

MDDDLMLALRLQEEWNLQEAERDHAQESLSLVDASWELVDPTPDLQALFVQFNDQFFWGQLEA  
VEVKWSVRMTLCAGICSYEGKGGMCSIRLSEPLLKLRPRKDLVETLLHEMIHAYLFVTNNDKD  
REGHGPEFCKHMRINSLTGANITVYHTFHDEVDEYRRHWWRCNGPCQHRPPYYGYVKRATNR  
EPSAHDYWWAEHQKTCGGTYIKIKEPENYSKKGKGKAKLGKEPVLAAENKGTfVYILLIFM

**Important features of the protein:****Signal peptide:**

amino acids 1-41

**N-glycosylation sites.**

amino acids 148-151, 217-220

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 184-187

**Casein kinase II phosphorylation sites.**

amino acids 30-33, 121-124, 154-157, 187-190, 192-195

**Tyrosine kinase phosphorylation site.**

amino acids 211-218

**N-myristoylation sites.**

amino acids 59-64, 85-90, 146-151

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 108-117

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**FIGURE 79**

CGGACGCGTGGGTGGCAACCAGGAGAAGCCAAACTTGGTCCCCCGGCTCGCGGAGTGCCTGCG  
AGCGGTGCTC**ATG**GCGCTCTATGAGGTCTTCTCTCACCCGGTCGAGCGCAGTTACCGCGCGGG  
GCTCTGCTCCAAAGCCGCGCTGTTCTGCTGCTGGCCGCTGCGCTCACGTACATCCCGCCGCT  
GCTGGTGGCCTTCCGGAGCCACGGGTTTTGGCTGAAGCGGAGCAGCTACGAGGAGCAGCCGAC  
CGTGCCTTCCAACACCAGGTGCTGCTCGTGGCCCTGCTCGGACCCGAAAGCGACGGGTTCCCT  
CGCCTGGAGCACGTTCCCCGCTTCAACCGGCTGCAAGGGGATCGCCTGCGCGTCCCGCTCGT  
TTCGACTAGAGAAGAAGACAGGAACCAGGATGGGAAGACGGACATGTTACATTTTAAGCTGGA  
GCTTCCCCTGCAGTCCACGGAGCACGTTCTCGGTGTGCAGCTCATCCTGACTTTCTCCTATCG  
ATTACACAGGATGGCGACCCTCGTGATGCAGAGCATGGCGTTTTCTCCAGTCTCCTTTTCTGT  
CCCCGGATCCCAGTTATACGTGAACGGAGACCTGAGGCTGCAGCAGAAGCAGCCGCTGAGCTG  
TGGTGGCCTAGATGCCCCGATACAACATATCCGTGATCAACGGGACCAGCCCCTTTGCCTATGA  
CTACGACCTCACCCATATTGTTGCTGCCTACCAGGAGAGGAACGTTACCACCGTCCTGAATGA  
TCCCAACCCCATCTGGCTGGTGGGCAGGGCCGAGATGCTCCATTTGTGATTAATGCTATCAT  
CCGATACCCTGTGGAAGTCATTTCTTATCAGCCAGGATTCTGGGAGATGGTAAAGTTTCGCTG  
GGTACAGTATGTCAGCATCCTGCTTATCTTCTCTGGGTGTTTGAAAGAATCAAGATCTTCGT  
GTTTCAGAATCAGGTGGTGACCACCATTCTGTGACAGTGACGCCCCGGGAGACTTGTGTAA  
GGAGCACTTATCC**TAG**AAAGGCCATTTCTGAAGACTCAGCAGGACCGTGGCTGCCTCATTGTC  
ATCTTCTGGGAACATCTTAGGACCTTTTGAAAGAGCCCAGCGGACACCTGCGGGCTTGTGTGC  
TTTTCCCTCAGAGACAACGGTTCTTTCCGTTTTTGCTCTACACAGTTCCGTATCTTCAGAGCT  
CCTGCAGAATTGTCAGGGACTAGTTTGTGGAAAGGTCTGAGAGTTCTGGAGGCTATAATTAG  
CTTTTTGGGTTTTCTTCTTTGCCTTAGCGTTGAATTTAGGAGAAAATTGCAGTCAGTTCAG  
ACATCTTGGAAGAGTCCCATCTCTGGTCAAGCAGAGACTTTTCTCTGTTGAACTGAGGAAC  
ACACTGTGCATTTCTTCTTCTGTTGTGAGCCACTCTTACTCTTTTCAGGGCTCTCTGTGAC  
AAACATGCCAATCACTAGCACTTGCACCCCTGGGCTTCTCCATTTCCCATTCACAGCTTTGA  
TTTCCAGAGCTGAGGCCTTTAACTGGAGACCTGGAGGGGCAGGGCCCCAAGGGCAAGGGCCGCA  
TTAGCACAGGCAATCAGGGAGGGCCGCTGAAGGACACTTGGACCGTCCACCTGCCCCAGCCCA  
ACAGTCAGTCATCTGTCATCAGCTCAGCTGAGCAGCCCTGGATCTTTGCCGTACTGTGACTGG  
GCTCTTTGCCCTATTTTTTCCCTCTGTCTGTGCCCTGGATGGCAGGCTGAAGTCAGAGGGGCT  
GTTTCATTCTCAGCCCCCTCAGCAGCACTGGGGGAAGAAAGCATTGTCACAACAGGTTCTTTC  
TGGCCCTCACCAACAGCCTGGGCACCTTGGCCCTCCTCCTCCTTGACAGCCCTCCCCCTTCT  
GCAAAGGACAGGGGCGACAGGGGTGGTGTGGGATTGGCTCCCGCTGCCTGACAACCACAAG  
TTTATTTGGAAGGCTAGCGGGAAGCCCAGCGGCTGGCGTTTCCCTGACTAAGGAACAGGGTG  
CCCATCAGAGTGGGGCGGGCAGCTTTGGGAAGGACACAAGAAGCAGTAAGAGTGTAAGAGGA  
TGCTGGCCTGGGCAGGCCAGTCCAGCCTGGCCACTAGCAGAATACCAAGCAGTCCAGTGGATT  
ACCCTCGTGGCTAAGCAAGTGTCTGCAGGAGCAGAGATGGCTGGAAGGGGCTCTGCACACGG  
AAGATGGCTTGTTCAGCCATTACCTCCTGAGGATGTGGGCAGTCTCCTCCAAGAACACATG  
GAGCTGCTTCTGATCCCAAGCAGGTCAATTGCCACTGGAAGGACATGGCCCCGGTGATCCATG  
CTTCATGCCCACCCAGAAACACACCCCTCAGTGTGTGCCTCAGTTTACTTTGGAGATCAGTTG  
TCGTTTTTAGTGCTCCTTTAGGCTTACTAAAACAGTTTTGGAAACAAAGCTATTTTGAAGTAT  
TCAAGCAGAGGAATTCCCTAACTGACCCCTTGTCTTTTTTTAATATTACAGGCTGTTTTAT  
ATGCCTAAATTTTTTTCTTAAGATCTAAACGAAAAATAGTTTCTTGTTTAAATTCACATAAGG  
CAATGAGATATGGAAAGATGACAAGATACGTATAAACATTGGTTTGCATCTTATTAAATTATT  
CTAATGCAAATCTTGTATAAAGAACCATGATGTTTTGTAACCTTTCTAATTAAAATGTTCAAA  
ATGAG

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**FIGURE 80**

MALYEVFSHPVERSYRAGLCSKAALFLLAAALTYIPPLLVAFRSHGFWLKRSSYEEOPTVRF  
QHQVLLVALLGPESDGFRAWSTFPAFNRLQGDRLRVPLVSTREEDRNQDGKTDMLHFKLELPL  
QSTEHLVGLVQLILTFSYRLHRMATLVMQSM AFLQSSFPVPGSQLYVNGDLRLQQKQPLSCGGL  
DARYNISVINGTSPFAYDYDLTHIVAAYQERNVTTVLNDPNPIWLVGRAADAPFVINAIIRYP  
VEVISYQPGFWEMVKFAWVQYVSILLIFLWVFERIKIFVFQNVVTTIPVTVTPRGDLCKEHL

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 268-284

**N-glycosylation sites.**

amino acids 194-198, 199-203, 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 51-55

**Tyrosine kinase phosphorylation site.**

amino acids 250-259

**N-myristoylation site.**

amino acids 187-193

**Cell attachment sequence.**

amino acids 307-310

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**FIGURE 81**

CCCCGGAGCTTCCCTGATGGTGGCCGCCCTCCGAGCCGGGGAGGAGCTGCCAGGGGCCAGCTGGGCAGGAGCCT  
GGGTCCGCTGCTGCTCCTGGCGTTGGGACACACGTGGACCTACAGAGAGGAGCCGGAGGACGGCGACAGAGA  
AATCTGCTCAGAGAGCAAAATCGCGACGACTAAATACCCGTGTCTGAAGTCTTCAGGCGAGCTCACCACATGCTA  
CAGGAAAAAGTGCTGCAAAGGATATAAATTTGTTCTTGACAATGCATCCCAGAAGATTACGACGTTTGTGCCGA  
GGCTCCCTGTGAACAGCAGTGCACGGACAACTTGGCCGAGTGTGTGTACTTGTATCCGGGATACCGATATGA  
CCGGGAGAGACACCGGAAGCGGGAGAAGCCATACTGTCTGGATATTGATGAGTGTGCCAGCAGCAATGGGACGCT  
GTGTGCCACATCTGCATCAATACCTTGGGCAGCTACCGCTGCGAGTGCCGGGAAGGCTACATCCGGGAAGATGA  
TGGGAAGACATGTACCAGGGGAGACAAATATCCCAATGACACTGGCCATGAGAAGTCTGAGAACATGGTGAAAGC  
CGAACTTGCTGTGCCACATGCAAGGAGTTCTACCAGATGAAGCAGACCGTGTGCAGCTGAAGCAAAAGATTGC  
TCTGCTCCCCAACAAATGCAGCTGACCTGGGCAAGTATATCACTGGTGACAAGGTGTGGCCTCAAACACCTACCT  
TCCAGGACCTCCTGGCCTGCCTGGGGGCCAGGGCCCTCCCGGCTCACCAGGACCAAAGGGAAGCCCAGGCTTCCC  
CGGTATGCCAGGCCCTCCTGGGCAGCCCGGGCCACGGGGCTCAATGGGACCCATGGGACCATCTCCTGATCTGTC  
CCACATTAAGCAAGGCCGGAGGGGCCCTGTGGGTCCACCAGGGGCACCAGGAAGAGATGGTTCTAAGGGGGAGAG  
AGGAGCGCCTGGGGCCAGAGGGTCTCCAGGACCCCTGGTCTTTGACTTCCTGCTACTTATGCTGGCTGACAT  
CCGCAATGACATCACTGAGCTGCAGGAAAAGGTGTTCGGGCACCGGACTCACTCTTCAGCAGAGGAGTTCCCTTT  
ACCTCAGGAATTTCCAGCTACCCAGAAGCCATGGACCTGGGCTCTGGAGATGACCATCCAAGAAGAAGTGAAC  
AAGAGACTTGAGAGCCCCAGAGACTTCTACCCATAGCACATCCCAACACCGTCACGCCAAAGGAAGAGAAAGAT  
CAACTCACCTGCAGTTAAACCATCTAAAGAGAAGAAAGACCACTGGAGACCTAGAAAACATACATTTTTCTCTTC  
TCTTCTCCTGACGTCTCTCCACTCCTCTCTTCCAAATACGATGCTATTTTCAGAGTCCCCTCCTAGGCCTGCAG  
ACATGAGGGAGTGAATGATTGATTTACCTGCTTCTCACTAAGAGTCCATTGGGGTGGTTTGCATTGTAACTTTTTC  
TTTTACATCCTATTTTCCAGGAACCTTTGGATTAAAGTACTCTCACAGTGTCTTAAATCATAAATCTTGAAGTT  
AAATTTGGCAGAGTATCAAAAGGGGAAAATGACAAAAGTGAAGTCTAAGAAAATGTGAGGCTACTTCTAAGATGT  
GTGTTACAATAGACCATAACTCCTCTAGTATCAAAATTTGGGGCTCTTCAGTTAAAAGGGGTGGGGAGGACAAA  
CGTGTGATGTGCTTTGGTGGAGAATTTTTCTGTGCTTCTAGTAGACTTAAATATTGTATCCCTTTGTCAA  
ACCTTGTTTTCCCAATTAATTAAAGAGAGGAGAGAATTAATGGCGTTTAGAGAAGATAGAAAAGAATCACAGT  
CATATATTTACTGTTATATAGATTGCCACATTCTAAAATTCAAATACGGTGCTTAAGGTTTCATGCCATGCTTAT  
CTGTAAGTATCCTATTTAGGGAAGAAGATTAACTCTCTTTTCAAAAAACAAAGTGAAATGCCTGGATTACAT  
TAAACAATGGGCTCTCGTTTGCTATAATATTTTAAAGCTGTTTAAATCAACAGTGGAGTCTGCTCTATAAATATA  
GATTATTTGTTCAATAAAGTGGCTGAGCTTAGAGAGAGGTGCAGAATTCCTGGTTCTGAGCAGGTGCCAGAGG  
TACCATTAGGTGCCATGATCCAGGCTGAACCAATATACAGTGGGGCTGAAGTCTGCAAGGAGGTTGCTGGCTTGG  
GCTGACCTCACTAATGCCATCAGCAGCGGTAGGTAAATTTTTCTCCTTGGGTATTACAAGTTTTTGTCTGGAGC  
CAACCAAGCTTGCCACCAACATATTGAGAGTAATACACTATTGAAAGTTATCTTGGATGGGGAGAAAAAATA  
GTGGTTTTCTTGTGCAAAAACCTTCTTCTCTATTCTCATTTTTTCTTAATTTCTTAAATTTAGTCCAAGTTC  
CAGTCTTTTTAGGCCTTCTCTTTGATTTATTTTCCCTGCATGTGAGAAGCAGTTCAGAAAAGGTCTATATCTC  
CACCTCCTAGTGAGTTAGAGTGTCTTCTCAGAGACCTCTGGGTGGCAAAGGGAAGCATGTTCTGCCAAGGTTT  
GCTGTGGATTGAGAAGCACCAGGAGCAAGAGACCAGAAGGATGATCTGCTCCTTTGTAACGTTGTTGAGGGCCCT  
CTTGTTTCCAATGAGCAGCTTATAGGTTACTCACAGTCCACTTTCTCACTGGACACACAAAGTGGCTCTTTATCT  
ACCTTTGCGGGAGATTTTCACTCTCCTGCAATGATCGTTCTCACACTCATATTAGCTCATGTTGGAATTTCCCA  
TCCTGCCATGTCCTTTCCCATTTCTTTTGGCTTTTTTGCCTCCACCTTTTAGCCACATCATTTAACTCCACTA  
CTGTGAAAGCTTGCTTAAAGAAAATCCCTCTTGGCCGGGTGTGGTAGCCACGCCTCTAATCCCAGCACTTTGGG  
AGGCTGAGGCGGGGAGATCAAGGTCAGGAGATCGAGACCAGCCTGACCAACATGGTGAAACCTGTCTCTACT  
AAAAATACAAAATTAGCTGGGCGTGTGGCACACACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAA  
TTACTTTAACCTGCGGGGGGAGCCTAGATTGCGCTACTGCACTCCAGCCTAGGCAACAGAGGGAGACTCTGTCTC  
ATTAAAAA

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**FIGURE 82**

MVPPPPSRGGAARGQLGRSLGPLLALLLALGHTWTYREEPEDGDREICSESKIATTKYPCLKSS  
GELTTCYRKKCKCKGYKFVLGQCIPEDYDVCAEAPCEQQCTDNFGRVLCTCYPGYRYDRERHRK  
REKPYCLDIDECASSNGTLCAHICINTLGSRCECREGYIREDDGKTCTRGDKYPNDTGHEKS  
ENMVKAGTCCATCKEFYQMKQTVLQLKQKIALLPNNAADLGKYITGDKVLASNTYLPGPPGLP  
GGQGPPGSPGPKGSPGFPMPGPPGQPGPRGSMGPMGSPDLSHIKQGRRGPVGPFGAPGRDG  
SKGERGAPGPRGSPGPPGSFDFLLMLADIRNDITELQEKVFGHRTSSAEFPLPQEFPSYP  
EAMDLGSGDDHPRRTETRDRLRAPRDFYP

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**N-glycosylation sites.**

amino acids 142-148, 182-188

**Tyrosine kinase phosphorylation site.**

amino acids 125-132

**N-myristoylation sites.**

amino acids 10-16, 143-149, 155-161, 196-202, 250-256

**Amidation site.**

amino acids 299-303

**Aspartic acid and asparagine hydroxylation site.**

amino acids 150-162

**Cell attachment sequence.**

amino acids 176-179

**Clq domain proteins.**

amino acids 247-280

**Calcium-binding EGF-like domain proteins pattern proteins.**

amino acids 144-165

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**FIGURE 83**

ATCTGAGTGAGCTAACTGACACAATGAACTGTCAGGCATGTTTCTGCTCCTCTCTCTGGCTC  
TTTTCTGCTTTTTTAACAGGTGTCTTCAGTCAGGGAGGACAGGTTGACTGTGGTGAGTTCCAGG  
ACCCCAAGGTCTACTGCACTCGGGAATCTAACCCACACTGTGGCTCTGATGGCCAGACATATG  
GCAATAAATGTGCCTTCTGTAAGGCCATAGTGAAAAGTGGTGGAAAGATTAGCCTAAAGCATC  
CTGGAAAATGCTTGAGTTAAAGCCAATGTTTCTTGGTGACTTGCCAGCTTTTGCAGCCTTCTTT  
TCTCACTTCTGCTTATACTTTTGCTGGTGGATTCCTTTAATTCATAAAGACATACCTACTCTG  
CCTGGGTCTTGAGGAGTTCAATGTATGTCTATTTCTCTTGATTCACCTGTCAATAAAGTACATTC  
TGCAAAAGCAAAAA

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**FIGURE 84**

MKLSGMFLLLSLALFCFLTGVFSQGGQVDCGEFQDPKVYCTRESNPHCGSDGQTYGNKCAFCK  
AIVKSGGKISLKHPGKC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**N-myristoylation sites.**

amino acids 26-32, 52-58, 56-62, 69-75

**Kazal serine protease inhibitors family signature.**

amino acids 40-63



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**FIGURE 85**

GGAGCAGACACACAGACCCGGGCGGAGGCCCTCTTCTAGCCCTGCGGGAACCGGACAGTTC  
CCCAACTGGGGACTCTGGAACCACAGCTCCTAAATCATCAAATTCTCAAGCTTTTTTTTTTCCC  
TCTCTTCGTCCCAGCCATCCCAGTCTTCTTCTTCTTTTTTTTTTTTTTAACCTATTGTTTTTT  
TCGCTCCTGTCATTATGAAAGTGGTCACGCCATTCAATATTAAGACTTGGAGGGAATTGGGGA  
AAGAAAAGAAAGAATCTAAAAGAAGAGAAGCGACCGGTGCTTTTAAGGGTGTCTAATTTTCAA  
AAGAGACGTCTGGGAGTATTTTGCTCTGGGCGTTTGGAGCAACTTCGCGGACAGCGGAGCTCG  
CCCAGCATGGATGTTCCAGGTTACAGGCGCCTTTCTTCTGAGAACGACCCTGGCCTTGAACG  
TCAGAGCCGGGGACGAAGGCCCGGAGGCTGCTGCGAGCTCCGCGCGTTCCTTCGCGCCCTT  
CCGCGCCGCTCGCGCCGGCGCCGGCCTCCACCCCGCGCGCCGCTCCCACCACTCCCGATGC  
AGGCGCCCGGCGGGGGGCCACTCGGGCTGCGGCTGATGATGCCCCGGGCGCCGGGGGGCGCTGC  
GCGAGCCTGGCGGCTGCGGATCCTGCCTGGGGGTGGCGCTGGCCCTGCTGTTGCTGCTACTGC  
CCGCCTGCTGCCCCGTGCGGGCGCAGAACGACACGGAGCCCATCGTGCTGGAGGGCAAGTGCC  
TGGTGGTGTGCGACTCCAGCCCGTTCGGCGGACGGCGCCGTCACCTCCTCCCTAGGCATCTCCG  
TGGCTCCGGCAGCGCCAAGGTGGCCTTCTCCGCCACGCGGAGCACCAACCACGAGCCGTCCG  
AGATGAGCAACCGCACCATGACCATCTATTTGACCAGGTATTAGTAAATATTGGCAACCACT  
TTGATCTTGCTTCCAGTATATTTGTAGCACCGAGAAAAGGGATTTATAGCTTCAGCTTCCACG  
TGGTCAAAGTGTATAACAGACAAACCATCCAGGTTCAGTTTAATGCAGAATGGCTACCCAGTGA  
TCTCGGCCTTTGTCAGGAGACCAGGATGTCACCAGAGAAGCTGCTAGCAATGGCGTGCTGCTGC  
TCATGGAAAGGGAAGACAAAGTGCATCTCAAACCTTGAGAGAGGCAACCTCATGGGGGGCTGGA  
AATACTCCACATTCTCGGGCTTCTTGGTGTTCCTCTATAACACAGAGCCCCCTAGATGGTG  
GGGGAATGGCAAACCTGGACCCAGGACTCCGCCCTTTAAACACCCTGAACTTACTGGAATTGG  
ACACCTTGTTTCCAACCTCCGTCAGACTGTTGCAGTAGAAGAATGATTTCTTTTGAACCTCC  
AGTACTTTTGTGTTTTGTTTTTGGAACTGACAATTCCTCGGGAACCTGGCCTCTAATTAGT  
TTTAGATGACAAGGTCTTAAGGAGAAATGAAATTATCGATTTGAGCAATTTGTACCTGTGATT  
GTAAAGTCAATATCGGATTTTATTGTTGGGACCATGGACCTCTTTTGTGTTGTATGTTGTATTG  
TCGTCCCAACGGAAGGAGAGCTCCTGACTCCAGGATGGGCTGCAGGTTGCAGTCAGGGCTTGA  
AGTAGGAGCCCAGCAAAGAACCACCTGCTGGACAGTCCTTGACATGTGTTCTGTGTGTGCTG  
TATAGCCTTAAGAAAAAGAATGGCTTCACTTTTCTGATTCTTCCCCCACCATGTGGCT  
GGGAGGACTTGGGAGGGGGATGGGGACATTGGGAACCTGTCAAGAAGTGCTTTATCCAGAGAA  
GCAAATTTTGCACGATTGGACTGCAATTTTTGTTTTGTATTGTTTGTGTTTTTTCTTGAAAAG  
CTTTACTTTTCTTTCCACACTCAGCTCTCCCTCCTCAACCCCACTTTTATTTTTCTTGCTGGG  
GTTGAGGAGAGAAAATATAGAATTCCTGGATAAGACCAAAACAAAACAAATATAAATACCT  
GTATGTTTTGTTTTAGACGAGACCAAACTAAACAAAAGTATCTGTTTATCAAAGTAAAAGTA  
ACACAATGGACAATTCTGCTTATTCTCTCAAAGAGATTCTAAGATGCACCTTTAGAACTATTA  
ATAGCAACCTGCATTTTTTTTTTAATTTATACTTCAGAATCCTTTAAGAACCTGGTGTTCTGA  
GTGGTCCTGAATCATATAAGTTGGTAATGGAAGCTGTAATGACCAAGTCCCCTAAACATACTA  
TGTCTTTGCCACGTGTGCTGTGACTTCTCTGTGGGTGATTTAATTTATTTGGATCCACCTCTG  
AGTGAGCGCACAGTGATCAGGTGCTTCAAAGCCAACAGACCAGCTCCTCTTCTCCGGATCCT  
CTTTTGATCTGCCCAGGAAAGGGATGCATTGACACTCTCCTGCATGCACCTGGCGAGAAGCCA  
CCTGAAAGTCACTGTGGTTAAAGATATTGGTGGAGGTACCCAGGAGCACTGTTACAAATCCT  
TCTTGTTTTGGCATCTCGTACAACATTATTAAGACACAGCTGAGAGTTGATGGGTGTGTAATG  
CATATGCCAAGGAAATGTCATAATCCCAAAGCAATCAAAAAGGAGACCTCAAACCAGATGTT  
AATTTGTTCTTTGTGTAACAATGTAACCAAAATATTGATGATAAAAGTCATAATTTAAGATTC  
AGAATAAATGGGTTTGATGTCTGGCAAAAAAAAAAAAAA

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**FIGURE 86**

MQAPGRGPLGLRLMMPGRRGALREPGGCGSCLGVALALLLLLLPACCPVRAQNDTEPIVLEGK  
CLVVCDSPPSADGAVTSSLGISVRSGSAKVAFSATRSTNHEPSEMSNRTMTIYFDQVLVNIGN  
HFDLASSIFVAPRKGIYSFSFHVVKVYNRQTIQVSLMQNGYPVISAFAGDQDVTREAASNGVL  
LLMEREDKVHLKLERGNLMGGWKYSTFSGFLVFPL

**Important features of the protein:****Signal peptide:**

amino acids 1-48

**N-glycosylation sites.**

amino acids 53-57, 110-114

**N-myristoylation sites.**

amino acids 26-32, 27-33, 29-35, 33-39, 76-82, 205-211

**Amidation site.**

amino acids 16-20

**Clq domain signature.**

amino acids 117-148

**Clq domain proteins.**

amino acids 115-149

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**FIGURE 87**

AGGGCCCGCGGGTGGAGAGAGCGACGCCCCGAGGGG**ATG**GCGGCAGCGTCCCGGAGCGCCTCTG  
GCTGGGCGCTACTGCTGCTGGTGGCACTTTGGCAGCAGCGCGCGGGCCGGCTCCGGCGTCTTCC  
AGCTGCAGCTGCAGGAGTTCATCAACGAGCGCGGCGTACTGGCCAGTGGGCGGCCTTGCGAGC  
CCGGCTGCCGGACTTTCTTCCGCGTCTGCCTTAAGCACTTCCAGGCGGTCTGTCTCGCCCCGAC  
CCTGCACCTTCGGGACCGTCTCCACGCCGGTATTGGGCACCAACTCCTTCGCTGTCCGGGACG  
ACAGTAGCGGCGGGGGGCGCAACCCCTCTCCAAGTGCCTTCAATTTACCTGGCCGGGTACCT  
TCTCGCTCATCATCGAAGCTTGGCACGCGCCAGGAGACGACCTGCGGCCAGAGGCCCTTGCCAC  
CAGATGCACTCATCAGCAAGATCGCCATCCAGGGCTCCCTAGCTGTGGGTGCAAGTGGTTAT  
TGGATGAGCAAACCAGCACCCCTCACAAGGCTGCGTACTCTTACCGGGTCATCTGCAGTGACA  
ACTACTATGGAGACAACTGCTCCCGCCTGTGCAAGAAGCGCAATGACCACTTCGGCCACTATG  
TGTGCCAGCCAGATGGCAACTTGTCTGCTGCGCGGTTGGACTGGGGAATATTGCCAACAGC  
CTATCTGTCTTTCGGGCTGTCTATGAACAGAATGGCTACTGCAGCAAGCCAGCAGAGTGCCTCT  
GCCGCCAGGCTGGCAGGGCGCGGTGTGTAACGAATGCATCCCCACAATGGCTGTGCCACG  
GCACCTGCAGCACTCCCTGGCAATGTACTTGTGATGAGGGCTGGGGAGGCCTGTTTTGTGACC  
AAGATCTCAACTACTGCACCCACCACTCCCCATGCAAGAATGGGGCAACGTGCTCCAACAGTG  
GGCAGCGAAGCTACACCTGCACCTGTGCGCCAGGCTACACTGGTGTGGACTGTGAGCTGGAGC  
TCAGCGAGTGTGACAGCAACCCCTGTGCAATGGAGGCAGCTGTAAGGACCAGGAGGATGGCT  
ACCACTGCCTGTGTCTCCGGGCTACTATGGCCTGCACTGTGAACACAGCACCTTGAGCTGCG  
CCGACTCCCCCTGCTTCAATGGGGGCTCCTGCCGGGAGCGCAACCAGGGGGCCAACTATGCTT  
GTGAATGTCCCCCAACTTCACCGGCTCCAAGTGCAGAGAAGAAAGTGGACAGGTGCACCAGCA  
ACCCCTGTGCCAACGGGGGACAGTGCCTGAACCGAGGTCCAAGCCGCATGTGCCGCTGCCGTC  
CTGGATTACGGGCACCTACTGTGAAGTCCACGTCAGCGACTGTGCCCCGTAACCCCTTGCGCCC  
ACGGTGGCACTTGCCATGACCTGGAGAATGGGCTCATGTGCACCTGCCCTGCCGGCTTCTCTG  
GCCGACGCTGTGAGGTGCGGACATCCATCGATGCCTGTGCCTCGAGTCCCTGCTTCAACAGGG  
CCACCTGCTACACCGACCTCTCCACAGACACCTTTGTGTGCAACTGCCCTTATGGCTTTGTGG  
GCAGCCGCTGCGAGTTCCCCGTGGGCTTGCCGCCCAGCTTCCCCTGGGTGGCCGTCTCGCTGG  
GTGTGGGGCTGGCAGTGCTGCTGGTACTGCTGGGCATGGTGGCAGTGGCTGTGCGGCAGCTGC  
GGCTTCGACGGCCGGACGACGGCAGCAGGGAAGCCATGAACAACTTGTGCGACTTCCAGAAGG  
ACAACCTGATTCTTGCCGCCAGCTTAAAAACACAAACCAGAAGAAGGAGCTGGAAGTGGACT  
GTGGCCTGGACAAGTCCAAGTGTGGCAAACAGCAAAACCACACATTGGACTATAATCTGGCCC  
CAGGGCCCCCTGGGGCGGGGGACCATGCCAGGAAAGTTTCCCCACAGTGACAAGAGCTTAGGAG  
AGAAGGCGCCACTGCGGTTACACAGTGAAAAGCCAGAGTGTGCGATATCAGCGATATGCTCCC  
CCAGGGACTCCATGTACCAGTCTGTGTGTTTGATATCAGAGGAGAGGAATGAATGTGTATTG  
CCACGGAGGT**TAA**GGCAGGAGCCTACCTGGACATCCCTGCTCAGCCCCGCGGCTGGACCTTC  
CTTCTGCATTGTTTACA

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**FIGURE 88**

MAAASRSASGWALLLLVALWQQRAAGSGVFQLQLQEFINERGVLASGRPCEPGCRTFFRVCLK  
HFQAVVSPGPCTFGTVSTPVLGTNSFAVRDDSSGGGRNPLQLPFNFTWPGTFSLIIEAWHAPG  
DDLREALPPDALISKIAIQGSLAVGQNWLLDEQTSTLTRLRYSYRVICSDNYYGDNC SRLCK  
KRNDHFGHYVCQPDGNLSCLPGWTGEYCQQPICLSGCHEQNGYCSKPAECLCRPGWQGRLCNE  
CIPHNGCRHGTCSTPWQCTCDEGWGGLFCDQDLNYCTHHSPCKNGATCSNSGQRSYTCTCRPG  
YTGVDCLELSECDSNPCRNGGSKDQEDGYHCLCPPGYGLHCEHSTLSCADSPCFNGGSCR  
ERNQGANYACECPPNFTGSNCEKKVDRCTSNPCANGGQCLNRGPSRMCRCPGFTGT YCELHV  
SDCARNPCAHGGTCHDLENGLMCTCPAGFSGRRCVRTSIDACASSPCFN RATCYTDLSTDTF  
VCNCPYGFVGSRCFFVGLPPSFPWVAVSLGVGLAVLLVLLGMVAVAVRQLRLRRPDDGSREA  
MNNLSDFQKDNLI PAAQLKNTNQKKELEVDCGLDKSNCGKQQNHTLDYNLAPGPLGRGTM PGK  
FPHSDKSLGEKAPLRHLHSEKPECRISAICSPRDSMYQSVCLISEERNECVIATEV

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 530-552

**N-glycosylation sites.**

amino acids 108-112, 183-187, 205-209, 393-397, 570-574, 610-614

**Glycosaminoglycan attachment site.**

amino acids 96-100

**Tyrosine kinase phosphorylation site.**

amino acids 340-347

**N-myristoylation sites.**amino acids 42-48, 204-210, 258-264, 277-283, 297-303, 383-389,  
415-421, 461-467, 522-528, 535-541, 563-569, 599-605, 625-631**Amidation site.**

amino acids 471-475

**Aspartic acid and asparagine hydroxylation site.**

amino acids 339-351

**EGF-like domain cysteine pattern signature.**amino acids 173-185, 206-218, 239-251, 270-282, 310-322, 348-360,  
388-400, 426-438, 464-476, 506-518**Calcium-binding EGF-like:**amino acids 224-245, 255-276, 295-316, 333-354, 373-394, 411-432,  
449-470

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**FIGURE 89**

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGAC  
TTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTCAGAGATCCTGCAGC  
CGCCCAGTCCCGGGCCCCCTCTCCCGCCCCACACCCACCCTCCTGGCTCTTCCTGTTTTTACTCC  
TCCTTTTTCATTTCATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCC  
GAGCGTGGAAGAATGGGGTTCCTCGGGACCGGCACTTGGATTCTGGTGTTAGTGCTCCCGATT  
CAAGCTTTCCCCAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCA  
GAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAACAAAAACATATCCT  
CCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGTGATAACTTGAACCTGCTAAAGGCA  
ATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCACTTGATAAT  
AAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGATTATGACTCT  
ACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATCAACTAGACGGG  
ACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAGAAAATGAC  
AGAGCCGTGTTTGACAAGATTGTTTCTAAACTACTTAATCTCGGCCTTATCACAGAAAGCCAA  
GCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAAC  
AATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCA  
GAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACA  
GTATCTAACACATTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGAC  
AACTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTTCAGAA  
AAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAG  
ATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTTCCTACCTTGAAAACCTGGAT  
GAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAATGCTACTGACAATATAAGCAAG  
CTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGACAGTACCAAGGAAGAAGCAGCT  
AAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCACAAAAGATGATAACTCCAACCCAGGA  
GGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTGGAAGCCATCAGAAAAAATATT  
GAATGGTTGAAGAAACATGACAAAAAGGGAAATAAAGAAGATTATGACCTTTCAAAGATGAGA  
GACTTCATCAATAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAAGAAGCC  
GAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAAATGGCAAAAGATCCAGGAGTCTTTCAAC  
TGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAATTTTTTGACCC  
AAGGGTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGC  
TTTCTTCCCGTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAA  
AAA

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**FIGURE 90**

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENK  
PGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDDYSTKSG  
LDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTL  
EDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPKVTMAAIQDGLAKGENDETVSNT  
LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVK  
YGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEEAAKMEK  
EYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFIN  
KQADAYVEKGILDKEEAIAIKRIYSSL

**Important features:****N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

**N-myristoylation sites:**

amino acids 143-148, 239-244

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**FIGURE 91**

TGCATCAGTGCCCAGGCAAGCCCAGGAGTTGACATTTCTCTGCCCAGCCATGGGCCTCACCCCT  
GCTCTTGCTGCTGCTCCTGGGACTAGAAAGGTCAGGGCATAGTTGGCAGCCTCCCTGAGGTGCT  
GCAGGCACCCGTGGGAAGCTCCATTCTGGTGCAGTGCCACTACAGGCTCCAGGATGTCAAAGC  
TCAGAAAGGTGTGGTGCCGGTTCTTGCCGGAGGGGTGCCAGCCCCTGGTGTCTCAGCTGTGGA  
TCGCAGAGCTCCAGCGGGCAGGCGTACGTTTCTCACAGACCTGGGTGGGGGCCTGCTGCAGGT  
GGAAATGGTTACCCTGCAGGAAGAGGATGCTGGCGAGTATGGCTGCATGGTGGATGGGGCCAG  
GGGGCCCCAGATTTTGCACAGAGTCTCTCTGAACATACTGCCCCAGAGGAAGAAGAAGAGAC  
CCATAAGATTGGCAGTCTGGCTGAGAACGCATTCTCAGACCCTGCAGGCAGTGCCAACCCTTT  
GGAACCCAGCCAGGATGAGAAGAGCATCCCCCTTGATCTGGGGTGCTGTGCTCCTGGTAGGTCT  
GCTGGTGGCAGCGGTGGTGCTGTTTGCTGTGATGGCCAAGAGGAAACAAGAATCCCTCCTCAG  
TGGTCCACCACGTCAGTGACTCTGGACCGGCTGCTGAATTGCCTTTGGATGTACCACACATTA  
GGCTTGACTCACCACCTTCATTTGACAATACCACCTACACCAGCCTACCTCTTGATTCCCCAT  
CAGGAAAACCTTCACTCCCAGCTCCATCCTCATTGCCCCCTCTACCTCCTAAGGTCCTGGTCT  
GCTCCAAGCCTGTGACATATGCCACAGTAATCTTCCCGGGAGGGAACAAGGTGGAGGGACCT  
CGTGTGGGCCAGCCCAGAATCCACCTAACAAATCAGACTCCATCCAGCTAAGCTGCTCATCACA  
CTTTAAACTCATGAGGACCATCCCTAGGGGTTCTGTGCATCCATCCAGCCAGCTCATGCCCTA  
GGATCCTTAGGATATCTGAGCAACCAGGGACTTTAAGATCTAATCCAATGTCCTAACTTTACT  
AGGGAAAGTGACGCTCAGACATGACTGAGATGTCTTGGGGAAGACCTCCCTGCACCCAACTCC  
CCCACTGGTTCTTCTACCATTACACACTGGGCTAAATAAACCCCTAATAATGATGTGCAAAAAA  
AA

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**FIGURE 92**

MGLTLLLLLLLLLGLEGQGIVGSLPEVLQAPVGSSILVQCHYRLQDVKAQKVWCRFLPEGCQPLV  
SSAVDRRAPAGRRFTLTDLGGGLLQVEMVTLQEEDAGEYGCMVDGARGPQILHRVSLNILPPE  
EEEETHKIGSLAENAFSDPAGSANPLEPSQDEKSIPLIWGAVLLVGLLVAAVVLFAVMAKRKQ  
ESLLSGPPRQ

**Important features of the protein:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 161-181

**N-myristoylation sites.**

amino acids 17-23, 172-178

**Amidation site.**

amino acids 73-79



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**FIGURE 93**

GGCGGCGTTGCCGGGCTCTCCGGAAGGAGACGTGGCGGCGGTTGGGCGGTTGATACCCGGGCG  
CTTTATAGTCCCGCCGCTCCTCCTCCACCTCCTCCTCCTCCTCCTCCTCCTGGGGCAGAG  
GAGGTTGTGGCGGTGGCTGGAGAAAAGCGGCGGCGGAGG**ATG**GAGGAAGGAGGCGGCGGCGTAC  
GGAGTCTGGTCCCGGGCGGGCCGGTGTTACTGGTCCTCTGCGGCCTCCTGGAGGCGTCCGGCG  
GCGGCCGAGCCCTTCCTCAACTCAGCGATGACATCCCTTTCCGAGTCAACTGGCCCCGGCACCG  
AGTTCTCTCTGCCCACAACTGGAGTTTTATATAAAGAAGATAATTATGTCATCATGACAACTG  
CACATAAAGAAAAATATAAATGCATACTTCCCCTTGTGACAAAGTGGGGATGAGGAAGAAGAAA  
AGGATTATAAAGGCCCTAATCCAAGAGAGCTTTTGGAGCCACTATTTAAACAAAGCAGTTGTT  
CCTACAGAATTGAGTCTTATTGGACTTACGAAGTATGTCATGGAAAACACATTCGGCAGTACC  
ATGAAGAGAAAAGAACTGGTCAGAAAATAAATATTACGAGTACTACCTTGGGAATATGTTGG  
CCAAGAACCTTCTATTTGAAAAAGAACGAGAAGCAGAAGAAAAGGAAAAATCAAATGAGATTC  
CCACTAAAAATATCGAAGGTCAGATGACACCATACTATCCTGTGGGAATGGGAAATGGTACAC  
CTTGTAGTTTGAACAGAACCGGCCCGAGATCAAGTACTGTGATGTACATATGTCATCCTGAAT  
CTAAGCATGAAATTCTTTCAGTAGCTGAAGTTACAACCTTGTGAATATGAAGTTGTCATTTTGA  
CACCCTCTTGTGCAGTCATCCTAAATATAGGTTTCAGAGCATCTCCTGTGAATGACATATTTT  
GTCAATCACTGCCAGGATCTCCATTTAAGCCCCCTCACCTGAGGCAGCTGGAGCAGCAGGAAG  
AAATACTAAGGGTGCCTTTTAGGAGAAATAAAGAGGGTGTGCGTTGGTGGAAATATGAATTCT  
GCTATGGCAAACATGTACATCAATACCATGAGGACAAGGATAGTGGGAAAACCTCTGTGGTTG  
TCGGGACATGGAACCAAGAAGAGCATATTGAATGGGCTAAGAAGAATACTGCTAGAGCTTATC  
ATCTTCAAGACGATGGTACCCAGACAGTCAGGATGGTGTACATTTTATGGAAATGGAGATA  
TTTGTGATATAACTGACAAACCAAGACAGGTGACTGTAAACTAAAGTGCAAAGAATCAGATT  
CACCTCATGCTGTTACTGTATATATGCTAGAGCCTCACTCCTGTCAATATATTCTTGGGGTTG  
AATCTCCAGTGATCTGTAAATCTTAGATACAGCAGATGAAAATGGACTTCTTTCTCTCCCA  
A**CTAA**AGGATATTAAAGTTAGGGGAAAGAAAAGATCATTGAAAGTCATGATAATTTCTGTCCC  
ACTGTGTCTCATTATAGAGTTCTCAGCCATTGGACCTCTTCTAAAGGATGGTATAAAATGACT  
CTCAACCACTTTGTGAATACATATGTGTATATAAGAGGTTATTGATAAACTTCTGAGGCAGAC  
ATTTGTCTCGCTTTTTTTCATTTTTGTTGTGTCTTATAAACTGACTGTTTTCTTTGCTTGGA  
TACTGTGATTCCAAAATAAATCTCATCCAAGCAAGTTAGAGTCCAGCCTAATCAAATGTCATA  
ATTGTTGTACCTAFTGAAAGTTTTTAAATAATAGATTTATTATGTAAATTATAGTATATGTAA  
GTAGCTAATGAAGTAAAGATCATGAAGAAAGAAATTGATAGGTGTAAATGAGAGACCATGTAA  
AATATGTAAATTCTAGTACCTGAAATCCTTTCAACAGATTTTATATAGCAACTGCTCTCTGC  
AAGTAGTTAACTAGAACTGGGCACATGGTAGAGGCTCACATGGGAGTTGTCCCTCACCTTG  
TTAATCTCAAGAACTCTTATTTATAATAGGTTGCTTCTCTCTCAGAACTTTTATCTATTACT  
TTTTTCTTCTTATGAGTATGTTTACTCTCAGAGTATCTATCTGATGTAGACAGTTGGTGTATGC  
TTCTGAGACTCAGAATGGTTTACTCTAACAAAACACTGTGCTGTCTATCCCTTGTACTTGCCT  
ACTGTAATATGGATTTCACTTCTGAACAGTTTACAGCACAATATTTATTTTAAAGTGAATAAA  
ATGTCCACAAGCAAAA

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**FIGURE 94**

MEEGGGGVRS LVPGGPVLLVLCGLLEASGGGRALPQLSDDIPFRVNWPGTEFSLPTTGVLVLYKE  
DNYVIMTTAHKEKYKCILPLVTSGDEEEEEKDYKGNPRELLEPLFKQSSCSYRIESYWTYEVC  
HGKHIRQYHEEKETGQKINIHEYLLGNMLAKNLLFEKEREAEKEKSNEIPTKNIEGQMTPLY  
PVGMGNGTPCSLKQNRPRSSTVMYICHPEKHEILSVAEVTTC EYEVVILTPLLCSHPKYRFR  
ASPVNDIFCQSLPGSPFKPLTLRQLEQQEEILRVPFRRNKEGVGWWKYEF CYGKHVHQYHEDK  
DSGKTSVVVGVTWNQEEHIEWAKKNTARAYHLQDDGTQTVRMVSHFYGN GDICDITDKPRQVTV  
KLKCKESDSPHAVTVYMLEPHSCQYILGVESPVICKILDTADENGLLSLPN

**Important features of the protein:****Signal peptide:**

amino acids 1-30

**Glycosaminoglycan attachment site.**

amino acids 28-32

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 337-341

**N-myristoylation sites.**amino acids 6-12, 23-29, 29-35, 49-55, 141-147, 152-158, 192-198,  
196-202**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 54-60

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**FIGURE 95**

TTCCGTTTCTGGGAGGAGTGAGGGGCAACGGGTCTGGAGAAAAAGGAAAAAGAAGGGCTCAGC  
GCCTCCCCGCCGGGCCGTGGACAGAGGGGCACAGTTTTCGGCAGGCGGGTGAGGTCTGAGGG  
CCCGCCGGAGATGTTTTCTTGTCTGAGCACGGTGCAACCCAGGTTACAGTTCCTCTGAGTCA  
TCTCATCAATGCCTTCCATACACCAAAAAACACTTCTGTTTCTCTCAGTGGAGTGTCTAGTTTC  
TCAAACCAGCATCGAGATGTAGTTCCTGAGCATGAGGCTCCCAGCAGTGAAGCTTCACTTAA  
CTTAAGGGACCTTGGATTATCTGAACATAAAATTTGGACAGATTGATCAGCTGGTAGAAAATCT  
ACTTCCTGGATTTTGTAAAGGCAAAAACATTTCTTCCCATTGGCATAACATCCCATGTCTCTGC  
ACAATCCTTCTTTGAAAATAAATATGGTAACCTAGATATATTTAGTACATTACGTTCTCTTG  
CTTGTATCGACATCATTCAAGAGCTCTTCAAAGCATTGTTTCTCAGATCTTCACTACTGGCCAGT  
TTTCATACAGTCTCGGGGTTTTAAACTTTGAAATCAAGGACACGACGTCTCCAGTCTACCTC  
CGAGAGATTAGCTGAAACACAGAATATAGCGCCATCATTCTGTAAGGGGTTTTCTTTTGGCGGA  
CAGAGGATCAGATGTTGAGAGTTTGGACAACTCATGAAAACCAAAAATATACCTGAAGCTCA  
CCAAGATGCATTTAAACTGGTTTTGCGGAAGGTTTTCTGAAAGCTCAAGCACTCACACAAAA  
AACCAATGATTCCTTAAGGCGAACCCGTCTGATTCTCTTCGTTCTGCTGCTATTCCGGCATTTA  
TGGACTTCTAAAAAACCCATTTTTATCTGTCCGCTTCCGGACAACAACAGGGCTTGATTCTGC  
AGTAGATCCTGTCCAGATGAAAAATGTCACCTTTGAACATGTTAAAGGGTGGAGGAAGCTAA  
ACAAGAATTACAGGAAGTTGTTGAATTCTTGAAAAATCCACAAAATTTACTATTCTTGAGG  
TAACTTCCAAAAGGAATTCTTTTAGTTGGACCCCCAGGGACTGGAAAGACACTTCTTGCCCG  
AGCTGTGGCGGGAGAAGCTGATGTTCTTTTTATTATGCTTCTGGATCCGAATTTGATGAGAT  
GTTTGTGGGTGTGGGAGCCAGCCGTATCAGAAATCTTTTTAGGGAAGCAAAGGCGAATGCTCC  
TTGTGTTATATTTATTGATGAATTAGATTCTGTTGGTGGGAAGAGAATTGAATCTCCAATGCA  
TCCATATTCAAGGCAGACCATAAATCAACTTCTTGCTGAAATGGATGGTTTTAAACCCAATGA  
AGGAGTTATCATAATAGGAGCCACAACTTCCCAGAGGCATTAGATAATGCCTTAATACGTCC  
TGGTCGTTTTGACATGCAAGTTACAGTTCCAAGGCCAGATGTAAAAGGTCGAACAGAAATTTT  
GAAATGGTATCTCAATAAAATAAAGTTTGATCAATCCGTTGATCCAGAAATTATAGCTCGAGG  
TACTGTTGGCTTTTTCCGGAGCAGAGTTGGAGAATCTTGTGAACCAGGCTGCATTAAGCAGC  
TGTTGATGGAAAAGAAATGGTTACCATGAAGGAGCTGGAGTTTTCCAAAGACAAAATTTCTAAT  
GGGGCCTGAAAGAAGAAGTGTGGAATTTGATAACAAAAACAAACCATCACAGCATATCATGA  
ATCTGGTCATGCCATTATTGCATATTACACAAAAGATGCAATGCCTATCAACAAAGCTACAAT  
CATGCCACGGGGGCCAACACTTGGACATGTGTCCCTGTTACCTGAGAATGACAGATGGAATGA  
AACTAGAGCCCAGCTGCTTGCACAAATGGATGTTAGTATGGGAGGAAGAGTGGCAGAGGAGCT  
TATATTTGGAACCGACCATATTACAACAGGTGCTTCCAGTGATTTTGATAATGCCACTAAAAT  
AGCAAAGCGGATGGTTACCAAATTTGGAATGAGTGAAAAGCTTGGAGTTATGACCTACAGTGA  
TACAGGGAAACTAAGTCCAGAAACCAATCTGCCATCGAACAAGAAATAAGAATCCTTCTAAG  
GGACTCATATGAACGAGCAAAACATATCTTGAAAACCTCATGCAAGGAGCATAAGAATCTCGC  
AGAAGCTTTATTGACCTATGAGACTTTGGATGCCAAAGAGATTCAAATTGTTCTTGAGGGGAA  
AAAGTTGGAAGTGAGATGATAACTCTCTTGATATGGATGCTTGCTGGTTTTATTGCAAGAATA  
TAAGTAGCATTGCAGTAGTCTACTTTTACAACGCTTTCCCCTCATTCTTGATGTGGTGTAATT  
GAAGGGTGTGAAATGCTTTGTCAATCATTTGTCACATTTATCCAGTTTGGGTTATTCTCATT  
TGACACCTATTGCAAATTAGCATCCCATGGCAAATATATTTGAAAAATAAAGAACTATCAG  
GATTGAAAACAAAAA

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**FIGURE 96**

MFSLSSTVQPQVTVPLSHLINAFTPKNTSVSLSGVSVSQNQHRDVVPEHEAPSSEPSLNLRD  
LGLSELKIGQIDQLVENLLPGFCKGKNISSHWHTSHVSAQSFFENKYGNLDIFSTLRSSCLYR  
HHSRALQSICSDLQYWPVFIQSRGFKTLKSRTTQLQSTSERLAETQNIAPSFVKGFLLRDRGS  
DVESLDKLMKTKNIPEAHQDAFKTGFAEGFLKAQALTQKTNDLSLRTRLILFVLLLFGIYGLL  
KNPFLSVRFRTTGLDSAVIDPVQMKNVTFEHVKGVEEAKQELQEVVEFLKNPQKFTILGGKLP  
KGILLVGPPGTGKTLLARAVAGEADVPFYYASGSEFDEMFGVGASRIRNLFREAKANAPCVI  
FIDELDSVGGKRIESPMHPYSRQTINQLLAEMDGFKPNEGVIIGATNFPEALDNALIRPGRF  
DMQVTVPRPDVKGRTEILKWYLNKIKFDQSVDPEIIARGTVGFSGAELENLVNQAALKAADV  
KEMVTMKELEFSKDKILMGPERRSVEIDNKNKTITAYHESGHAIAYYTKDAMPINKATIMPR  
GPTLGHVSLLPENDRWNETRAQLLAQMDVSMGGRVAEELIFGTDHITTGASSDFDNATKIAGR  
MVTKFGMSEKLGVMYSDTGKLSPETQSAIEQEIRILLRDSYERAKHILKTHAKEHKNLAEAL  
LTYETLDAKEIQIVLEGKKLEVR

**Important features of the protein:****Transmembrane domain:**

amino acids 238-259

**N-glycosylation sites.**amino acids 28-32, 90-94, 230-234, 278-282, 535-539, 584-588,  
623-627**N-myristoylation sites.**

amino acids 35-41, 266-272, 286-292, 325-331, 357-363, 599-605

**Amidation site.**

amino acids 387-393, 709-713

**ATP/GTP-binding site motif A (P-loop).**

amino acids 322-330

**AAA-protein family proteins**

amino acids 315-336, 343-386, 405-451

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**FIGURE 97**

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTCCCCTGTGGGTCTGAGGG  
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA  
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT  
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG  
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG  
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTAGGCCTAAGATGAAAGCCTCTAGT  
CTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG  
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT  
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT  
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC  
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC  
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA  
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG  
GAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTTCGAGGTCAAGAGCTCCAGTCT  
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTACTGTACTAGTCTTGTGCT  
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGATTGTCTTTATGCATCCCC  
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTCTGCTATTGGATATATT  
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG  
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT  
ACAGTAAAAAAAAAAACCTTGTAATCTAGAAAGAGTGGCTAGGGGGGTATTTCATTTGTAT  
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC  
TACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG  
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG  
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 98**

MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSEIRGSVQAKDGNIDIR  
ILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSLTIKKDLRLC  
HAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE

**Signal sequence:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 107-110, 140-143

**N-myristoylation site.**

amino acids 51-56

**Interleukin 10:**

amino acids 9-176

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**FIGURE 99**

[illegible]

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**FIGURE 100**

MRLLPEWFLLLLFGPWLLRKAVSAQIPESGRPQYLGLRPAAAGAGAPGQQLPEPRSSDGLGVGR  
AWSAWPTNHTGALARAGAAGALPAQRTKRKPSIKAARAKKIFGWGDFYFRVHTLKFSLLVTG  
KIVDHVNGTFSVYFRHNSSSLGNLSVSIVPPSKRVEFGGVWLPGPVPHPLQSTLALEGVLPGL  
GPPLGMAAAAAGPGLGGSLLGGALAGPLGGALGVPGAKESRAFNCHVEYEKTNRARKHRPCLYD  
PSQVCFTTEHTQSQAAWLCAKPFKVICIFVSFLSFDYKLVQKVC PDYNFQSEHPYFG

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 273-288

**N-glycosylation sites.**

amino acids 72-76, 133-137, 143-147, 149-153

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 93-97

**N-myristoylation sites.**amino acids 35-41, 58-64, 60-66, 81-87, 84-90, 184-190, 194-200,  
203-209, 205-211, 206-212, 209-215, 217-223, 221-227, 224-230**Cytochrome b/b6 Qo site signature.**

amino acids 5-11



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**FIGURE 101**

AATGCCCCATGCGCACCCACAGCTCGCGCTCCTGCAAGTGTTCTTTCTGGTGTTCCCCGATG  
GCGTCCGGCCTCAGCCCTCTTCCTCCCCATCAGGGGCAGTGCCCACGTCTTTGGAGCTGCAGC  
GAGGGACGGATGGCGGAACCCTCCAGTCCCCTTCAGAGGCGACTGCAACTCGCCCCGGCCGTGC  
CTGGACTCCCTACAGTGGTCCCTACTCTCGTGACTCCCTCGGCCCCTGGGAATAGGACTGTGG  
ACCTCTTCCCAGTCTTACCGATCTGTGTCTGTGACTTGACTCCTGGAGCCTGCGATATAAATT  
GCTGCTGCGACAGGGACTGCTATCTTCTCCATCCGAGGACAGTTTTCTCCTTCTGCCTTCCAG  
GCAGCGTAAGGTCTTCAAGCTGGGTTTGTGTAGACAACTCTGTTATCTTCAGGAGTAATTCCC  
CGTTTCCTTCAAGAGTTTTTCATGGATTCTAATGGAATCAGGCAGTTTTGTGTCCATGTGAACA  
ACTCAAACCTTAACTATTTCCAGAAGCTTCAAAAGGTCAATGCAACCAACTTCCAGGCCCTGG  
CTGCAGAGTTTGGAGGCGAATCATTCACTTCAACATTCCAAACCTCAATCACCACCATCTTTTT  
ACAGGGCTGGGGACCCATTCTTACTTACTTCCCCAAGTGGTCTGTAATAAGCTTGCTGAGAC  
AACCTGCAGGAGTTGGAGCTGGGGGACTCTGTGCTGAAAGCAATCCTGCAGGTTTCTTAGAGA  
GTAAAAGTACAACCTGCACTCGTTTTTTCAAGAACCTGGCTAGTAGCTGTACCTTGGAATTCAG  
CCCTCAATGCTGCCTCTTACTATAACTTCACAGTCTTAAAGGTTCGAAGAAGCATGACTGATC  
CACAGAATATGGAGTTCCAGGTTCTGTAACTTACCTCACAGGCTAATGCTCCTCTGTTGG  
CTGGAAACACTTGTCAGAATGTAGTTTCTCAGGTCACCTATGAGATAGAGACCAATGGGACTT  
TTGGAATCCAGAAAGTTTCTGTCAGTTTGGGACAAACCAACCTGACTGTTGAGCCAGGCGCTT  
CCTTACAGCAACACTTCATCCTTCGCTTCAGGGCTTTTCAACAGAGCACAGCTGCTTCTCTCA  
CCAGTCCTAGAAGTGGGAATCCTGGCTATATAGTTGGGAAGCCACTCTTGGCTCTGACTGATG  
ATATAAGTTACTCAATGACCCTCTTACAGAGCCAGGGTAATGGAAGTTGCTCTGTTAAAAGAC  
ATGAAGTGCAGTTTGGAGTGAATGCAATATCTGGATGCAAGCTCAGGTTGAAGAAGGCAGACT  
GCAGCCACTTGCAAGCAGGAGATTTATCAGACTCTTCATGGAAGGCCAGACCAGAGTATGTTG  
CCATCTTTGGTAATGCTGACCCAGCCCAGAAAGGAGGGTGGACCAGGATCCTCAACAGGCACT  
GCAGCATTTACAGCTATAAACTGTACTTCCTGCTGTCTCATAACAGTTTCCCTGGAGATCCAGG  
TATTGTGGGCATATGTAGGTCTCCTGTCCAACCCGCAAGCTCATGTATCAGGAGTTTCGATTCC  
TATACCAGTGCCAGTCTATACAGGATTCTCAGCAAGTTACAGAAGTATCTTTGACAACCTCTTG  
TGAACCTTTGTGGACATTACCCAGAAGCCACAGCCTCCAAGGGGCCAACCCAAAATGGACTGGA  
AATGGCCATTGCACTTCTTTCCCTTCAAAGTGGCATTTCAGCAGAGGAGTATTCTCTCAAAAAT  
GCTCAGTCTCTCCCATCCTTATCCTGTGCCTCTTACTACTTGAGTTCTCAACCTAGAGACTA  
TGTGAAGAAAAGAAAATAATCAGATTTTCAGTTTTCCCTATGAGAACTCTGAGGCAGCCACTT  
ATCTTGGCTAAATAGAACCTCACCTGCTCATGACCAGAGAGCATTTAGGATAATAGATGACCT  
AACTGAAGGAATCCTTGTATATGAAAGGAGTTATTTTAGAAAAGCAATAAAAATATTTTATTC  
ATCNTAAAAA

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**FIGURE 102**

M RTPQLALLQVFFLVFPDGV RPQPSSSPSGAVPTSLELQRGTDGGTLQSPSEATATRPV PGL  
PTVVPTLVTPSAPGNRTVDLFPVLPICVCDLTPGACDINCCDRDCYLLHPRTVFSFCLPGSV  
RSSSWVCVDNSVIFRSNSPFPSRVFMD SNGIRQFCVHVNNNSNLNYFQKLQKVNATNFQALAAE  
FGGESFTSTFQTQSPPSFYRAGDPILTYFPKWSVISLLRQPAGVGAGGLCAESNPAGFLESKS  
TTCTRFFKNLASSCTLDSALNAASYNFTVLKVPRSM TDPQNMEFQVPVILTSQANAPLLAGN  
TCQNVVSQVTYEIEIETNGTFTGIQKVS VSLGQTNLTVEPGASLQQHFILRFRAFQQSTAASLTSP  
RSGNPGYIVGKPLLALTD DISYSMTLLQSQGN GSCSVKRHEVQFGVNAISGCKLRLKKADCSH  
LQQEIYQTLHGRPRPEYVAIFGNADPAQKGGWTRILNRHCSISAINCTSCCLIPVSLEIQVLW  
AYVGLLSNPQAHVSGVRFLYQCQSIQDSQQVTEVSLTTLVNFVDITQKPQPPRGQPKMDWKWP  
FDFFPFKVAFSRGVFSQKCSVSPILILCLLLLGV LNLETM

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 484-505, 581-600

**N-glycosylation sites.**amino acids 78-82, 165-169, 179-185, 279-285, 331-337, 347-351,  
410-414, 487-491**N-myristoylation sites.**

amino acids 30-36, 41-47, 124-130, 232-238, 236-242, 409-415

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 420-431

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**FIGURE 103**

CCTAATTCTCAAGGTGATGCTATTTAGGAAGTCATAACTCATGTGAGTGGAGCCATGTGGGAT  
TAAGAAGTGATAGGAGAGCTTGCTGTCTGTCTCTGCTCTCCACTGTGTGAGGATACAACAGGA  
AGACAGCCATCTGGTGAGGAAGAGAGGGCCCTCGCCAGATACCGGACCTGCTGACACCTTGAT  
CTTGGA CTTCCTTCCAGGAAGGCCTGACCTCAGTTGTTCCAGGGTAAAGAATTTGGGCA  
GTGCCCACACCCACGCTGTTGGATAACATTTCTTCACCATAACAGTGAGGGTGAATGTGTACA  
CGCCAGCTTCCTGCCTGTTACTCTCCACAGTATGCGAAGAATATCCCTGACTTCTAGCCCTG  
TGCGCCTTCTTTTGTCTGTGCTACTAATAGCCTTGAGATCATGGTTGGTGGTCACT  
CTCTTTGCTTCAACTTCACTATAAAATCATTGTCCAGACCTGGACAGCCCTGGTGTGAAGCGC  
AGGTCTTCTTGAATAAAAATCTTTTCCTTCAGTACAACAGTGACAACAACATGGTCAAACCTC  
TGGGCCTCCTGGGGAAGAAGGTATATGCCACCAGCACTTGGGGAGAATTGACCCAAACGCTGG  
GAGAAGTGGGGCGAGACCTCAGGATGCTCCTTTGTGACATCAAACCCAGATAAAGACCAGTG  
ATCCTTCCACTCTGCAAGTCGAGATGTTTTGTCAACGTGAAGCAGAACGGTGCCTGGTGCAT  
CCTGGCAGTTCGCCACCAATGGAGAGAAATCCCTCCTCTTTGACGCAATGAACATGACCTGGA  
CAGTAATTAATCATGAAGCCAGTAAGATCAAGGAGACATGGAAGAAAGACAGAGGGCTGGAAA  
AGTATTTTCAGGAAGCTCTCAAAGGGAGACTGCGATCACTGGCTCAGGGAATTCTTAGGGCACT  
GGGAGGCAATGCCAGAACCGACAGGCAGAAGATCCACCTAGAGGTGATACCACGGCGGCGCAG  
AGTTGTTACCTGTGGTCCTCGATCGCTGACAGCCTGGCTCCCACTGCTGTGTGTTCCCTGA  
GTCAAGTGGAGGCGGAGCCTGCAATGAGCGGAGATCGCGCCTCTGCATTCCAGTCTTGGCAAC  
AGAGCAAGACTCCGTCTCAAAAAAAAAAATTTTTTTTCAGTACATATTTTTTAAAGATAGG  
GCTGGGCACAGCAGCTCACATCTATAATCCCAACACTTTGGGAGGCCTAGGCAGGAGGATCAC  
TTGAGCCCAGGAATCTGAAGCTGCAGTGAGCCTTTGCTCGTGAGATTGTGGACCTATGATCCT  
ACCACCAGCCCACCTGGTTCTAACACCCCTCCTCTATGTGTGAGAGGGAGAGAAGAAAAGTG  
AGGGAGAAAAGAGAGATAAGCAAAGAACAGAGAGGAAAATGGAAAATAAGAGGAAATTGGGG  
GAATTAAACAGAGGGGAGGGCATGGATCCCCGGGAGTTAGAAGAGTAGCAGCTTGTGGATTAC  
TACGCAGTGGAGGAAGAAGAGTTGTTGGAAATTATTTGAGAGGTAGTATAATCATTGTGAGG  
CAGTTTTCTGCATTACCATTTCTCACAGACTAAGTTACTCATAAGCAAACGTGCAATTCACA  
TTACACTGAAATTCTTCCCTAATACATCATTTGCATTGGAATAAAGTACGGTTTTCAAACAAC  
CTGATATAGCAGAACTGACTGTATAAATTATGTGAGCACAGTGCAAGTAATTCTTTGTTTGT  
TGTTTGTTTTTTTGAGACAGAGTCTCACTCTATCTCCAGGCTGGAGTGTAGTGGTGCGATCC  
CGGCTCACTGCAACCTCGATCTCCAGGCTCAAGCGATTCCCCTGCCTCAGCCTCCTGAGTAG  
CTGGGATTACAGGCATGAGCCACCACGCCCGGCTAATTTTTGTATTTTGTAGTAGACGGGGT  
TTCACCTGTTGGCCAGGCTGGTCTCGAACTACGGACCTCAGGTGATCTGCCCCCTCAGCCT  
CTCAAAGTGCTGGGATTATAGCATGAGCCACTGAGCCCAGACACAAGTAGTTCTTTCTGATAA  
ACACTTTAACTGAATGCA

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**FIGURE 104**

MRRISLTSSPVRLLLFLLLLLIALEIMVGGHSLCFNFTIKSLSRPGQPWCEAQVFLNKNLFLQ  
YNSDNNMVKPLGLLGKKVYATSTWGELTQTLGEVGRDLRMLLCDIKPQIKTSDPSTLQVEMFC  
QREAERCTGASWQFATNGEKSLLFDAMNMTWTVINHEASKIKETWKKDRGLEKYFRKLSKGDC  
DHWLREFLGHWAMPEPTGRRST

**Important features of the protein:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 11-30 (possible type II protein)

**N-glycosylation site.**

amino acids 36-39, 154-157

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 2-5, 182-185, 209-212

**Casein kinase II phosphorylation site.**

amino acids 86-89, 93-96, 142-145, 185-188

**N-myristoylation site.**

amino acids 46-51

**Amidation site.**

amino acids 77-80, 207-210

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**FIGURE 105**

TTTTCCGAGTGACCTTCTTGATGCTGGCTGTTTCTCTCACCGTTCCCCTGCTTGGAGCCATGA  
TGCTGCTGGAATCTCCTATAGATCCACAGCCTCTCAGCTTCAAAGAACCCCCGCTCTTGCTTG  
GTGTTCTGCATCCAAATACGAAGCTGCGACAGGCAGAAAGGCTGTTTGAAAATCAACTTGTTG  
GACCGGAGTCCATAGCACATATTGGGGATGTGATGTTTACTGGGACAGCAGATGGCCGGGTGC  
TAAAACTTGAAAATGGTGAAATAGAGACCATTGCCCCGTTTGGTTCGGGCCCTTGCAAAACCC  
GAGATGATGAGCCTGTGTGTGGGAGACCCCTGGGTATCCGTGCAGGGCCCAATGGGACTCTCT  
TTGTGGCCGATGCATACAAGGGACTATTTGAAGTAAATCCCTGGAAACGTGAAGTGAAACTGC  
TGCTGTCCTCCGAGACACCCATTGAGGGGAAGAACATGTCCTTTGTGAATGATCTTACAGTCA  
CTCAGGATGGGAGGAAGATTTATTTACCGATTCTAGCAGCAAATGGCAAAGACGAGACTACC  
TGCTTCTGGTGATGGAGGGCACAGATGACGGGCGCCTGCTGGAGTATGATACTGTGACCAGGG  
AAGTAAAAGTTTTATTGGACCAGCTGCGGTTCCCGAATGGAGTCCAGCTGTCTCCTGCAGAAG  
ACTTTGTCTGCTGGTGGCAGAAACAACCATGGCCAGGATACGAAGAGTCTACGTTTCTGGCCTGA  
TGAAGGGCGGGGCTGATCTGTTTGTGGAGAACATGCCTGGATTTCAGACAACATCCGGGCCA  
GCAGCTCTGGGGGGTACTGGGTGGGCATGTCGACCATCCGCCCTAACCCCTGGGTTTTCCATGC  
TGGATTTCTTATCTGAGAGACCCTGGATTAAAAGGATGATTTTAAAGCTCTTTAGTCAAGAGA  
CGGTGATGAAGTTTGTGCCGCGGTACAGCCTCGTCCTAGAACTCAGCGACAGCGGTGCCTTCC  
GGAGAAGCCTGCATGATCCCGATGGGCTGGTGGCCACCTACATCAGCGAGGTGCACGAACACG  
ATGGGCACCTGTACCTGGGCTCTTTCAGGTCCCCCTTCCCTCTGCAGACTCAGCCTCCAGGCTG  
TTTAGCCCTCCCAGATAGCTGCCCCTGCCACGCAGGCCAGGAGTCTTCACACTCAGGCACCAG  
GCCTGGTCCAGGAGGAGCTGTGGACACAGTCGTGGTTCAAGTGTCCACATGCACCTGTTAGTC  
CCTGAGAGGTGGTGGGAATGGCTGCTTCATTCCCTCGAGGATGCCCCGGGCCCCACCTGGGCTTG  
TCTTTCTGTTTAGAGGGGAAGTGTAACATATCTGCCATGAGGAACATAAATTCATGTAAAGCCA  
TTTTCTCTTAAACAAAACAAAACCTTTCTAAGTACAATCATTCTCTAGGATTTGGGAAGCTCCT  
TGCACTTGGAACAGGGCTCAGGTGGGTGGAGCAGTAAGGCACTACCCAGAGAGCTTGCTGCTG  
CGGCCCTGTCTGCGGCCTCAAAGTTCTTCTTTACTATATATAACGTGCGGTCATACCTTTCT  
TCGTTGTGGTGGGGATGGAAGAGCAGAGGGAGCATGGCCCAGGGGTGTTGAGGCCAGCGGTGA  
GAGCCGTGTTAGCCAAGACATGGAACCTGTGTTCTCAAGGGTTATGTGGGGCGTGGGCTCTCCA  
TAGTGTGTATGAAAAGCTTGTTGACTCTAGCGGCTCAGAGAGGACTTTGCTGGGTTTCTTTCT  
GTGAATATCTCCGTGCTGACCATGCTGGAATTGGATGATTCTGCAATTCGGGACCTACTGCAG  
GGGTCCGTTTAGTAACGTCTTGTCTGTGATCTTTGTTCTTGACCTCTAGACCCCAAGATGTGA  
ACAGTGCACGTGTTAATGTCATCTTTGCTCATGTGTTATAAGCCCCAAGTTGCTGTATATTTT  
CACAAGTATGTCTACACACTGG

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**FIGURE 106**

MLAVSLTVPLLGAMMLLESPIDPQPLSFKEPPLLLGVLHPNTKLRQAERLFENQLVGPESIAH  
IGDVMFTGTADGRVVKLENGEIETIARFGSGPCKTRDDEPVCGRPLGIRAGPNGTLFVADAYK  
GLFEVNPWKREVKLLLLSSETPIEGKNMSFVNDLTVTQDGRKIYFTDSSSKWQRRDYLLLVMEG  
TDDGRLLLEYDVTREVKVLLDQLRFPNGVQLSPAEDFVLVAETTMARIRRVYVSGLMKGGADL  
FVENMPGFDPNIRPSSSGGYWGMSTIRPNPGFSMLDFLSERPWIKRMIFKLFSQETVMKFVP  
RYSLVLELSDSGAFRRSLHDPDGLVATYISEVHEHDGHLYLGSRSPFLCRLSLQAV

**Important features of the protein:****Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 1-21 (possible type II)

**N-glycosylation sites.**

amino acids 116-119, 152-155

**Casein kinase II phosphorylation sites.**

amino acids 19-22, 27-30, 98-101, 146-149, 221-224, 286-289, 332-335

**N-myristoylation sites.**

amino acids 71-76, 92-97, 189-194, 244-249, 338-343

**Amidation site.**

amino acids 164-167

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**FIGURE 107**

AACGAAGCGTGCGCGCTTTGGTAACCGGCTAGAAATCCCGCACGCGCGCCTGCCTCCTCTCCC  
CAGGCCTGAGCTGCCCCCTCCCACTGCCTTTCCTTCTTCCCGCGAGTCAGAAGCTTCGCGAGGG  
CCCAGAGAGGGCGGTGGGGTGGGCGACCCTACGCCAGCTCCGGGCGGGAGAAAGCCCACCCTCT  
CCCGCGCCCCAGGAAACCGCCGCGCTTCGGCGCTGCGCAGAGCCATGGAATTCTCCTGGCTGG  
AGACGCGCTGGGCGCGGCCCTTTTACCTGGCGTTTCGTGTTCTGCCTGGGCCCTGGGGCTGCTGC  
AGGCCATTAAGCTGTACCTGCGGAGGCAGCGGCTGCTGCGGGACCTGCGCCCCCTTCCAGCGC  
CCCCACCCACTGGTTCCTTGGGCACCAGAAGTTTATTTCAGGATGATAACATGGAGAAGCTTG  
AGGAAATTATTGAAAAATACCCCTCGTGCCTTCCCTTTCTGGATTGGGCCCTTTCAGGCATTTT  
TCTGTATCTATGACCCAGACTATGCAAAGACACTTCTGAGCAGAACAGATCCCAAGTCCCAGT  
ACCTGCAGAAATTCTCACCTCCACTTCTTGGAAGGACTAGCGGCTCTAGACGGACCCAAGT  
GGTTCAGCATCGTCGCTACTAACTCCTGGATTCCATTTTAAACATCCTGAAAGCATAACATTG  
AGGTGATGGCTCATTCTGTGAAAATGATGCTGGATAAGTGGGAGAAGATTGTCAGCACTCAGG  
ACACAAGCGTGGAGGTCTATGAGCACATCAACTCGATGTCTCTGGATATAATCATGAAATGCG  
CTTTCAGCAAGGAGACCAACTGCCAGACAAACAGCACCCATGATCCTTATGCAAAGCCATAT  
TTGAACTCAGCAAAATCATATTTACCGCTTGTACAGTTTGTGTATCACAGTGACATAATTT  
TCAAACCTCAGCCCTCAGGGCTACCGCTTCCAGAAGTTAAGCCGAGTGTGAATCAGTACACAG  
ATACAATAATCCAGGAAAGAAAGAAATCCCTCCAGGCTGGGGTAAAGCAGGATAAACTCCGA  
AGAGGAAGTACCAGGATTTTCTGGATATTGTCTTTCTGCCAAGGATGAAAGTGGTAGCAGCT  
TCTCAGATATTGATGTACACTCTGAAGTGAGCACATTCTGTTGGCAGGACATGACACCTTGG  
CAGCAAGCATCTCCTGGATCCTTTACTGCCTGGCTCTGAACCCTGAGCATCAAGAGAGATGCC  
GGGAGGAGGTGAGGGGCATCCTGGGGGATGGGTCTTCTATCACTTGGGACCAGCTGGGTGAGA  
TGTCGTACACCACAATGTGCATCAAGGAGACGTGCCGATTGATTCTGTCAGTCCCGTCCATTT  
CCAGAGATCTCAGCAAGCCACTTACCTTCCCAGATGGATGCACATTGCCTGCAGGGATCACCG  
TGGTTCTTAGTATTTGGGGTCTTCACCACAACCCTGCTGTCTGGAAAAACCCAAAGGTCTTTG  
ACCCCTTGAGGTTCTCTCAGGAGAATTCTGATCAGAGACACCCCTATGCCTACTTACCATTCT  
CAGCTGGATCAAGGAACTGCATTGGGCAGGAGTTTGCCATGATTGAGTTAAAGGTAACCATTG  
CCTTGATTCTGCTCCACTTCAGAGTGACTCCAGACCCACCAGGCCTCTTACTTTCCCCAACCC  
ATTTTATCCTCAAGCCCAAGAATGGGATGTATTTGCACCTGAAGAACTCTCTGAATGTTAGA  
TCTCAGGGTACAATGATTAAACGTACTTTGTTTTTCGAAGTTAAATTTACAGCTAATGATCCA  
AGCAGATAGAAAGGGATCAATGTATGGTGGGAGGATTGGAGGTTGGTGGGATAGGGGTCTCTG  
TGAAGAGATCCAAAATCATTTCTAGGTACACAGTGTGTGCTAGATCTGTTTCTATATAACT  
TTGGGAGATTTTTCAGATCTTTTCTGTTAACTTTCACTACTATTAATGCTGTATACACCAATA  
GACTTTCATATATTTTCTGTTGTTTTTAAATAGTTTTTCAGAATTATGCAAGTAATAAGTGCA  
TGTATGCTCACTGTCAAAAATTCCTAACACTAGAAAATCATGTAGAATAAAAATTTTAAATCT  
CACTTCACTTAGCCGACATTCATGCCCTGACCAATCCTACTGCTTTTCTTAAAAACAGAATA  
ATTTGGTGTGCAATTCTTTCAGACTTTTCTTATACATTTTATATGTAGAAATGTAGCAATGTA  
TTTGTATAGATGTGATCATTCCCTATATTGTTATTGATTTTTTCACTTAATAAAAATTCACCT  
TATTCCTTAAAA

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**FIGURE 108**

MEFSWLETRWARPFYLAFFVFCALGLLQAIKLYLRRQRLRLDLRPFAPPTHWFLGHQKFIQD  
DNMEKLEEIIIEKYPRAPFWIGPFQAFCCIYDPDYAKTLLSRTDPKSQYLQKFSPLLKGKGLA  
ALDGPKEFQHRRLTPGFHFENILKAYIEVMAHSVMMMLDKWEKICSTQDTSVEVYEHINSMSL  
DIIMKCAFSKETNCQTNSTHDPYAKAIFELSKIIFHRLYSLLYHSDIIFKLSPOGYRFQKLSR  
VLNQYTDITIIQERKKSLOAGVKQDNTPKRKYQDFLDIVLSAKDESGSSFSDDIVHSEVSTFLL  
AGHDTLAASISWILYCLALNPEHQERCREEVGILGDGSSITWDQLGEMSYTTMCIKETCRLI  
PAVPSISRDLISKPLTFPDGCTLPAGITVVLISWGLHHNPAVWKNPKVFDPLRFSQENSQDRHP  
YAYLPFSAGSRNCIGQEFAMIELKVTIALILLHFRVTPDPTRPLTFPNHFILKPKNGMYLHLK  
KLSEC

**Important features of the protein:****Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 310-330, 397-413, 459-473

**N-glycosylation site.**

amino acids 206-210

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 265-269, 504-520

**N-myristoylation sites.**

amino acids 25-31, 298-304, 353-359, 450-456, 456-462

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 447-457

**Cytochrome P450 cysteine heme-iron ligand proteins.**

amino acids 444-475



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**FIGURE 109**

GGCGTTCCGGGCCTCAACTTTGGCGTCGTGAGATTCTTGTGAGGCGTCTGCCTGGAAGCCGGC  
AGCAATTTTGCTTCTTTAAAGAGAAAAAGAAGGCTAGGGACTCAGATTCCTGGATTCTGAGAT  
CCAGACCAGCTCCTCCCAGACCTCTCCAGAAGAAGCCATGGGAACCCCTCGTATCCAGCATTT  
GCTGATCCTCCTGGTCCTAGGAGCCTCCCTCCTGACCTCGGGCCTAGAGCTGTATTGTCAAAA  
GGGTCTGTCCATGACTGTGGAAGCAGATCCAGCCAATATGTTTAACTGGACCACAGAGGAAGT  
GGAGACTTGTGACAAAGGGGCACTTTGCCAGGAAACCATACTAATAATTAAAGCAGGGACTGA  
GACAGCCATTTTGGCCACGAAGGGCTGCATCCCGGAAGGGGAGGAGGCCATAACAATTGTCCA  
GCACTCTTCACCTCCCGGCCTGATCGTGACCTCCTACAGTAACTACTGTGAGGATTCCTTCTG  
TAATGACAAAGACAGCCTGTCTCAGTTTTGGGAGTTCAGTGAGACCACAGCTTCCACTGTGTC  
AACAAACCCTCCATTGTCCAACCTGTGTGGCTTTGGGGACCTGTTTCAGTGCTCCTTCTCTTCC  
CTGTCCCAATGGTACAACCTCGATGCTATCAAGGAAACTTGAGATCACTGGAGGTGGCATTGA  
GTCGTCTGTGGAGGTCAAAGGCTGTACAGCCATGATTGGCTGCAGGCTGATGTCTGGAATCTT  
AGCAGTAGGACCCATGTTTGTGAGGGAAGCGTGCCACATCAGCTGCTCACTCAACCTCGAAA  
GACTGAAAATGGGGCCACCTGTCTTCCCATTCTGTTTGGGGGTACAGCTACTGCTGCCATT  
GCTGCTGCCATCATTTATTTCACTTTTCCTAAGAAGGCACTTCTGGGCCTGGGTCTGAGGACAT  
CTTTTTTGACTGGGAGCCTTCTTACTGTTGAGGTTCAACAAGCTGAGGAGTAGATGGGAATTT  
GAGGGAGAATACAGAGATACTATGAACGTATTTGACATTTTAAATAACAATTTCTGCTATAATT  
TTTGTATGCAGTAGGCGTTACTAATAAACATTTCTGCTGTGA

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**FIGURE 110**

MGTPRIQHLLILLVLGASLLTSGLELYCQKGLSMTVEADPANMFNWTTEEVEETCDKGALCQET  
ILIIKAGTETAILATKGCIPEGEEAITIVQHSSPPGLIVTSYSNYCEDSFNDKDSLSQFWEF  
SETTASTVSTTLHCPTCVALGTCFSAPSLPCPNGTTRCYQGKLEITGGGIESSVEVKGCTAMI  
GCRLMSGILAVGPMFVREACPHQLLTQPRKTENGATCLPIPVGWLQLLLPLLLPSFIHFS

**Important features of the protein:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 184-201

**N-glycosylation sites.**

amino acids 45-49, 159-163

**N-myristoylation sites.**amino acids 31-37, 70-76, 99-105, 147-153, 160-166, 174-180,  
175-181

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**FIGURE 111**

CGAGAAGAGGACAGAGGAGACTGAGCAAAGGGGGGTGGGCTCCAGGCGACCCCTAGCCCAATTCTGCCCCTCCAT  
CCCAAGGGGCGAGAGAAATTGCTTTCTTTGCTGACTCCTACGAGGAAAAAAAAAAAAAAAAAAAAAACCATTAA  
AGGGAAAGATAAACGGAGACGGAGGAAAGGTGGCAGCCAGATTACTTAGAGAGGCACAGAGGAGAGATCGGGG  
TGAGTCGCCATGCGGACTCCCAGGGCCCCAGCACCCGCCCTCCCCAGCTGCTGTTCTAATTCTGCTGAGCTGT  
CCCTGGATCCAGGGTCTGCCCCGAAGGAGGAGGAGATATTGCCAGAGCCTGGAAGTGAGACCCCCACGGTGGCC  
TCTGAGGCCCTGGCTGAAGTCTTTCATGGGGCCCTGCTGAGGAGGGGGCCAGAGATGGGCTACCTGCCAGGATCT  
GATCCGGACCCACGCTAGCCACCCCTCCGGCCGGCCAGACTCTCGCAGTGCCCTCCCTGCCACGGGCCACTGAG  
CCGGGGACAGGGCCTCTGACAAACAGCCGTCAACCCCTAACGGGGTCAGGGGGGACAGGGCCACTGCGCCAGAACTG  
CTGACCCCGCCCCCAGGAACACAGCCCCACCCCAACCCAGCCCTGCCTCCCCAGGGCCTCCCTTGGGCCTGAG  
GGAGGAGAGGAGGAGACGACACCACCATCATCACCACGACAACTGTTACCACTACGGTGACCAGCCCAGTTCTG  
TGTAATAACAACATCTCCGAGGGCGAAGGGTATGTGGAGTCTCCAGATCTGGGGAGCCCCGTACGCCGACCCCTG  
GGGCTCCTGGACTGCACTTACAGCATCCATGTCTACCCTGGCTACGGCATTGAGATCCAGGTGCAGACGCTGAAC  
CTGTACAGGAAGAGGAGCTCCTGGTGTGGCTGGTGGGGGATCCCCAGGCCTGGCCCCCGACTCCTGGCCAAAC  
TCATCCATGCTTGGAGAAGGACAAGTCTTTCGGAGCCCCAACCAACCGGCTGCTTCTGCACTTCCAGAGCCCACGG  
GTCCCAAGGGCGGTGGCTTCAGGATCCACTATCAGGCCTACCTCCTGAGCTGTGGCTTCCCTCCCGGGCCGGCC  
CATGGGGACGTGAGTGTGACGGACCTGCACCCCTGGGGGCACTGCCACCTTTCACTGTGATTTCGGGCTACAGCTG  
CAGGGAGAGGAGACCCTCATCTGCCTCAATGGCACCCTGGCCATCCTGGAACGGTGAACCCCCAGCTGCATGCA  
TCCTGTGGTGGCACCATCCACAATGCCACCCTGGGCGCATCGTGTCCCCAGAGCCTGGGGGAGCCGTAGGGCCC  
AACCTCACCTGCCGTTGGGTCAATTGAAGCAGCTGAGGGGGCCGGCTGCACCTGCACTTTGAAAGGGTCTCGCTG  
GATGAGGACAATGACCGGCTGATGGTGCCTCAGGGGGCAGCCCCCTATCCCCGTGATCTATGATTTCGGACATG  
GACGATGTCCCGAGCGGGGTCTCATCAGTGACGCCCAGTCCCTCTACGTGGAGCTGCTGTGAGAGACACTGCC  
AATCCCCTGCTGTTAAGCCTTCGATTTGAAGCCTTTGAGGAGGATCGTGTCTCGCCCCCTTCTGGCACATGGA  
AATGTCACTACCACGGACCCTGAGTATCGCCAGGGGCACTGGCAACCTTCTCGTGCCTCCCAGGATATGCCCTG  
GAGCCCCCTGGGCCCCCAATGCCATCGAATGTGTGGATCCCACAGAACCCCACTGGAACGACACAGAGCCGGCC  
TGCAAAGCCATGTGTGGAGGGGAGCTGTGGAACCCAGCTGGCGTGGTCTCTCTCCGACTGGCCCCAGAGCTAT  
AGCCCGGGCCAAAGACTGCGTGTGGGGCGTGACAGTCCAGGAAGAGAAGCGCATCTTGCTCCAAGTTGAGATATTG  
AATGTGCGGGAAGGGGACATGCTGACGCTGTTCGACGGGGACGGTCCCAGCGCCCCGAGTCTTGGCCCCAGCTGCGG  
GGACCTCAGCCGCGCCGCGCCTTCTCTCCTCTGGGCCCCGACCTCACACTGCAGTTTCAGGCACCGCCCCGGCCC  
CCAAATCCAGGCCTGGGCCAGGGCTTCGTATTGCACTTCAAAGAGGTCCCGAGGAACGACAGCTGCCCGAGCTG  
CCACCTCCGGAGTGGGGCTGGAGAACGGCATCCCACGGGGACCTGATCCGGGGCACGGTGCTCACCTACCACTGC  
GAGCCTGGCTACGAGCTGCTAGGCTCCGACATTTCTCACTTGCCAGTGGGACCTGTCTTGGAGCGCCGCGCCGCC  
GCCTGCCAAAAGATCATGACTTGTGCTGACCCCTGGCGAGATTGCCAACGGGCACCGCACCGCCTCGGACGCCGGC  
TTCCCCGTTGGCTCCCAGTCCAGTACCGCTGCCTGCCAGGGTACAGCCTCGAGGGGGCAGCCATGCTCACCTGC  
TACAGCCGGGACACAGGCACACCCAAGTGGAGCGATAGGGTCCCCAAATGCGCCTTGAAGTACGAGCCGTGCCTG  
AACCCGGGGGTTCCCAGAAATGGCTACCAGACGCTGTACAAGCACCCTACCAGCGGGCGAGTCTCTGCGCTTC  
TTCTGCTATGAGGGCTTTGAGCTTATCGGCGAGGTACCATCACCTGTGTGCGCCGGCCACCCCTCCCAGTGGACC  
AGCCAGCCCCCACTCTGCAAAGTGACCCAGACCACAGATCCATCACGGCAGCTGGAAGGGGGGAACCTGGCCCTG  
GCCATCCTGCTGCCTCTAGGCTTGGTCAATTGTCTCGGAGTGGCGTTTACATCTACTACCAAGCTTCAGGGGA  
AAGTCCCTTTTTCGGCTTCTCGGGCTCCCACTCCTACAGCCCCATCACCGTGGAGTCCGACTTCAGCAACCCGCTG  
TATGAAGCTGGGGATACGCGGGAGTATGAAGTTTCCATCTGAACCCCAAGACTACAGCTGCAGGACCCAGGACGC  
CCCTCCCCCTCCTCATTCGGGCAGAGGGAAATACGGGACCCGGTCTCTGCCTCCTGGCTGCCCTCCTCCCTGGCTG  
TGTAATAGTCTCCCTATCCCACGAGGGGGCTTTGATGGCCCTGGAGATCCTACAGTAAATAAACAGCATCCTG  
CCGCCCCAAAAA

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**FIGURE 112**

MGTPRAQHPPPPQLLFLILLSCPWIQGLPLKEEEILPEPGSETPTVASEALAE LLHGALLRRG  
PEMGYLP GSDPDPTLATPPAGQTLAVPSLPRATEPGTGPLTTAVTPNGVRGAGPTAPELLTTP  
PGTTAPPPSPASPGPPLGPEGGEEETTTTIIITTTVT TTTVTSPVLCNNNISEGEGYVESPD  
GSPVSR TLGLLDCTYSIHVYPGYGIEIQVQTLNLSQEEELLVLAGGGSPGLAPRLLANSSMLG  
EGQVLRSP TNRLLLHFQSPRVPRGGGFRIHYQAYLLSCGFPPRPAHGDVSVTDLHPGGTATFH  
CDSGYQLQGEETLICLNGTRPSWNGETPSCMASCGGTIHNATLGRIVSPEPGGAVGPNLTCRW  
VIEAAEGRRLLH LHFERSLDEDNDRMLMVRSGGSPLSPVIYDSMDVPERGLISDAQSLYVEL  
LSETPANPLLLSLRFEAFEEEDRCFAPFLAHGNVTTTDPEYRPGALATFSCLPGYALEPPGPPN  
AIECVDPT EPHWNDTEPACKAMCGGELSEPAGVVLSPDW PQSYSPGQDCVWGVHVQEEKRILL  
QVEILNVREGDMLT LFDGDGPSARVLAQLRGPQPRRLLSSGPD LTLQFQAPP GPPNPGLGQG  
FVLHFKEVPRNDTCPELPPPEWGWRTASHGDLIRGT VLT YQCEPGYELLGSDILT CQWDLWS  
AAPPACQKIMTCA DPGEIANGHRTASDAGFPV GSHVQYRCLPGYSLEGAAMLTCYSRDTGT PK  
WSDRVPKCAL KYEPCLNPGVPENGYQTLYKH HYQAGESLRFFCYEGFELIGEVTITCVPGHPS  
QWTSQPPLCKVTQT TDP SRQLEGGNLALAILLPLGLVIVL GSGVYIYYTKLQKSLFGFSGSH  
SYSPITVESDFSNPLYEAGDTREYEVSI

**Important features of the protein:****Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 842-864

**N-glycosylation sites.**amino acids 176-180, 222-226, 247-251, 332-336, 355-359, 373-377,  
473-477, 517-521, 641-645**Tyrosine kinase phosphorylation site.**

amino acids 61-69

**N-myristoylation sites.**amino acids 2-8, 84-90, 111-117, 114-120, 190-196, 198-204,  
235-241, 309-315, 333-339, 351-357, 472-478, 484-490, 528-534,  
626-632, 665-671, 775-781, 842-848**Amidation site.**

amino acids 384-388

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

**CUB domain proteins profile.**

amino acids 202-218, 376-392, 553-569

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**FIGURE 113**

GCCGCGGGCGGAGCTGCCTGCCGGTCCCGCGCCGCGCGTCCGCACTCCTCGGCCCTCGGGCGGTTCGATGGGACGG  
GGCGCCGCGGAGCAGGAGGCGCGCCCGTCCGGGTGCTCGGGCCGCGCGGGAGCCCACTGTGGGGCTCGGGCATG  
GCGGGCCGAGGACCTGAGCTCTCCTCAGGGGAGCGGGAGGCAGCTGCTGGCCGGCGATGGGGACGGAGTGGGG  
CCGTGCGCGCCGCGCGGAGCCGTGAGCGCCGAGCCACCGCCGCGCTACCTCAGCCCTTCGCGAAGCGCCGGCA  
GCTCGGGAACATGGCCCTGGAGCGGCTCTGCTCGGTCCCTCAAAGTGTTGTTAATAACAGTACTGGTAGTGGAAGG  
GATTGCCGTGGCCCAAAAACCAAGATGGACAAAATATTGGAATCAAGCATATTCTGCAACCCAGTGTGGCAT  
TTGGGTTTGAACCCAGCAATGGAGGTCATTTTGCTTCGCCAAATTATCCTGACTCATATCCACCAACAAGGAGTG  
TATCTACATTTTGAAGCTGCTCCAGTCAAAGAATAGAGTTGACCTTTGATGAACATTATTATATAGAACCATC  
ATTTGAGTGTGGTTTGATCACTTGAAGTTTCGAGATGGGCCATTTGGTTTTCTCTCTCTTATAGATCGTTACTG  
TGGCGTGAAAAGCCCTCCATTAAATAGATCAACAGGGAGATTTCATGTGGATTAAAGTTTAGTTCTGATGAAGAGCT  
TGAAGGACTGGGATTTTCGAGCAAAATATTCAATTTATCCAGATCCAGACTTTACTTACCTAGGAGGTATTTTAAA  
TCCCATTCAGATTGTGAGTTCGAGCTCTCGGGAGCTGATGGAATAGTGCGCTCTAGTCAGGTAGAACAAGAGGA  
GAAAACAAAACCCAGGCCAAGCCGTTGATTGCATCTGGACCATTAAAGCCACTCCAAAAGCTAAGATTTATTTGAG  
GTTCTTAGATTATCAAATGGAGCACTCAAATGAATGCAAGAGAACTTCGTTGCAGTCTATGATGGAAGCAGTTT  
TATTGAAAACCTGAAGGCCAAGTTTTCGAGCACTGTGGCCAATGATGTAATGCTTAAACAGGAATTGGAGTGAT  
TCGAATGTGGGCAGATGAAGGTAGTGGGCTTAGCAGGTTTCGAATGCTCTTTACTTCCCTTTGTGGAGCCCTCCCTG  
CACAAGCAGCACTTTCTTTTGGCATAGCAACATGTGCATCAATAATCTTTAGTCTGTAATGGTGTCCAAAATTG  
TGCATACCTTGGGATGAAAATCATTGTAAGAAAAGTAGTTACACTTTCAAACAGGGACATGAGTGCCCTGAGCAGGCCCTGGA  
TGGAACAATTATTGGCATTACTTCAGGGATTGTCTTGGTCTTCTCATTATTTCTATTTTAGTACAAGTGAAACA  
GCCTCGAAAAAAGGTTCATGGCTTGCAAAACCGCTTTTAAATAAAACCGGGTTCCAAGAAGTGTTTGATCCTCCTCA  
TTATGAAGTGTTCCTAAGGGACAAAGAGATTTCTGCAGACCTGGCAGACTTGTGGAAGAATTGGACAACCTA  
CCAGAAGATGCGCGCTCCTCCACCGCCTCCCGCTGCATCCACGACCACCACTGTGGGTGCGAGGCCCTCCAGCGT  
CAAACAAAGCAGGACCAACCTCAGTTCCATGGAACCTTCTTTCCGAAATGACTTTGCACAACCACAGCCAATGAA  
AACATTTAATAGCACCTTCAAGAAAAGTAGTTACACTTTCAAACAGGGACATGAGTGCCCTGAGCAGGCCCTGGA  
AGCCGAGTAATGGAGGAGATTCCCTGTGAAATTTATGTGAGGGGGCGAGAAGATTCTGCACAAGCATCCATATC  
CATTGACTTCTAAATCTTCTGCTAATGGTGATGTGAATCTTAGGGTGTGTACGTACGCAGCCTCCAGGGCACCAT  
ACTGTTTCCAGCAGCCAACCTTTTCTCCCATCACAACCTACGAAGACCTTGATTTACCGTTAACCTATTGTATGG  
TGATGTTTTTATCTCTCAGGCAGTCTATATATGTTAAACCAATCAAGGAACCTTACTTATTAGTGGAACAAT  
AATCATCTCTATTGCTTGGTGTCAATTTATAGGAAGCACTGCCAGTTAAAGAGCATTAGAAGAGGTGGTTGGATGG  
AGCCAGGCTCAGGCTGCCTCTTCGTTTTAGCAACAAGAAGAACTGCTCTTGACTGATAACAGCTCTGTCAATATTT  
TGATGCCACAATAAACTTGATTTTTTTTTTACATTCCTTTTATTTTTCTCTTCTAAATTTAATTTGTTTTATAA  
GCCTATCGTTTTACCATTTCAATTTCTTACATAAGTACAAGTGGTTAATGTACCACATACTTCAGTATAGGCATT  
TGTTCTTGAGTGTGCAAAATACAGCTAGTTACTGTGCCAATTAAGACCCAGTTGATTTACCCATCTGTTTCT  
TCTTGGCTAATCTCTGACTTCTGCCTTTTAATTACTGGGCCCTTATTCCTTATTTCTGTGAGAAATAATAGAT  
GATATGATTTATTACCTTTCAATTATATTTTCTCAGTTTATACTAGAAAATTTTATAATCCTGGGATATATGTAC  
CATTGTGAGCTATGACTAAAAATTTGAAAAGATAAAAATTTCTAGCAAGCCCTTGAAGTTTACCAAGTATAGTC  
ACATTCAGTGACAGCCCATTCATTCCAGTAAAGAATCATTTCATTCACTTTGGGAGAGGCCTATAATTACATTTA  
TTTGCAATGTTTCTCTTCGCTAGATTGTTACATAGCTCCCATCTGTTGGTTTTGCTTACAGCATATGGTAACCA  
AGGTTAGATGCCAGTTAAATTCCTTAGAAATTGGATGAGCCTTGAGATTGCTTCTTAAGTGGGACATGACATTT  
TTCTAGCTCTTATCAAGATAACAACCTCCACTTTTTTTAACTGCACTTTTGACTTTTTTTATGGTATAAAAA  
CAATAATTTATAAACATAAAAGCTCATTGTGTTTTTTTAGACTTTTGATATTATTTGATACTGTACAACTTTATT  
AAATCAAGATGAAAGACCTACAGGACAGATTCCTTTTCACTGTTTACATCAGTGGCTTTGATGCAAAATATGCTGT  
GTTGGACCTGGACGCTATAACTTATTGTAAAGACCTTGGAATGTGGACATAAGCTCTTTCTTTCTTTTGTAC  
TGATTTAGTTTGTGATAAATTTTCACTGTGTGATATTTATGCTCTAAATCACTACACAAATCCCATATTAATA  
TATACATTGTACCTGAAAAAAA

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**FIGURE 114**

MALERLCSVLKVLITVLVVEGIAVAQKTQDGQNIQIKHIPATQCGIWVRTSNGGHFASPNYP  
DSYPPNKECIYILEAAPRQRIELTFDEHYIIEPSFECDHLEVRDGPFGFSPLIDRYCGVKS  
PPLIRSTGRFMWIKFSSDEELEGLGFRKYSFIPDPDFTYLGGILNPIPDCQFELSGADGIVR  
SSQVEQEETKPGQAVDCIWTIKATPKAKIYLRLDYQMEHSNECKRNFVAVYDGSSSIENLK  
AKFCSTVANDVMLKTGIGVIRMWADEGSRLSRFRMLFTSFVEPPCTSSTFFCHSNMCINNSLV  
CNGVQNCAYPWDENHCKEKKKAGVFEQITKTHGTIIGITSGIVLVLLIISILVQVKQPRKKVM  
ACKTAFNKTGFQEVFDPHYELFSLRDKEISADLADLSEELDNYQKMRRSSTASRCIHDHHC  
SQASSVKQSRTNLSSMELPFRNDFAPQPMKTFNSTFKKSSYTFKQGHECPEQALEDRVMEEI  
PCEIYVRGREDQAQASISIDF

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 348-369

**N-glycosylation sites.**

amino acids 311-315, 385-389, 453-457, 475-479

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 426-430, 479-483

**N-myristoylation sites.**amino acids 22-28, 32-38, 54-60, 186-192, 279-285, 318-324,  
348-354, 352-358, 441-447

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**FIGURE 115**

GGTCTCTGTCCTTGGCTGTGGCTCCTGCGCTCTGGCTGAGCCATGTTTCCTTCTCCTCGCCCTC  
CTCACTGAGCTTGGGAAGACTGCAAGCCCACGAAGGTTCTGAAGGAATATTTCTGCATGTCACA  
GTTCCACGGAAGATTAAGTCAAATGACAGTGAAGTTTCAGAGAGGAAGATGATTACATCATT  
ACAATTGATGGACAACCTTACACTCTACATCTCGGAAAACAATCATTCTTACCCCAAGACTTT  
TTGGTTTATACATATAATGAACTGGATCTTTGCATTCTGTGTCTCCATATTTTATGATGCAT  
TGCCATTACCAAGGATATGCTGCCGAATTTCCAAATTCATTTGTGACACTCAGTATATGTTCT  
GGTCTCAGGGGATTTCTCCAGTTTGAATAATATCAGTTATGGAATTGAACCAGTAGAATCTTCA  
GCAAGATTTGAGCATATAATTTATCAAATGAAAAATAATGATCCAAATGTATCCATTTTAGCA  
GTAAATTACAGTCATATTTGGCAGAAAGACCAGCCCTACAAAGTTCCTTTAAACTCACAGATA  
AAAAATCTTTCAAACTATTACCCCAATATCTGGAAATATACATTATAGTGGAAAAAGCTTTG  
ATGTTTACCCAGTTCAAATTGACTGTTATACTGTCTTCCTTGGAAATTGTGGTCAAATGAAAAC  
CAGATTTCCACCAGTGGGGATGCTGATGATATATTACAAAGATTTTGGCATGGAAACGGGAC  
TATCTCATCCTACGGCCCCATGACATAGCATACTTACTTGTTTACAGGAAACATCCTAAATAT  
GTGGGAGCAACATTTCTGCGACCGTATGCAATAAAAGCTATGATGCAGGTATTGCTATGTAT  
CCAGATGCAATAGGTTTGGAGGGATTTTCGGTTATTATAGCTCAACTGCTTGGCCTTAATGTA  
GGATTAACATATGATGACATCACTCAGTGTTTCTGTCTGAGAGCTACATGCATCATGAATCAT  
GAAGCAGTGAGTGCCAGTGGTAGAAAGATTTTAGCAACTGCAGCATGCACGACTATAGATAT  
TTTGTTCAAAATTTGAGACTAAATGCCTTCAGAAGCTTTCAAATTTGCAACCATTACATCAA  
AATCAACCAGTGTGTGGTAATGGGATTTTGAATCCAATGAAGAATGTGACTGTGGTAATAAA  
AATGAATGTCAATTTAAGAAGTGCTGTGATTATAACACATGTAACTGAAGGGCTCAGTAAAA  
TGTGGTTCTGGACCATGTTGTACATCAAAGTGTGAGTTGTCAATAGCAGGCACTCCATGTAGA  
AAGAGTATTGATCCAGAGTGTGATTTTACAGAGTACTGCAATGGAACCTCTAGTAATTGTGTT  
CCTGACACTTATGCACTGAATGGCCGTTTGTGCAAGTTGGGAACTGCCTATTGCTATAACGGA  
CAATGTCAAACCTACTGATAACCAGTGTGCCAAGATATTTGGAAAAGGTGCTCAAGGTGCTCCA  
TTTGCCTGTTTTAAAGAAGTTAATTCTCTGCATGAAAGATCTGAAAACCTGTGGTTTTAAAAAT  
TCACAACCATTACCTTGTGAACGGAAGGATGTTCTCTGTGGAAAATTAGCTTGTGTTTCAGCCA  
CATAAAAATGCTAATAAAAGTGACGCTCAATCTACAGTTTATTTCATATATTCAAGACCATGTA  
TGTGTATCTATAGCCACTGGTTCCTCCATGAGATCAGATGGAACAGACAATGCCTATGTGGCT  
GATGGCACCATGTGTGGTCCAGAAATGTACTGTGTAAATAAAACCTGCAGAAAAGTTTCATTTA  
ATGGGATATAACTGTAATGCCACCACAAAATGCAAAGGGAAAGGGATATGTAATAATTTTGGT  
AATTGTCAATGCTTCCCTGGACATAGACCTCCAGATTGTAAATTCAGTTTGGTTCCCCAGGG  
GGTAGTATTGATGATGGAATTTTCAGAAATCTGGTGACTTTTATACTGAAAAGGGCTACAAT  
ACACACTGGAACAACCTGGTTTATTCTGAGTTTCTGCATTTTCTGCCGTTTTTCATAGTTTTC  
ACCACTGTGATCTTTAAAGAAATGAAATAAGTAAATCATGTAACAGAGAGAATGCAGAGTAT  
AATCGTAATTCATCCGTTGTATCAGAAAGCGATGACGTGGGACATTAAATATTGCACAGAAGTT  
CCATAGCAAATAACCTAAAGGAACGAATGTGCTTTATTTATAACCTTACGTTATCCCCAATGC  
ATTGTAAATGTCAAACCTTTGGAAAATAAAGCCTGCGTGCCCTCCC

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**FIGURE 116**

MFLLLALLTELGRLLQAHEGSEGIFLHVTVPRIKISNDSEVSEKMIYIITIDGQPYTLHLGKQ  
SFLPQNFLVYTYNETGSLHSVSPYFMMHCHYQGYAAEFNSFVTLISCSGLRGFLQFENISYG  
IEPVESARFEHIIYQMKNNDPNVSILAVNYSHIWQKDQPYKVPLNSQIKNLSKLLPQYLEIY  
IIVEKALMFTQFKLTVILSSLELWSNENQISTSGDADDILQRFLAWKRDYLILRPHDIAYLLV  
YRKHPKYVGATFPGTVCNKSYDAGIAMYPDAIGLEGFSVIIAQLLGLNVGLTYDDITQCFCLR  
ATCIMNHEAVSASGRKIFSNCSMHDYRYFVSKFETKCLQKLSNLQPLHQNPVCGNGILESNE  
ECDGKNECQFKKCCDYNTCKLKGSVKCGSGPCCTSKCELSIAGTPCRKSIDPECDFTTEYCN  
GTSSNCVPTDYALNGRLCKLGTAYCYNGQCQTTDNQCAKIFGKGAQGAPFACFKEVNSLHERS  
ENCGFKNSQPLPCRKDVLCGKLACVQPHKNANKSDAQSTVYSYIQDHVCVSIATGSSMRSDG  
TDNAYVADGTMCPEMYCVNKTCKRVHLMGYNCNATTKCKGKGICNNFGNCQCFPGHRPPDCK  
FQFGSPGGSIDDGNFQKSGDFYTEKGYNTHWNNWFILSFCIFLPFFIVFTTVIFKRNEISKSC  
NRENAEYNRNSSVSESDDVGH

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 665-684

**N-glycosylation sites.**amino acids 36-39, 76-79, 122-125, 149-152, 156-159, 177-180,  
270-273, 335-338, 441-444, 537-540, 587-590, 601-604, 703-706**Casein kinase II phosphorylation sites.**amino acids 74-77, 208-211, 221-224, 304-307, 337-340, 346-349,  
376-380, 415-418, 499-502, 639-642, 708-711**Tyrosine kinase phosphorylation site.**

amino acids 243-249

**N-myristoylation sites.**amino acids 53-58, 79-84, 266-271, 298-303, 372-377, 403-408,  
408-413, 442-447, 462-467, 469-474, 488-493, 567-572, 610-615,  
616-621, 634-639**Amidation site.**

amino acids 328-331



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**FIGURE 117**

CCCACGCGTCCGCGGACGCGTGGGGCTCAGTGGGCGTCGCGCGAAGGCTAAGGGAGTGTGGCG  
GGCGGCTCCGGGAGCCAAC**ATG**CCTCGGTATGCGCAGCTGGTCATGGGCCCCGCGGGCAGCGG  
GAAGAGCACCTACTGTGCCACCATGGTCCAGCACTGTGAAGCCCTCAACCGGTCTGTCCAAGT  
TGTAACCTGGATCCAGCAGCAGAACAACCTCAACTACTCCGTGATGGCTGACATCCGGGAAC  
GATCGAGGTGGATGATGTAATGGAGGATGATTCTCTGCGATTCCGTCCCAACGGAGGATTGGT  
ATTTTGCATGGAGTACTTTGCCAATAATTTTGGCTGGGAGAACTGTCTTGGCCATGTAGA  
GGACGACTATATCCTTTTTGATTGTCCAGGTCAGATTGAGTTGTACACTCACCTGCCTGTGAT  
GAAACATCTGGTCCAGCAGCTCGAGCAGTGGGAGTTCCGAGTCTGTGGAGTTTTTCTTGTTGA  
TTCTCAGTTCATGGTGGAGTCATTCAAGTTTATTTCTGGCATCTTGGCAGCCCTGAGTGCCAT  
GATCTCTCTAGAAATTCGCAAGTCAACATCATGACAAAAATGGATCTGCTGAGTAAAAAAGC  
AAAAAAGGAAATTGAGAAATTTTAGATCCAGACATGTATTCTTTATTAGAAGATTCTACAAG  
TGACTTAAGAAGCAAAAAATTCAAGAACTGACTAAAGCTATATGTGGACTGATTGATGACTA  
CAGCATGGTTCGATTTTTTACCTTACGATCAGTCAGATGAAGAAAGCATGAACATTGTATTGCA  
GCATATTGATTTTGCCATTCAATATGGAGAAGACCTAGAATTTAAAGAACCAAGGAACGTGA  
AGATGAGTCTTCCTCTATGTTTGACGAATATTTTCAAGAATGCCAGGATGAAT**TGA**AGAGTTTA  
CTAAAAGTAACCATCTAAAGAGCTTGTGGCCAAACCAGCAGAACATTCTTCTCTTCAAAGGAT  
GCAATAGTAGAAAGCTACTTATTTTAATGAAAAAAGTAAACTTCGTTCTTTATCAGCCTCA  
TGCCTGAATCAAATTTTTAATTATTCTGAACTGCTGCTGTTTAAAGTGGAATCTTTTAGTAT  
TATAACAGCATCACTTTAGATTTTGTAAGTCAAATTGAAATGAATGCACATAGATTTATATA  
TAAATTAGCACCTGAGCTAAGGTTAAGGCCGGTCTAAACTTATTTTCACTTTTTGTATTATTT  
TTGAGATGCAGGAATTACTGTAACAAAATATGTATGTCCGAAGGGAAAAAGCTGCAAGGATAT  
ATATAAGACCACTGCTTATCTGTATCTTCCATTTTCCTATATTGAAAATGTATATTATTTAT  
ATAACTTAAAAAGTAAAAATAACTATGTTTTGAGAT

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**FIGURE 118**

MPRYAQLVMGPAGSGKSTYCATMVQHCEALNRSVQVVNLDPAAEHFNYSVMADIRELIEVDDV  
MEDDSLRFPGNGGLVFCMEYFANNFDWLENCLGHVEDDYILFDCPGQIELYTHLPVMKHLVQQ  
LEQWEFRVCGVFLVDSQFMVESFKFISGILAALSAMISLEIPQVNIMTKMDLLSKKAKKEIEK  
FLDPDMYSLLEDSTSDLRSKKFKKLTKAICGLIDDYSMVRFLPYDQSDEESMNIVLQHIDFAI  
QYGEDLEFKEPKEREDESSSMFDEYFQECQDE

**Important features of the protein:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 151-170

**N-glycosylation sites.**

amino acids 31-35, 47-51

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 212-216

**Tyrosine kinase phosphorylation site.**

amino acids 189-197

**N-myristoylation sites.**

amino acids 13-19, 76-82, 154-160

**ATP/GTP-binding site motif A (P-loop).**

amino acids 10-18

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**FIGURE 119**

GGGCGCTGGGAGACACCGGACGCCCCGCTCGGCTGCGCTGCGGCTCAGGCCCCCGCTCGGGCCC  
GACCCGCTCGGTACCGCCGGCTCGGGCGCGCACCTGCCGGCTGCGGCCCCAGGGCCATGCGG  
AGGCCCACGAGGAGGCCGGCGGCCACGCGCATCCCGTAGCCCAGGTGGCCCAGGTCTGCACCG  
CGGCGGCCTCGGCGGCC**ATGG**AGCCCCCGTATTGCTGACGGCGCACTACGATGAGTTCCAAGA  
GGTCAAGTACGTGAGCCGCTGCGGCGCGGGGGGCGCGCGGGGGCCTCCCTGCCCCCGGGCTT  
CCCGTTGGGCGCTGCGCGCAGCGTCACCGGGGCCCGGTCCGGGCTGCCGCGCTGGAACCGGCG  
CGAGGTGTGCTGCTGTGCGGGCTGGTGTTCGCCGCCGGCCTCTGCGCCATTCTGGCGGCTAT  
GCTGGCCCTCAAGTACCTGGGCCCCGGTCGCGGCCGGCGGCGGCGCCTGTCCCGAGGGCTGCCC  
TGAGCGCAAGGCCTTCGCGCGCGCCGCTCGCTTCCTGGCCGCCAACCTGGACGCCAGCATCGA  
CCCATGCCAGGACTTCTACTCGTTGCGCTGCGGCGGTTGGCTGCGGCGCCACGCCATCCCCGA  
CGACAAGCTCACCTATGGCACCATCGCGGCCATCGGCGAGCAAAACGAGGAGCGCCTACGGCG  
CCTGCTGGCGCGGCCCGGGGGTGGGCTGGCGGCGCGGCCAGCGCAAGGTGCGCGCCTTCTT  
CCGCTCGTGCCTCGACATGCGCGAGATCGAGCGACTGGGCCCCGCGACCCATGCTAGAGGTCAT  
CGAGGACTGCGGGGGCTGGGACCTGGGCGGCGCGGAGGAGCGTCCGGGGGTGCGGCGCGATG  
GGACCTCAACCGGCTGCTGTACAAGGCGCAGGGCGTGTACAGCGCCGCCGCGCTCTTCTCGCT  
CACGGTCAGCCTGGACGACAGGAACCTCTCGCGCTACGTTCATCCGCATTGACCAGGATGGGCT  
CACCCTGCCAGAGAGGACCCTGTACCTCGCTCAGGATGAGGACAGTGAGAAGATCCTGGCAGC  
ATACAGGGTGTTCATGGAGCGAGTGCTCAGCCTCCTGGGTGCAGACGCTGTGGAACAGAAGGC  
CCAAGAGATCCTGCAAGTGGAGCAGCAGCTGGCCAACATCACTGTGTGAGAGTATGACGACCT  
ACGGCGAGATGTCAGCTCCATGTACAACAAGGTGACGCTGGGGCAGCTGCAGAAGATCACCCC  
CCACTTGCGGTGGAAGTGGCTGCTAGACCAGATCTTCCAGGAGGACTTCTCAGAGGAAGAGGA  
GGTGGTGCTGCTGGCGACAGACTACATGCAGCAGGTGTGCGAGCTCATCCGCTCCACACCCCA  
CCGGGTCCTGCACAACTACCTGGTGTGGCGCGTGGTGGTGGTCTGAGTGAACACCTGTCCCC  
GCCATTCCGTGAGGCACTGCACGAGCTGGCACAGGAGATGGAGGGCAGCGACAAGCCACAGGA  
GCTGGCCCCGGTCTGCTTGGGCCAGGCCAATCGCCACTTTGGCATGGCGCTTGGCGCCCTCTT  
TGTACATGAGCACTTCTCAGCCGCCAGCAAAGCCAAGGTGCAGCAGCTAGTGAAGACATCAA  
GTACATCCTGGGCCAGCGCCTGGAGGAGCTGGACTGGATGGACGCCGAGACCAGGGCTGCTGC  
TCGGGCCAAGCTCCAGTACATGATGGTGTGCTGCGCTACCCGGACTTCTGCTGAAACCCGA  
TGCTGTGGACAAGGAGTATGAGTTTGAGGTCCATGAGAAGACCTACTTCAAGAACATCTTGAA  
CAGCATCCCCCTCAGCATCCAGCTCTCAGTTAAGAAGATTGCGCAGGAGGTGGACAAGTCCAC  
GTGGCTGCTCCCCCACAGGCGCTCAATGCCTACTATCTACCCAACAAGAACCAGATGGTGT  
CCCCGCGGGCATCCTGCAGCCACCCCTGTACGACCCTGACTTCCCACAGTCTCTCAACTACGG  
GGGCATCGGCACCATCATTGGACATGAGCTGACCCACGGCTACGACGACTGGGGGGGCCAGTA  
TGACCGCTCAGGGAACCTGCTGCACTGGTGGACGGAGGCCTCCTACAGCCGCTTCTGCGAAA  
GGCTGAGTGCATCGTCCGTCTCTATGACAACCTCACTGTCTACAACCAGCGGGTGAACGGGAA  
ACACACGCTTGGGGAGAACATCGCAGATATGGGCGTCCCTCAAGCTGGCCTACCACGCCTATCA  
GAAGTGGGTGCGGGAGCACGGCCAGAGCACCCACTTCCCCGGCTCAAGTACACACATGACCA  
GCTCTTCTTCATTGCCTTTGCCCAGAACTGGTGCATCAAGCGGCGGTGCGAGTCCATCTACCT  
GCAGGTGCTGACTGACAAGCATGCCCCTGAGCACTACAGGGTGTGGGCAGTGTGTCCAGTT  
TGAGGAGTTTGGCCGGGCTTTCCACTGTCCCAAGGACTCACCCATGAACCCTGCCCCACAAGTG  
TTCCGTGTGG**TG**AGCCTGGCTGCCCCGCTGCACGCCCCCACTGCCCCCGCACGAATCACCTCC  
TGCTGGCTACCGGGGACGGCATGCACCCGGTGCCAGCCCCGCTCTGGGCAACCACTGCCTTCC  
AGCCCCCTCCAGGACCCGGTCCCCCTGCTGCCCCCTCACTTCAGGAGGGGCCTGGAGCAGGGTGA  
GGCTGGACTTTGGGGGGCTGTGAGGGAAATATACTGGGGTCCCCAGATTCTGCTCTAAGGGGG  
CCAGACCCTCTGCCAGGCTGGATTGTACGGGCCACCTTCGCTGTGTCTTGCTGCAAAGTC  
TGGTCAATAAATCACTGCACTGTTAAAAA

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**FIGURE 120**

MEPPYSLTAHYDEFQEVKYVSRGAGGARGASLPPGFPLGAARSVTGARSGLPRWNRREVCLL  
SGLVFAAGLCAILAAMLALKYLGPVAAGGGACPEGCPEKAFARAARFLAANLDASIDPCQDF  
YSFACGGWLRRAIPDDKLTGTIAAIGEQNEERLRLLARPGGGPGGAAQRKVRAFFRSCLD  
MREIERLGPRPMLEVEDCGGWDLGGAERPGVAARWDLNRLLYKAQGVYSAAALFSLTVSLD  
DRNSSRYVIRIDQDGLTLPERTLYLAQDEDSEKILAAAYRVFMERVLSLLGADAVEQKAQEILQ  
VEQQLANITVSEYDDLRRDVSSMYNKVTLGQLQKITPHLRWKWLLDQIFQEDFSEEEEVLLA  
TDYMQQVSQILIRSTPHRVLHNYLVWRVVVLSEHLSPPFREALHELAQEMEGSDKPQELARVC  
LGQANRHFGMALGALFVHEHFAASKAKVQQLVEDIKYILGQRLEELDWMDAETRAAARAKLQ  
YMMVMVGYPDFLLKPDADVKEYEFEVHEKTYFKNILNSIPFSIQLSVKKIRQEVDKSTWLLPP  
QALNAYYLPKNQMVFPAFILQPTLYDPDFPQSLNYGGIGTIIGHELTHGYDDWGGQYDRSGN  
LLHWWTEASYSRFLRKAECIVRLYDNFTVYNQRVNGKHTLGENIADMVGLKLAYHAYQKWVRE  
HGPEHPLRLKYTHDQLFFIAFAQNWCIRRSQSIYLQVLTDKHAPEHYRVLGVSVSQFEEFGR  
AFHCPKDSMPNPAHKCSVW

**Important features of the protein:****Transmembrane domain:**

amino acids 64-88

**N-glycosylation sites.**

amino acids 255-259, 322-326, 656-660

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 722-726

**N-myristoylation site.**amino acids 24-30, 26-32, 27-33, 40-46, 47-53, 65-71, 148-154,  
169-175, 170-176, 237-243, 450-456, 604-610, 607-613**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 85-96

**Prenyl group binding site.**

amino acids 772-777

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 609-619

**Neutral zinc metallopeptidases, zinc-binding region proteins.**

amino acids 609-619

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**FIGURE 121**

CGGACTGCCCCGACCGCGCGATGGAGTCGACCGGCAGCGTCGGGGAGGCCCCGGGCGGACCCC  
GGGTGCTGGTGGTGGGCGGCGGCATCGCGGGGCTGGGCGCGGCGCAGAGGCTCTGCGGCCACT  
CCGCCTTCCCGCACCTGCGGGTCCTGGAGGCCACGGCCCCGCGCCGGGGGCCGCATCCGCTCGG  
AGCGCTGCTTCGGTGGCGTGGTGGAGGTGGGCGCGCACTGGATCCATGGGCCCTCCCGGGGTA  
ACCCCGTCTTCCAGCTGGCTGCTGAGTACGGGCTGCTGGGGGAGAAGGAGCTGTCCCAGGAGA  
ACCAGCTGGTGGAGACCGGGGGTCACGTGGGCCTGCCCTCCGTGAGCTACGCCAGCTCCGGGG  
CCAGCGTGAGCCTCCAGCTGGTGGCGGAGATGGCGACTCTGTTCTACGGCCTGATAGACCAGA  
CCCGGGAGTTCTTGCACGCTGCAGAGACCCCGGTGCCAGCGTCGGGGAGTACCTCAAGAAGG  
AGATTGGCCAGCACGTGGCCGGCTGGACAGAGGATGAGGAGACCAGGAAGCTGAAGCTGGCCG  
TCCTGAACTCCTTCTTCAACCTGGAATGCTGTGTGAGCGGCACCCACAGCATGGACCTGGTGG  
CCCTGGCACCCCTTTGGGGAGTATACCGTGCTGCCGGGGCTGGACTGCACCTTTTCTAAGGGCT  
ATCAAGGACTCACAACTGCATGATGGCCGCCCTGCCGGAGGACACTGTAGTTTTTTGAGAAGC  
CTGTGAAGACCATCCACTGGAACGGGTCTTCCAGGAGGCAGCCTTTCCCGGGGAGACCTTTC  
CAGTGTGCGTAGAGTGTGAGGATGGAGACCGGTTCCCGGCGCACCATGTCATCGTCACCGTGC  
CCTTAGGTTTTCTTAGGGAACATTTGGACACCTTCTTTGACCCTCCCCTGCCGGCTGAGAAGG  
CAGAAGCAATCAGGAAGATAGGCTTTGGGACCAACAACAAAATCTTCCTGGAGTTTGAGGAGC  
CCTTCTGGGAGCCAGACTGCCAGCTGATCCAGCTGGTGTGGGAGGACACGTCGCCCCCTGGAGG  
ATGCTGCCCCCTGAGCTACAGGACGCCTGGTTCCGGAAGCTCATTGGCTTTGTGGTCTTGCCTG  
CCTTTGCGTCTGTCCACGTTCTCTGTGGGTTTATTGCCGGACTTGAGTCTGAGTTCATGGAGA  
CTCTGTGCGATGAAGAAGTACTTCTGTGTCTCACCCAAGTGCTCCGGAGAGTGACAGGAAACC  
CACGGCTCCCCGCGCCCAAGAGCGTCTGCGGTCTCGCTGGCACAGCGCCCCGTACACTAGGG  
GGTCTACAGCTACGTGGCCGTGGGCAGTACTGGGGGCGACCTGGACCTGCTGGCTCAGCCCC  
TCCCTGCAGACGGCGCCGGCGCCAGCTCCAGATCCTGTTTGCGGGGAAGCCACACATCGCA  
CGTTTTACTCCACGACGCACGGGGCTCTGCTGTGCGGATGGAGGGAGGCCGACCGCCTCCTCA  
GTCTGTGGGCCCCGCAGGTGCAGCAGCCCAGGCCGAGGCTCTAGCTGGGCCCAGCCTACTCTG  
TTCCACCCGTGTCGGGGGTAGGCTGGGACCGTCATTTCTTCTGACAGATTTAGTCTGGCTTG  
AAATTTGGGGATGTTAATGAGGGTCTCTGGTTTTTTGGTAACAGGGCCACCTTCTCAGTTCT  
TGTGTCTGTTATTGGAGTCTGGCCAGGGTTGACTTGAGCTGAGACACCAGATGCTCACGGAGA  
TGCTGGACACATAAAGCAAGTTACAGCCACAAAAA

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**FIGURE 122**

MESTGSVGEAPGGPRVLVVGGGIAGLGAAQRLCGHSAFPHLRVLEATARAGGRIRSERCFGGV  
VEVGAHWIHGPSRGNPVFQLAAEYGLLGEKELSQENQLVETGGHVGLPSVSYASSGASVSLQL  
VAEMATLFYGLIDQTREFLHAAETPVPSVGEYLLKKEIGQHVAGWTEDEETRKLKLAVLNSFFN  
LECCVSGTHSMDLVALAPFGEYTVLPGLDCTFSKGYQGLTNCMMAALPEDTVVFEKPVKTIHW  
NGSFQEAAPGETFPVSVECEDGDRFPAHHVIVTVPLGFLREHLDTFFDPPLPAEKAEAIRKI  
GFGTNNKIFLEFEFPFWEPCQLIQLVWEDTSPLEDAAPELQDAWFRKLIGFVVLPAFASVHV  
LCGFIAGLESEFMETLSDEEVLLCLTQVLRRTGNPRLPAPKSVLRSRWHSAPYTRGSYSYVA  
VGSTGGDLDLLAQPLPADGAGAQLQILFAGEATHRTFYSTTHGALLSGWREADRLLSLWAPQV  
QQPRPRL

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 364-385

**N-glycosylation site.**

amino acids 253-257

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 408-412

**N-myristoylation sites.**amino acids 20-26, 21-27, 25-31, 105-111, 119-125, 164-170,  
216-222, 227-233, 443-449, 484-490**Aminooxidase Flavin containing amine oxidase:**

amino acids 23-497

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**FIGURE 123**

CGGACGCGTGGGGGAAGATGGATAAATAATTCTGTACACGTGCCCTGGCCTCTGGAGCTCAGCTGCCAGTCCAC  
GTCTAGGGAATCTTAGCATCTGGGACCAAGACACTTTACAGCAATCATCACCCTTTGCAGAGGAGGTGAGCTCAC  
CAGGACTCATCTGCCATTTTCAGACCTTTTGTCTACCTGCCAGGTGGCCCCCACTGCTGACGAGAGATGGTGA  
TCTCTCAGTCTCCCCGACTCCTTGAAGCCAGTATCGCTGACCAGCAGTCTTGTCTTCCTCATGCACCTCCTCCT  
CCTTCAGCCTGGGGAGCCGAGCTCAGAGGTCAAGGTGCTAGGCCCTGAGTATCCCATCCTGGCCCTCGTCGGGGA  
GGAGGTGGAGTTCCCGTGCCACCTATGGCCACAGCTGGATGCCAGCAATGGAGATCCGCTGGTTCCGGAGTCA  
GACCTTCAATGTGGTACACCTGTACCAGGAGCAGCAGGAGCTCCCTGGCAGGCAGATGCCGGCGTTCCGGAACAG  
GACCAAGTTGGTCAAGGACGACATCGCCTATGGCAGCGTGGTCTGCAGCTTACAGCATCATCCCCTCTGACAA  
GGGCACATATGGCTGCCGCTTCCACTCCGACAACCTTCTCTGGCGAAGCTCTCTGGGAAGTGGAGGTAGCAGGGCT  
GGGCTCAGACCCTCACCTCTCCCTTGAGGGCTTCAAGGAAGGAGGCATTGAGCTGAGGCTCAGATCCAGTGGCTG  
GTACCCCAAGCCTAAGGTTTCAGTGGAGAGACCACCAGGGACAGTGCCTGCCTCCAGAGTTTGAAGCCATCGTCTG  
GGATGCCCAGGACCTGTTTCAGTCTGGAAACATCTGTGGTTGTCCGAGCGGGAGCCCTCAGCAATGTGTCCGTCTC  
CATCCAGAATCTCCTCTTGAGCCAGAAGAAAGAGTTGGTGGTCCAGATAGCAGACGTGTTCTGACCCGGAGCCTC  
TGCGTGGAAAGAGCGCGTTTCGTGCGGACCCCTGCCGCTGCTGTGGTCTCGCGGCGCTGGCGCTGGCGCTCCTCCG  
GAAGCAGCGGAGAAGCCGAGAAAAGCTGAGGAAGCAGGCGGAGAAGAGACAAGAGAACTCACTGCAGAGCTGGA  
AAAGCTTACAGACAGAGCTTGACTGGAGACGGGCTGAAGGCCAGGCTGAGTGGAGAGCAGCCAAAAATATGCA  
GGATGTGACGCTGGACCCGGCCTCGGCGCACCCACAGCCTGGAGGTGTGAGGATGGCAAGAGCGTGTCTTCCCG  
CGGGGCGCCCGCAGGCCCCGGCGCCTGGCCACCCGACGCGGTTCTCGGAGCAGACGTGCGCGCTGAGCCTGGAGCG  
GTTCTCCGCGCGCCGCACTACTGGGAGGTGCACGTGGGCGCGCGCAGCCGCTGGTCTTGGGCGCCTGCCTGGC  
CGCGGTGCGCGCGCGCGGGGCTGCGCGCCTGAGCCCTGCGGCGGCTACTGGGTGCTGGGGCTGTGGACGGCTG  
CGAGTACTTCGTCTTGGCCCCGACCCGCTGCGGCTCACCTGCGCGTGCCCCCGCGCGCCTGGGCGTCTTCTCT  
GGACTACGAGGCGGAGAGCTGTCTTCTTCAACGTGTCCGACGGCTCCACATCTTACCTTCCACGACACCTT  
CTCGGGCGCGCTCTGTGCGTACTTCAGGCCAGGGCCCCACGACGGCGCGAACATCCGGATCCCCTGACCATCTG  
CCCCGTGCCGTTAGAGGGACGGGCGTCCCCGAAGAGAAAGACAGTACACCTGGCTACAGCCCTATGAGCCCGC  
GGACCCCGCCTGGACTGGTGGTGAAGGCGCCCTCGTGGCGCGGGACTGGCCCCGGGGGGCCCCCTGGATCCAG  
GCCAGCGCTTTGCTCTCTCTGCTCTGAAGGGAGCAGGTGCACCAGCCAAATGTGAGCGAGGGGGACAAAGA  
GAGGGACCTTTGCCCTACGTAGATGTGTATGTGTAGTGCGATTTTCTTCAAGGAAAGGAGACAAGTCCAAAGCTCG  
TTTGTGGATTGTGGGACTGAGCGAAGGAGTACAAATATATCCACGTCGCTCAGAGCTGGGGTGTCTCAGGTGGG  
GGTGGGCAAGAAGCCAGCATGGAAGAAAGAAGGGAGAAAACCTTTGGTACTGCCTTAGAGGGATCAGTTAATTTG  
TATAGTTTTATATTTTTGTATATGTTTGTAGCTTAAAAAGGTGAGATGCAATAACACTTCGTAAGCAACGA  
GTTACCTAAGTAAGGCTCAGATCCTAGTTTTTAAAAACCATTTCCCATTAATGAAGTTGGAGGAACAGCTGCT  
TCTGAGCCGGGGCAAAAATTTCAAGGTGAGCCTGGAGCATTGTGTGTGGTGAAGTAAAAATAAGGCTCAAAACGT  
GACGGCAACCCGGCAAAAAGGTTAGGGAGCCAGGCCGAAGGGGCGCTCACTGACCAATTGTGGGACAATTTGAACAT  
CAGGATGAATAATGACAGGAGAGATTATAACACACTGAATAAAAAACATAATCCATGAGTTCATGTAATACTCAA  
ATTTCTTTTTTAAAAAGGAGAAACAGGAAGGTTTCTTTTGAGGTGAAATCTAATTATTGGTGAGAGTCTTGAGA  
ACAGGCTGTTTCCAGTCTCAAAGCAGTAACCTTATACACTACTTATAAGTTTGAAGGGGAAAGGTTACCTTTAC  
AATGGAGACATCTACCAGATCATCCAAGTGATTAAATTTAACATCATCAATGATGGGACCAAGGACATTATTAGT  
TTGACAACTGGGGAAAGAAGTGTCTTACCCCCCTACCCCAAGACATTCTCTGTGCGCCAGGCTGGAGTGCA  
GCCTCAACCTCCTGGGCCCCAAGTGATCCTCCACCTCAGCACACAACACCATGCCCAATTTAAGTGCGTTATAG  
AGACGGGGGTCTCACTTTGTTACCCAGGCTGGTCTCAACTCCTGCGCTCAAGCAATCCTCCACCTGGGCGCTCC  
CAAAATGCTGGGTGTACAGGCATGAGCCGCTGTGCCTGGCTTCAATTTTTCAGAGTGAGACATTTGTACTGTGGCTA  
TGTAAGGAGAACATTCTTGTCTTAGCAAAACATACTGAAGTTTTTAGATATTAATTACCACAGTGTCTGCCACTGA  
ATTTCCAGTGACTAAGTGGAATAATATAAAACATATGAATATAAAGAAAGAAAGAGACAAGTCAAATGTAGTAAA  
ATGACAACTTGGTGAAGTCTAGGTGACTGGTGCAGAGATGTTTATTGTACTATCAATGTGGCTTTGCTGTGGGT  
TTGAAATTTGCAAACTAAGAGTTGGGTGGCGGGGAGAAGGATACCAAAAACTAAGTGATTATCTTTGGATG  
GGAAATGTTTGGTAATTGCATTCTTAAATGTCTTCTTTGTATTTTTAATGTTCAATAATGTATATGTATCAG  
TTCTGTAATAAAGGGGAAAACACTTTTCA

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**FIGURE 124**

MVDLSVSPDSLKPVS LTSSLVFLMHLLLLQPGEPSSEVKVLGPEYPILALVGEEVEFPCHLWP  
QLDAQQMEIRWFRSQTFNVVHLYQEQQELPGRQMPAFRNRTKLVKDDIAYGSVVLQLHSIIPS  
DKGTYGCRFHS DNFSGEALWELEVAGLGSDPHLSLEGFKEGGIQLRLRSSGWYPKPKVQWRDH  
QGQCLPPEFEAIVWDAQDLFSLETSVVVRAGALSNVSVSIQNLLLSQKKELVVQIADVFPVGA  
SAWKSAFVATLPLLLVLAALALGVLRLKQRRSREKLRKQAEKRQEKLTAELEKLTQTELDWRRAE  
GQAEWRAAQKYAVDVTLDPASAHPSLEVSEDGKSVSSRGAPPGPAPGHPQRFSEQTCALSLE  
FSAGRHYWEVHVGRRSRWFLGACLAAPRAGPARLSPAAGYWVLGLWNGCEYFVLAPHRVALT  
LRVPPRRLGVFLDYEAGELSFNVS DGS HIFTFHDTFSGALCAYFRPRAHDGGEHPDPLTICP  
LPVRGTGVPEENDSDTWLQPYEPADPALDWW

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 247-272

**N-glycosylation sites.**

amino acids 102-106, 139-143, 224-228, 464-468, 516-520

**Tyrosine kinase phosphorylation site.**

amino acids 105-114

**N-myristoylation sites.**

amino acids 129-135, 220-226, 399-405, 423-429, 480-486

**Amidation site.**

amino acids 390-394



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**FIGURE 125**

TATAGTCCCAGCTACTCATGGGGCTGATGCAGGTTGAGGCAGGAGGTTTCATGAGCCCAGGAGGTTGGAGCTGTAA  
TGAGCTAGGATTCTGCCTCTGCACTCCTAGCTGGATGACAGAGCAAGACCCTGTCTCAAAAAAGAAAAA  
AAAAAGAATGCATGAACCAGACATGACAGTTCCTGGCCTCAAAGATCTTCCAAAGGAAATGATTTTTTTTAAAC  
ACCAATGCTGCAGGAAAAAGCAACATATTTAAGTTATCCAATAACACCTATCCAATAATTGTAAATCATTATCAT  
GACATGGTAGAGTTGTTTATATTTCTTTTCTTTTAGGTGAAACACCATTCAAAGTCGTAGTCAAATCTCTTTCA  
CCTAAAGAGTTGGTCCGGATACATGTCCCTAAACCTTTGGACAGGAATGATGGAACATTTTTTGATGAGATATAGG  
ATGTATGAAACTGTCGATGAAGGCCTGAAGATAGAGGTCCTTTATGGTGATGAACATGTGGCTCAGTCTCCCTAT  
ATTTTGAAGGACCAGTGATACCATGAGTACTGTGAGTGTCCGGAAGATCCTCAGGCCTGGCAGAAGACTCTTTCT  
TGTCACCAAGGAACCACAGATTGCAAAAGATTTTGCTTCCTTTCCAGCATCAATCTCCAGCAAATGCTAAAA  
GAAGTCCCCAAAAGGTTTGGGGATGAGAGAGGTGCCATTGTTTATTACACGATTCTCAATAACCATGTTTACCGG  
AGATCTTTAGGGAAATACACAGACTTCAAGATGTTCTCTGATGAGATTTGTTATCATTGACAAGAAAGGTCCTT  
CTCCAGATTTAGAAATTTATGTTAATCTTGGAGATTGGCCTTGGAGCATCGAAAAGTCAATGGAACCCCTAGC  
CCCATACCTATCATTTCATGGTGTGGCTCTCTGGATTCAAGAGATGTTGTCTTCCAACGTATGACATACCCAC  
TCCATGCTTGAAGCCATGCGGGGTGTACAAATGATCTCCTCTCTATTAGGGAAATACAGGCCTTCTGGATC  
AATAAAGCAGAGAGAGCTTTCTTCAAGGTTAGAGACAGCCGAGAGGAGAGGCTCCAGTTGGTACAGCTGTCCAAA  
GAAATCCTCAGCTACTAGATGCAGGAATTACAGGATATTTCTTTTCCAAGAGAAAGAAAGGAGCTTGGAAAA  
GCCAAGTTGATGGGTTTTCTTTGATTTCTTTAAGTACAAGTATCAAGTAAATGTGGATGGGACCGTGGCTGCTTAC  
AGATATCCATATCTCATGCTGGGCGACAGTCTGGTTTTAAAGCAGGACTCGCCATATTATGAACATTTCTCATG  
GCACTAGAACCTTGAAGCATTATGTTCCAATTAAGAAATCTGAGTGATTTATTAGAGAAAGTTAAATGGGCT  
AAGGAAATGATGAAGAAGCCAAGAAGATTGCAAAAGAAGGACAGTTGATGGCTAGGGACCTACTACGCCACAC  
AGGCTTTACTGCTACTATTACCAAGTACTGCAGAAATATGCCGAGCGCCAGTCCAGCAAACCCGAAGTACGTGAT  
GGAATGGAACCTGTTCTCAGCCAGAAGATAGCACAGCCATCTGCCAGTGCCACAGGAAAAAGCCTTCAAGAGAA  
GAACCTTGAAGTCTCAGCCCAGAATCACACTCCTGTGTATCCCGGCTACACTTAAAGGAAAGATTGAATCTAAGCTGT  
GAAGGACAGTATAGAAGACTGCACCAAGTGGACTAGTTCTCCCGTGGCTTTATATATGTAGATGGATATAGCAG  
TACTGGTTGAGTATCCCTCATCTGAAATGCTTAGGACCAGGAGTGTTCAGGCTTCAGATTTTTTAAGATTTGGG  
AATATTTGCATGTACATGAAGGATCTTGGGGATGAGATCCAAGTCTAAACACAAAATTCATTTATATTTTAT  
ATATACCTTGTTCACATACCCTGAAGGTAATTTTATATAATATTTTTTAATAATTTGTGCATGAACAAAGTTTGT  
ATACATTGAACTGTCAGAAAGCAAAGGTGTCACTATCTTAGCGACCCAAGTGGTGGTGTGAGCACTCAAAAGTT  
TTGGATTTTGGGGTATTTTCAAGATTTTGTATGAGGAATGTTCAACCTGTATTTGAACAAGCATTACCA  
AATATCATTGAATATTAATATCTTTTGGCTAAAACTGCTATTATCAGCATCATAGTTTCTCTAAAAAGAAAAT  
TGGGGATCATAGCCGATAGAGAGACTTGCTAAAAATATAATCAGCCTCTGCAAACTGTTTACATATTTATGGT  
TTACATATTTTATTGGTTTATTTCTATCCCTGTTCACTTTTTCTCTTCCACTTCCAATTATGAAGAGAAAATAT  
TTGTTTCAAGGTTGTCCCCCGCCCCCGTCACTGCATAATTTCTCCTCTTACAAGCTGCTTTTGGCTTTTCAATA  
TAACAGCTTCTTTTAGAAGGTCTGATAAGGATATTTAAGGAAGAAGAGATGACTCTGTTATTAAGGTGGCAT  
GGAGACTGTGGAGGGAATATTTTTTAAAGCACTACTCATATCTTTAACTAAATTTTGCCAAAGCCGAGACAA  
CATTAAAGGAGAAATGTACCTTAAGTTAGTAATTTCAAATCTATCTGAGTTGTATACCCATCAAAGACAATACAG  
TTATTAACATAGATGAAGGTATGCTATAGGCATCATTATTATCTCTATATTGAATAGGTGAAAGATACTGTAG  
TCAGGTGAAAGGCATTCATCATTTTTAAGCTGAAAAGGGGATCCTTGAAAACACTGAAAACCTCTACAACATCT  
TCAGGAAGCCTGCTATCTTGGGATTCACTAATAATAGGCCAAGAACAAGGCAAGCATCCATTCTCACTCCACC  
ACTTTTCTATTTTCACTGGGTGTCTTGGTACGATGAAGACTTTGGAAATTTCTTTCTTTTAGGACAGGGTCA  
GGATTTAGGACTCATAGCCTGAAAGCTCATTACATACTCCTTGTAACTCAGTCCAGGTTTCAAGTTCACTAAAG  
TGCATGTTCTAAAAACAAGAGCTATCCTCATTCCAAATTTTAAATATGTACTCTGGCCGGTTGCAGTGGCTCAGG  
CCTGTAATCCCAGCACTTTGGCAGGCCGAGATGGGCGGATCTTTGAGGTGAGGAGTTGAGACCAGCCTGGCCA  
ACATGGTGAACCCCGTCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGCATTTGCCTGTAATCCCAGCT  
ACTCGGGAGGCTGAGGCAGGAGAACTCACTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTACACCCTG  
CACTCCAGCCTGGGTGACAGAGTGAGACTCCATCTCAAAAACGAAAATAAAAAATATGATTCTCCTAA  
CTGAAATATTTACTTAATCTGGAAAACAATGTAATTTTTTAAAGTGGTTACATCTATTTCTGTGAAGAACA  
TAAACAGAATTTTTTGACTAAGCATAACCAATTTTCAAGACAGTCTAATCAATGCCAAGTATCCAAGGCAAACTC  
TAATACCCATCCATTGTGCAAAACCACAAGCAGCGAAGTATTAATAAGAGCAAGCTGTCTGAGCCCATACCTA  
ATGAATTTGTGTCTTAAATATTGTACATTGTGTTTGGGCTTGTCAAACTGGGATTATGGCAAGAAAGGTTGCC  
TAACTCATACCTTTCTGCCTCAAATTCAGGTGCTAAAGGCTAATGGCATTTTAAACATCTTACATTTTAAAA  
TTTATATTGCCTCTGCCAAACAGGCCTAATAGTTAAAGCAAGTTGAGACAAACCAGGCAGATTGAGTGTGGGA  
ACAGGAAGGATGTGCTTTAAAAAAGGTGGAATCCCTCAAAAATTTCTATAGGGAGACAGCAGCCTTAATCTACA  
TAATCTTCTATCTCGCAATTCAGCCGACGCTTTAAAGAGTTAGTGTTAATGGCTTTCTGGTTTGAACAAAA  
ATGCATCTATGTGGTTGAAAGTTTGGGAGGAGATTACCAATATCTGAGGAGAAGATGGAGTGAAGGGAATTTCT  
ACTTTTGTCTTTTATACCTTTCTATAATATTTAGATTTTTTTTTTACTGTAAGTATGGATCAATTTGCAAAATAAG  
AAAAATGCCAACCTTAGAAAAGACAATAATGCACAAAAGATATAAACAGGAACAGCAAATATTTATTTTTTTC  
CATTTTGTCTTTTTTAAATCTATGTTTAGAATTTATATCTTGGGACTTATGTATATATATACCTTTTAAATAAA  
ATAAATTTTCTAAATAAAAAGTTG

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**FIGURE 126**

MVELFIFLFLLLGETPFKVVVKSLSPELVRIHVPKPLDRNDGTFLMRYRMYETVDEGLKIEVL  
YGDEHVAQSPYILKGPVYHEYCECPEDPQAWQKTLSCPTKEPQIAKDFASFPSINLQQMLKEV  
PKRFGDERGAIVHYTILNNHVYRRSLGKYTDFKMFSDEILLSLTRKVLLPDLEFYVNLGDWPL  
EHRKVNGTPSPIPIISWCGSLDSRDVVLPTYDITHSMLEAMRGVTNDLLSIQGNTGPSWINKT  
ERAFFRGRDSREERLQLVQLSKENPQLLDAGITGYFFFQEKELGKAKLMGFFDFFKYKYQV  
NVDGTVAAARYPYLMLGDSLVLKQDSPYYEHFYMALEPWKHYVPIKRNLSDLLEKVKWAKEND  
EEAKKIAKEGQLMARDLLQPHRLYCYYYQVLQKYAERQSSKPEVRDGMELVPQPEDSTAICQC  
HRKKPSREEL

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 250-254, 363-367

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 444-448

**N-myristoylation site.**

amino acids 208-214, 319-325, 388-394

**Endoplasmic reticulum targeting sequence.**

amino acids 448-453

**Mitochondrial energy transfer proteins signature.**

amino acids 25-34

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**FIGURE 127**

AGCCGTCGGAGGGAGCCGGAGCGCTTCTCCCGAGTTGGTGATAGATTGGTGGTCATCCAACAT  
GCAGAAATGAATGAGCAGTGAAAAGCAGCAGAGCCGATGGGTCATGAGGATGTAAGTGCGTTT  
GAAGGCTTCCACACCCTCTACTCCAGGAATCATGAATAAACTGGAGGATAAGCAGGACCAGAT  
GATACCA**ATGA**AGAGAAGTTTACAGGCCCTCTATTGCCAACTGTTAAGTTTCCTGCTGATCTTG  
GCACTGACCGAAGCGCTGGCATTGTCATCCAGGAACCATCTCCCAGGGAATCTCTTCAGGTC  
CTCCCTTCAGGCACTCCCCCGGGAACCATGGTGACAGCACCCACAGCTCTACCAGACATACT  
TCTGTGGTGATGCTGACCCCCAATCCCGATGGACCCCCCTCACAGGCTGCAGCTCCCATGGCA  
ACACTGACACCCCGTGACAGAGGGGCACCCTCCTACGCACACCATCTCCACCATCGCTGCGACA  
GTAACCGCCCCCTATTCTGAAAGCTCCCTGTCCACAGGGCCCGCTCCAGCAGCCATGGCAACC  
ACATCCTCCAAGCCAGAGGGCCGCCCTCGAGGGCAGGCTGCCCCCACCATCCTGCTGACAAAG  
CCACCGGGGGCCACCAGCCGCCCCACCACAGCGCCCCCGCACTACCACACGCAGGCCCCC  
AGGCCCCCAGGCTCTTCCCGAAAAGGGGCTGGTAATTCATCACGCCCTGTCCCGCCTGCACCT  
GGTGGCCACTCCAGGAGTAAAGAAGGACAGCGAGGACGAAATCCAAGCTCCACACCTCTGGGG  
CAGAAGCGGGCCCTGGGGAAAATCTTTAGATCTACAAGGGCAACTTCACAGGGTCTGTGGAA  
CCAGAGCCCTCTACCCTCACCCCCAGGACCCCACTCTGGGGCTACTCCTCTTCACCACAGCCC  
CAGACAGTGGCTGCGACCACAGTGCCCAGCAATACCTCATGGGCACCCACCACCACCTCCCTG  
GGGCCTGCAAAGGACAAGCCAGGCCTTCGCAGAGCAGCCCAGGGGGGTGGTTCTACCTTCACC  
AGCCAAGGAGGGACACCAGATGCCACAGCAGCCTCAGGTGCCCTGTGAGTCCACAAGCTGCC  
CCAGTGCCTTCTCAGCGCCCCCACCACGGTGACCCACAGGATGGCCCCAGCCATAGTGACTCT  
TGGCTTACTGTTACCCCTGGCACCAGCAGACCTCTGTCTACCAGCTCTGGGGTCTTCACGGCT  
GCCACGGGGGCCACCCAGCTGCCTTCGATACCAGTGTCTCAGCCCCCTCCCAGGGGATTCCCT  
CAGGGAGCATCCACAACCCCAAGCTCCAACCCATCCCTCCAGGGTCTCAGAAAGCACTATT  
TCTGGAGCCAAGGAGGAGACTGTGGCCACCCTCACCATGACCGACCGGGTGCCAGTCTCTC  
TCCACAGTGGTATCCACAGCCACAGGCAATTTCTCAACCGCTGGTCCCCGCCGGGACCTGG  
AAGCCTGGGACAGCAGGGAACATCTCCCATGTGGCCGAGGGGGACAAACCGCAGCACAGAGCC  
ACCATCTGCCTGAGCAAGATGGATATCGCCTGGGTGATCCTGGCCATCAGCGTGCCCATCTCC  
TCCTGCTCTGTCCTGCTGACGGTGTGCTGCATGAAGAGGAAGAAGAAGACCGCCAACCCGGAG  
AACAACTGAGCTACTGGAACAACACCATCACCATGGACTACTTCAACAGGCATGCTGTGGAG  
CTGCCCAGGGAGATCCAGTCCCTTGAAACCTCTGAGGACCAGCTCTCAGAGCCCCGCTCCCCA  
GCCAATGGCGACTATAGAGACACTGGGATGGTCCTTGTTAACCCTTCTGTCAAGAAACACTG  
TTTGTGGGAAACGATCAAGTATCTGAGATCT**TAA**CTACAGCAGGCATCACTTTGCCATTCCGTA  
TTTTTCGTCTCTAAATTATAAATATACAAATATATATTATAAATATAACCTTGTGTAACCC  
TGACTTAATGAGAAACATTTTCAGCTTTTTTTCCTATGAATTGTCAACATCTTTTTTACAAGT  
GTGGTTTAAAAAAAAAAAAAACTTTACAGAATGATCTGTGGCTTTATAAAATAAAGGTATTTCT  
AAGCAAAAAAAAAAAAAAAAAA

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**FIGURE 128**

MKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESLQVLPSGTPPGTMVTAPHSSTRHTSV  
VMLTPNPDGPPSQAAAPMATLTPRAEGHPPTHISTIAATVTAPYSESSLSTGPAPAAMATTS  
SKPEGRPRGQAAPTILLTKPPGATS RPTTAPPRTTTTRRPPRPPGSSRKAGNSSRPVPPAPGG  
HSRSKEGQRGRNPSSTPLGQKRPLGKIFQIYKGNFTGSVEPEPSTLTPRTPLWGYSSSPQPQT  
VAATTVPNSNTSWAPTTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDATAASGAPVSPQAAPV  
PSQRPHHGDPQDGPSHSDSWLTVTPGTSRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPOG  
ASTTPQAPTHPSRVSESTISGAKEETVATLTMTDRVPSPLSTVVSTATGNFLNRLVPAGTWKP  
GTAGNISHVAEGDKPQHRATICLSKMDIAWVILAI SVPISSCSVLLTVCCMKRKKKTANPENN  
LSYWNNTITMDYFNRHAVELPREIQSLETSEDQLSEPRSPANGDYRDTGMVLVNPFCQETLFV  
GNDQVSEI

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 469-487

**N-glycosylation sites.**

amino acids 178-182, 223-227, 261-265, 446-450, 504-508, 509-513

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 495-499

**N-myristoylation sites.**amino acids 44-50, 48-54, 175-181, 222-228, 279-285, 286-292,  
288-294, 296-302, 351-357, 374-380, 427-433, 442-448**TonB-dependent receptor proteins signature 1.**

amino acids 1-44

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**FIGURE 129**

AGGCGAGGCGCGGCGCCGCTGCACACACGCACACGGAGCT**ATG**GGGTGCCATGTTGCCACCAG  
CTGCCACGTGGCCTGGCTTTTGGTGCTGATCTCTGGATGCTGGGGCCAGGTGAACCGGTGCC  
CTTCTTCACCAACCACTTCTTTGATACATACTGCTGATCAGCGAGGACACGCCTGTGGGTTC  
TTCTGTGACCCAGTTGCTGGCCCAAGACATGGACAATGACCCCTGGTGTGGCTGTCTGG  
GGAGGAGGCCTCTCGCTTCTTTGCAGTGGAGCCTGACACTGGCGTGGTGTGGCTCCGGCAGCC  
ACTGGACAGAGAGACCAAGTCAGAGTTCACCGTGGAGTTCTCTGTGACGACACCAGGGGGT  
GATCACACGGAAGGTGAACATCCAGGTGCGGGATGTGAATGACAACGCGCCACATTTACAA  
TCAGCCCTACAGCGTCCGCATCCCTGAGAATACACAGTGGGGACGCCCATCTTCATCGTGAA  
TGCCACAGACCCCGACTTGGGGGCAGGGGGCAGCGTCTCTACTCCTTCAGCCCCCTCCCA  
ATTCTTCGCCATTGACAGCGCCCGCGGTATCGTCACAGTGTGATCCGGGAGCTGGACTACGAGAC  
CACACAGGCCTACCAGCTCACGGTCAACGCCACAGATCAAGACAAGACCAGGCCTCTGTCCAC  
CCTGGCCAACTTGGCCATCATCATCACAGATGTCCAGGACATGGACCCCATCTTCATCAACCT  
GCCTTACAGCACCAACATCTACGAGCATTCTCCTCCGGGCACGACGGTGCATCATCACCGC  
CATAGACCAGGATAAAGGACGTCCCCGGGGCATTGGCTACACCATCGTTTCAGGGAATACAA  
CAGCATCTTTGCCCTGGACTACATCAGCGGAGTGTGACCTTGAATGGCCTGCTGGACCGGGA  
GAACCCCTGTACAGCCATGGCTTCATCTGACTGTGAAGGGCACGGAGCTGAACGATGACCG  
CACCCCATCTGACGCTACAGTCACACGACCTTCAATATCCTGGTTATTGACATCAATGACAA  
TGCCCCGGAGTTCAACAGCTCCGAGTACAGCGTGGCCATCACTGAGCTGGCACAGGTGGCTT  
TGCCCTTCCACTCTTCATCCAGGTGGTGGACAAGGATGAGAATTGGGCCTGAACAGCATGTT  
TGAGGTGTACTTGGTGGGGAACAACTCCCACCACTTCATCATCTCCCCGACCTCCGTCCAGGG  
GAAGGCGGACATTCGTATTTCGGGTGGCCATCCCCTGAGCTACGAGACCGTGGACCGCTACGA  
CTTTGATCTCTTTGCCAATGAGAGTGTGCCTGACCATGTGGGCTATGCCAAGGTGAAGATCAC  
TCTCATCAATGAAAATGACAACCGGCCCATCTTCAGCCAGCCACTGTACAACATCAGCCTGTA  
CGAGAACGTCACCGTGGGGACCTCTGTGCTGACAGTCCTGGTGAGTCCCCGCTTCACTGCAGG  
GCCACTGAGCTCTCCAGGGCCGACTGTGGTGAGGCACCCAGAGGGATTTTGTCCAAGGGACCT  
CAGCAATCAGGGAAGGAGGCACCCCCAAATCCCTGAGCTGTGTTTGGTGTAT**TAA**ATAAA  
GTTTTTGGACTCTTCAGGAAGGGGCTCCCTTGACCTAGGTTGCAATATGGAAAAGGAGCCAAC  
CTGAGGGGTGACGAGACTGAGCTGAGGACACTGGTTTTCTGCCTTTCCTGAGAGAGACTCAG  
TGAGGGTGGGCTGGGAGCCCTGGAAGCCCCCTCAAATGGGTGGGAAGGTGCCAGCCATCCTTG  
AGAAGGGCAACCCTCTCCATGTGAGCACAGGCACAGAGAGGGGCAGGCGCCTGGAGGGTACC  
GGGGCACCCCCAGCTGCCCATGGCTGGACTTGCCCTTTGACAAGGGGCCCTCCAGTGTCAAT  
TGTATCTGTCACTACTCTTGGTTGCAAGGGACAGAAACCCTTAAGTAGTTCAAGCAAAAAGG  
ATCCAACACCTTGAGAAAGCCGAGGTGGGCGGATCACTTGAGGTGCGGAGTTTGAGACCAGCC  
TGGCCAACATGGCAAAACCCCGTCTCTACTAAAAATACAAAATTAGCCGGGTGTGGTGGCAC  
ACGCCTGTAGTCCCAGCTACTAGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGCGG  
AGGTTGCAGTGAGCCGAGATTGTGTCACTGCCCTCCAGCCTGGGCGACAGAGCCAGATTCTGT  
CTC

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**FIGURE 130**

MGCHVATSCHVAWLLVLISGCWGQVNRLPFFTNHFFDTYLLISEDTPVGSSVTQLLAQDMDND  
PLVFGVSGEEASRFFAVEPDTGVVWLRQPLDRETKSEFTVEFSVSDHQGVITRKVNIQVGDVN  
DNAPT FHNQPYSVRIPENTPVGTPIFIVNATDPDLGAGGSVLYSFQPPSQFFAIDSARGIVTV  
IRELDYETTQAYQLTVNATDQDKTRPLSTLANLAIITDVQDMDPIFINLPYSTNIYEHSPPG  
TTVRIITAIDQDKGRPRGIGYTIVSGNTNSIFALDYISGVLTLNGLLDRENPLYSHGFILTVK  
GTELNDDRTPSDATVTTTTFNILVIDINDNAPEFNSSEYSVAITELAQVGFALPLFIQVVDKDE  
NLGLNSMFEVYLVGNNSHHFIISPTSVQ GKADIRIRVAIPLDYETVDRYDFDLFANESVPDHV  
GYAKVKITLINENDNRPIFSQPLYNISLYENVTVGTSVLTVLVSPRFTAGPLSSPGPTVVRHP  
EGFCPRDLSNQGRRHPQIPELCLLVY

**Important features of the protein:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 355-374

**N-glycosylation sites.**amino acids 155-159, 206-210, 349-353, 393-397, 434-438, 466-470,  
472-476**N-myristoylation sites.**

amino acids 2-8, 49-55, 162-168, 270-276, 278-284, 316-322

**Amidation site.**

amino acids 515-519

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**Leucine zipper pattern.**

amino acids 298-320

**PTS HPR component serine phosphorylation site signature.**

amino acids 377-393

**Cadherins extracellular repeated domain signature.**

amino acids 120-131, 336-347

**Cadherins extracellular**

amino acids 120-144, 336-360

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**FIGURE 131**

GTGGGCCGCCCCTGCTGCTGCCGTCC**ATG**CTGATGTTTGCGGTGATCGTGGCCTCCAGCGGGC  
TGCTGCTCATGATCGAGCGGGGCATCCTGGCCGAGATGAAGCCCCTGCCCTGCACCCGCCCCG  
GCCGCGAGGGCACAGCCTGGCGCGGGAAAGCCCCCAAGCCTGGGGGCCTGTCCCTCAGGGCTG  
GGGACGCGGACTTGCAAGTGCGGCAGGACGTCCGGAACAGGACCCTGCGGGCGGTGTGCGGAC  
AGCCAGGCATGCCCCGGGACCCCTGGGACTTGCCGGTGGGGCAGCGGCGCACCCCTGCTGCGCC  
ACATCCTCGTAAGTGACCGTTACCGCTTCTCTACTGCTACGTCCCCAAGGTGGCCTGCTCTA  
ACTGGAAGCGGGTGATGAAGGTGCTGGCAGGCGTCCTGGACAGCGTGGACGTCCGCCTCAAGA  
TGGACCACCGCAGTGACCTGGTGTTCCTGGCCGACCTGCGGCCTGAGGAGATTGCTACCGCC  
TGCAGCACTACTTTAAGTTCCTGTTTGTGCGGGAGCCCTTGGAACGCCTCCTCTGCTTACC  
GCAACAAGTTTGGCGAGATCCGAGAGTACCAGCAACGCTATGGGGCTGAGATAGTGAGGCGGT  
ACAGGGCTGGAGCGGGGCCAGCCCTGCAGGCGACGATGTCACATTCCCCGAGTTCCTGAGAT  
ACCTGGTGGATGAGGACCCTGAGCGCATGAATGAGCATTGGATGCCCCTGTACCACCTGTGCC  
AGCCTTGTGCCGTGCACTATGACTTTGTGGGCTCCTATGAGAGGCTGGAGGCTGATGCAAATC  
AGGTGCTGGAGTGGGTACGGGCACCACCTCACGTCCGATTTCCAGCTCGCCAGGCCTGGTACC  
GGCCAGCCAGCCCCGAAAGCCTGCATTACCACTTGTGCAGTGCCCCCGGGCCCTGCTGCAGG  
ATGTGCTGCCTAAGTATATCCTGGACTTCTCCCTCTTTGCCTACCCACTGCCTAATGTCACCA  
AGGAGGCGTGTGAGCAG**TGA**CCATGGGTGTGGGGCCAGCAGCTGGTGGGGACTGGTTTCAACG  
CCAGCTTTCTGTGCTTCTGCCTGTCATTCCGAGAACTCTGGCTCTGGGGCTTGGGGCTTCTC  
AGGATCCTGGATGGCAGAGACTGCCCTCAGAAGTTCCTTGTCCAGGGTGGGCACCCACAGTGA  
CTCAGAGGACAGGGCTAGGCAGGAGACCTGCTGCTCCTCATTTGGGGGGATCTCTTGGGGGGCA  
GACACCAGTTTGCCAATGAAGCAACACATCTGATCTAAAGACTGGCTCCAGACCCCGGGCTGC  
CAGGATTATGCAGTCCACTTGGTCTACCTTAATTTAACCTGTGGCCAAACTCAGAGATGGTAC  
CAGCCAGGGGCAAGCATGACCAGAGCCAGGGACCCTGTGGCTCTGATCCCCCATTTATCCACC  
CCATGTGCCTCAGGACTAGAGTGAGCAATCATACCTTATAAATGACTTTTGTGCCTTTCTGCT  
CCAGTCTCAAATTTCTACACCTGCCAGTTCTTTACATTTTTCCAAGGAAAGGAAAACGGAA  
GCAGGGTTCTTGCTGGTAGCTCCAGGACCCAGCTCTGCAGGCACCCAAAGACCCTCTGTGCC  
CAGCCTCTTCCTTGAGTTCTCGGAACCTCCTCCCTAATTCTCCCTTCCTTCCCCACAAGGCCT  
TTGAGGTGTGACTGTGGCTGGTATATCTGGCTGCCATTTTTCTGATGCATTTATTTAAATTT  
TGTACTTTTTGATAGAACCCTTGTAAGGGCTTTGTTTTCTAATAGCTGACTTTTTAATAAAG  
CAGTTTTATATAT

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**FIGURE 132**

MLMFAVIVASSGLLLMIERGILAEMKPLPLHPPGREGTAWRGKAPKPGGLSLRAGDADLQVRQ  
DVRNRTLRAVCGQPGMPRDPWDLVPGQRRRTLLRHILVSDRYRFLYCYVPKVACSNWKRVMKVL  
AGVLDSVDVRLKMDHRSDLVFLADLRPEEIYRLQHYFKFLFVREPLERLLSAYRNKFGEIRE  
YQORYGAEIVRRYRAGAGPSPAGDDVTFPEFLRYLVDEDPERMNEHWMPVYHLCQPCAVHYDF  
VGSYERLEADANQVLEWVRAPPHVRFPARQAWYRPASPESLHYHLC SAPRALLQDVL PKYILD  
FSLFAYPLPNVTKEACQQ

**Important features of the protein:****Signal peptide:**

amino acids 1-23

**N-glycosylation sites.**

amino acids 67-71, 325-329

**Tyrosine kinase phosphorylation sites.**

amino acids 152-159, 183-183

**N-myristoylation sites.**

amino acids 89-95, 128-134



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**FIGURE 133**

CGGCAGTTCTGGCCCCTGCAGCTGGAGGTACCCTGAGTTCTGAGGGTCGTAGTGCTGTTTCTG  
GTATTCTCATCGCGGTACCTCTACCGGTGTGGACAAGTAAAGTTTGAATCAGCTTCTCCATG  
GCCTGGGCACCAGTTCCCGGCTGAGCCATTTTCCTTTTGGCTAAAAGTCCCCGCCAGAGGCC  
AATTCGTCGCGGCGGCGGTGGAGATCGCAGGTCGCTCAGGCTTGCAGATGGGTCAAGGGTTGT  
GGAGAGTGGTCAGAAACCAGCAGCTGCAACAAGAAGGCTACAGTGAGCAAGGCTACCTCACCA  
GAGAGCAGAGCAGGAGAATGGATGCGAGCAACATTTCTAACACCAATCATCGTAAACAAGTCC  
AAGGAGGCATTGACATATATCATCTTTTGAAGGCAAGGAAATCGAAAGAACAGGAAGGATTCA  
TTAATTTGGAAATGTTGCCTCCTGAGCTAAGCTTTACCATCTTGTCTACCTGAATGCAACTG  
ACCTTTGCTTGGCTTCATGTGTTTGGCAGGACCTTGCGAATGATGAACTTCTCTGGCAAGGGT  
TGTGCAAATCCACTTGGGGTCACTGTTCCATATACAATAAGAACCCACCTTTAGGATTTTCTT  
TTAGAAAATTGTATATGCAGCTGGATGAAGGCAGCCTCACCTTTAATGCCAACCCAGATGAGG  
GAGTGAACACTTTTATGTCCAAGGGTATCCTGGATGATTGCGCAAAGGAAATAGCAAAGTTTA  
TCTTCTGTACAAGAACTAAATTGGAAAAACTGAGAATCTATCTTGATGAAAGGAGAGATG  
TCTTGGATGACCTTGTAACATTGCATAATTTTAGAAATCAGTTCTTGCCAAATGCACTGAGAG  
AATTTTTTCGTCATATCCATGCCCCCTGAAGAGCGTGGAGAGTATCTTGAAACTCTTATAACAA  
AGTTCTCACATAGATTCTGTGCTTGCAACCCTGATTTAATGCGAGAACTTGGCCTTAGTCCTG  
ATGCTGTCTATGTACTGTGCTACTCTTTGATTCTACTTTCCATTGACCTCACTAGCCCTCATG  
TGAAGAATAAAATGTCAAAAAGGGAATTTATTGAAATACCCGTCGCGCTGCTCAAAATATTA  
GTGAAGATTTTGTAGGGCATCTTTATGACAATATCTACCTTATTGGCCATGTGGCTGCAATAA  
AAGCACAATTGCTAGGACTTCAGTTTTTACTTCAGACTAAAGCTACCCAAGGACTTAGCAGAT  
ATGGGGGTTACATCAGTGCTGGTCATTGTAGCCTGAGTATACAATCAAGCTTCAGTGTGCAAC  
CTTTTTTCTTTTGCCATTTTCTATTTTAGTAATTTCTTGGGGAATAAATAATTTGCAGA  
ATTTTTCTAATTTTGTATACGTTTTGCACAAAGCAGAGCCACTGTCTAACACAGCTGTT  
AACGAATGATAAACTGACATTATACTCTAAAAGATGGTGTATTTGTGCATTAGATTTGCCTGA  
AAAACCTTATCCATTTCCATTCTTTATACAAATACCATGTAATGTGTACATATTTAACTAAAG  
AGATTTATAGTCATAATTATTTTATTGTAAAGATTTTAACTAAAGTTTTCTTTCTCTC

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**FIGURE 134**

MGQGLWRVVRNQQLQQEGYSEQGYLTREQSRRMDASNISNTNHRKQVQGGIDIYHLLKARKSK  
EQEGFINLEMLPPELSFTILSYLNATDLCLASCVWQDLANDELLWQGLCKSTWGHCSIYNKNP  
PLGFSFRKLYMQLDEGSLTFNANPDEGVNYFMSKGILDDSPKEIAKFIFCTRTLWKKLRIL  
DERRDVLDLVTLHNFRNQFLPNALREFFRHIHAPEERGEYLETLITKFSHRFCACNPDLMRE  
LGLSPDAVYVLCYSLILLSIDLTSPHVKNKMSKREFIRNTRRAAQNISEDFVGHLYDNIYLG  
HVAA

**Important features of the protein:****Transmembrane domain:**

amino acids 253-272

**N-glycosylation sites.**

amino acids 37-41, 87-91, 298-302

**N-myristoylation site.**

amino acids 110-116

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**FIGURE 135**

GGCACGAGGGAGCCTCCGTTAGGGGGTGGGAAAGGACTTTGCCATAGGTCGCTGAGGCCACCA  
TCTGCTCTCTTACTGGCCAAGGGCGTAAAAAGATAGTCTTCCCATTAGCTAGAGAGCAAACCC  
CAGAAAGCCTATTGGCTGCGCCGTCCGCGGGCCTTGGTCCGCTTTGAAGGCGGGCTGCGGCTG  
CGAGAGGAGGGCGGGCGGGAGGCTAGCTGTTGTGCTGGTTGCTCGGAGGCACGTGTGCAGTCC  
CGGAAGCGGCGAGGGGAAACTGCTCCGCGCGCGCCGCGGGAGGAGGAACCGCCCGGTCTTTTA  
GGGTCCGGGGCCCGGCCGGGGCCATGGATTCAATGCCTGAGCCCGCGTCCCGCTGTCTTCTGCTT  
CTTCCCTTGCTGCTGCTGCTGCTGCTGCTGCTGCCGGCCCCGGAGCTGGGCCCCGAGCCAGGCC  
GGAGCTGAGGAGAACGACTGGGTTTCGCCTGCCAGCAAATGCGAAGTGTGTAAATATGTTGCT  
GTGGAGCTGAAGTCAGCCTTTGAGGAAACCGGCAAGACCAAGGAGGTGATTGGCACGGGCTAT  
GGCATCCTGGACCAGAAGGCCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGTTAATCGAA  
GTCACTGAGACCATTTGCAAGAGGCTCCTGGATTATAGCCTGCACAAGGAGAGGACCGGCAGC  
AATCGATTTGCCAAGGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACACAAAGGG  
GTCAAGGTGGTGTATGGACATCCCCTATGAGCTGTGGAACGAGACTTCTGCAGAGGTGGCTGAC  
CTCAAGAAGCAGTGTGATGTGCTGGTGGAAGAGTTTGAGGAGGTGATCGAGGACTGGTACAGG  
AACCACCAGGAGGAAGACCTGACTGAATTCCTCTGCGCCAACCACGTGCTGAAGGGAAAAGAC  
ACCAAGTTGCCTGGCAGAGCAGTGGTCCGGCAAGAAGGGAGACACAGCTGCCCTGGGAGGGAAG  
AAGTCCAAGAAGAAGAGCAGCAGGGCCAAGGCAGCAGGCGGCAGGAGTAGCAGCAGCAAACAA  
AGGAAGGAGCTGGGTGGCCTTGAGGGAGACCCAGCCCCGAGGAGGATGAGGGCATCCAGAAG  
GCATCCCCTCTCACACACAGCCCCCCTGATGAGCTCTTGAGCCCCACCCAGCATCCTCTGTCTCTG  
AGACCCCTGATTTTGAAGCTGAGGAGTCAGGGGCATGGCTCTGGCAGGCCGGGATGGCCCCGC  
AGCCTTCAGCCCCTCCTTGCCCTTGGCTGTGCCCTCTTCTGCCAAGGAAAGACACAAGCCCCAG  
GAAGAACTCAGAGCCGTCATGGGTAGCCACGCCGTCCTTTCCCCTCCCCAAGTGTTTCTCTC  
CTGACCCAGGGTTCAGGCAGGCCTTGTGGTTTCAGGACTGCAAGGACTCCAGTGTGAACTCAG  
GAGGGGCAGGTGTCAGAACTGGGCACCAGGACTGGAGCCCCCTCCGAGACCAAACCTACCAT  
CCCTCAGTCCTCCCCAACAGGGTACTAGGACTGCAGCCCCCTGTAGCTCCTCTCTGCTTACCC  
CTCCTGTGGACACCTTGCACTCTGCCTGGCCCTTCCCAGAGCCCAAAGAGTAAAAATGTTCTG  
GTTCTGATTTCTGAAAAAAAAAAAAAAAAAAATTCCT

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**FIGURE 136**

MDSMPEPASRCLLLLPLLLLLLLLLLPAPELGPSQAGAEENDWVRLPSKCEVCKYVAVELKSAF  
EETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTETICKRLLDYSLHKERTGSNRFAKGM  
SETFETLHNLVHKGVKVMDIPYELWNETSAEVADLKKQCDVLVEEFEEVIEDWYRNHQEEDL  
TEFLCANHVLKGGKDTSCLAEQWSGKKGDTAALGGKKSKKKSSRAKAAGGRSSSSKQRKELGGL  
EGDPSPEEDEGIQKASPLTHSPDEL

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**N-glycosylation site.**

amino acids 153-157

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 227-231, 228-232

**Tyrosine kinase phosphorylation site.**

amino acids 142-150

**N-myristoylation sites.**amino acids 36-42, 74-80, 86-92, 125-131, 222-228, 237-243,  
250-256, 263-269**Amidation sites.**

amino acids 212-216, 222-226

**ATP/GTP-binding site motif A (P-loop).**

amino acids 62-70

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**FIGURE 137**

CACGCCTCCCGCTGCCAGCCCGGCACCGGGATCTTAATCAGTCACTATGAAAACCTCATTAGCT  
CCACAGCAATGAGTCCTCCACTGCTGAAGCTTGGCGCTGTGCTTAGTACCATGGCAATGATCT  
CAAACCTGGATGTCCCAAACCTCTCCCATCCTTGGTGGGACTGAACACCACGAGGCTGTGACTC  
CGGATACCTTAACCTCAGATTAGTCCTAAAGAAGGGTGGCAGGTGTACAGCTCAGCTCAGGATC  
CTGATGGGCGGTGCATTTGCACAGTTGTTGCTCCAGAACAAAACCTGTGTTCCCGGGATGCCA  
AAAGCAGGCAACTTCGCCAACTACTGGAAGAGGTTTCAAGACATGTCCAGTCTATTGAAGTCT  
TAAACTTGAGAACTCAGAGAGATTTCCAATATGTTTTAAAAATGGAACCCAAATGAAAGGGC  
TGAAGGCAAAATTTCCGGCAGATTGAAGATGATCGAAAGACACTTATGACCAAGCATTTTTCAGG  
AGTTGAAAGAGAAAAATGGACGAGCTCCTGCCTTTGATCCCCGTGCTGGAACAGTACAAAACAG  
ATGCTAAGTTAATCACCCAGTTCAAGGAGGAAATAAGGAATCTGTCTGCTGTCCTCACTGGTA  
TTCAGGAGGAAATTGGTGCCTATGACTACGAGGAACCTACACCAAGAGTGCTGAGCTTGGA  
CAAGACTTCGTGACTGCATGAAAAAGCTAACATGTGGCAAACCTGATGAAAATCACAGGCCAG  
TTACAGTCAAGACATCTGGAACCCGATTTGGTGTCTGGATGACAGACCTTTAGCATCTGAGA  
AAAACAACAGAGTCTGGTACATGGACAGTTATACTAACAATAAAATTGTTTCGTGAATACAAAT  
CAATTGCAGACTTTGTCTAGTGGGGCTGAATCAAGGACATACAACCTTCCTTTCAAGTGGGCAG  
GAACTAACCATGTTGTCTACAATGGCTCACTCTATTTTAAACAAGTATCAGAGTAAATCATCA  
TCAAATACAGCTTTGATATGGGGAGAGTGCTTGCCCAACGAAGCCTGGAGTATGCTGGTTTTTC  
ATAATGTTTACCCCTACACATGGGGTGGATTCTCTGACATCGACCTAATGGCTGATGAAATCG  
GGCTGTGGGCTGTGTATGCAACTAACCAAGATGCAGGCAATATTGTCATCAGCCAACCTTAACC  
AAGATACCTTGGAGGTGATGAAGAGCTGGAGCACTGGCTACCCCAAGAGAAGTGCAGGGGAAT  
CTTTTCATGATCTGTGGGACACTGTATGTCACCAACTCCCCTTAACCTGAGCCAAGGTGTATT  
ATTCCTATTCCACCAAAACCTCCACATATGAGTACACAGACATTCCTTCCATAACCAATACT  
TTCACATATCCATGCTTGACTACAATGCAAGAGATCGAGCTCTCTATGCCTGGAACAATGGCC  
ACCAGGTGCTGTTCAATGTCACCCTTTTCCATATCATCAAGACAGAGGATGACACATAGGCAA  
ATGTGACATGTTTTTCAATTGATTTAAACAGTGTGATTTGTGATAAACTCTATAAGACCCCTTCC  
GTTTTTTTCTTCACTATTATTTTTTCATCATTTCTCCAAAGCAAAGCATTTTTTATTGTAAAGTT  
GGTGTTCAAAAACATAGCTGAGCTTGTCTAACTTACCATGTTGGAACACATCTTAACCTTCT  
AAATTTACAAGGCCTATCATGTCCTTGTGATGAAAAGCACTAAAAAAGAGTTTAAAGT  
GGCTAAAGTCATAGTTTTTGCAAGAGATTAATGATCTGCCTTATATTAGAGTCAGAGACTAATG  
GTGGCTTAAATGCACGAATGTCTTTTTTTTTTAAACTGTGCTTTTTTTACTGTCTTTTGCTCCA  
TCTCAGGAAATATTTTGGTAGGAATTAGGAGAACAAAAGCACTTTTATCCCATTTATTTCTT  
TAAAAATGTAAGGATTTTCAATTTATATTGAAAAATAATATTAATCATTTTGTGCTGTTAACACAA  
TTCTCTGATGCGGTGCTGTACAGTCATTTTTTAAATCTCTTGCTAACATTTTATTGGCAGTATG  
TATTTCTACCATTTGTAACCACCATTTGTGCTATTGTATCTCTTCACTTCTGTGAAAGTAATATT  
TTTTATAAANACACTGNAATTTTAAAAAACAAAAAACAAAAA

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**FIGURE 138**

MSPPLLKLGAVLSTMAMISNWMSTLPSLVGLNTRLSTPDTLTQISPKEGWQVYSSAQDPDG  
RCICTVVAPEQNLCSDAKSRQLRQLLEKVQNMSQSIEVLNLRTQRDFQYVLKMETQMKGLKA  
KFRQIEDDRKTLMTKHFQELKEKMDLLPLIPVLEQYKTDAKLITQFKEEIRNLSAVLTG IQE  
EIGAYDYEELHQRVLSLETRLRDCMKKLTGKLMKITGPVTVKTSGTRFGAWMTDPLASEKNN  
RVWYMSYTNKIVREYKSIADFVSGAESRTYNLPFKWAGTNHVVYNGSLYFNKYQSNIIKY  
SFDMGRVLAQRSLEYAGFHNVPYTWGGFSDIDLMADEIGLWAVYATNQAGNIVISQLNQDT  
LEVMSWSTGYPKRSAGESFMICGTLYVTNSHLTGAKVYYSYSTKTSTYEYTDIPFHNQYFHI  
SMLDYNARDRALYAWNNGHQVLFNVTLEFHIKTEDDT

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 33-37, 95-99, 179-183, 299-303, 465-469

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 215-219

**Tyrosine kinase phosphorylation site.**

amino acids 106-114

**N-myristoylation sites.**

amino acids 9-15, 31-37, 235-241, 239-245

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**FIGURE 139**

GAAGCAGTGCAGAGAGGAGAGCGGAGCGGAGCTGCCGCTGAGCAAAGGCCTTCACCA**ATG**CCCC  
AGTCCCCCGGCTGCTGCTCCGTCTGGGCCCCGCTGCCTCCACTGCCTGTATAGCTGCCACTGGA  
GGAAATGCCCCAGAGAGAGGATGCAAACCAGCAAGTGCGACTGTATCTGGTTTGGCCTGCTCT  
TCCTCACCTTCCTCCTTTCCCTGAGCTGGCTGTACATCGGGCTCGTCCTTCTCAATGACCTGC  
ACAACTTCAATGAATTCCTCTTCCGCCGCTGGGGACACTGGATGGACTGGTCCCTGGCATTCC  
TGCTGGTCATCTCTACTGGTCACATATGCATCCTTGCTATTGGTCCTGGCCCTGCTCCTGC  
GGCTTTGTAGACAGCCCCCTGCATCTGCACAGCCTCCACAAGGTGCTGCTGCTCCTCATTATGC  
TGCTTGTTGGCGGCTGGCCTTGTTGGGACTGGACATCCAATGGCAGCAGGAGTGGCATAGCTTGC  
GTGTGTCACTGCAGGCCACAGCCCCATTCTTCATATTGGAGCAGCCGCTGGAATTGCCCTCC  
TGGCCTGGCCTGTGGCTGATACCTTCTACCGTATCCACCGAAGAGGTCCCAAGATTCTGCTAC  
TGCTCCTATTTTTTGGAGTTGTCCTGGTCATCTACTTGGCCCCCTATGCATCTCCTCACCTT  
GCATCATGGAACCCAGAGACTTACCACCCAAGCCTGGGCTGGTGGGACACCGAGGGGGCCCCCA  
TGCTGGCTCCCGAGAACACCCTGATGTCCTTGCGGAAGACAGCTGAATGCGGAGCTACTGTGT  
TTGAGACTGATGTGATGGTCAGCTCCGATGGGGTCCCCTTCCTCATGCATGATGAGCACCTCA  
GCAGGACCACGAATGTAGCCTCTGTATTCCCAACCCGAATCACAGCCCACAGCAGTGACTTCT  
CCTGGACTGAACTGAAGAGACTCAATGCTGGATCCTGGTTCCCTAGAGAGGGCACCCTTCTGGG  
GGGCCAAACCGCTGGCAGGCCCTGATCAGAAAGAGGCTGAGAGTCAGACGGTACCAGCATTAG  
AAGAGCTATTGGAGGAAGCTGCAGCCCTCAACCTTTCCATCATGTTGACTTGCGCCGACCCC  
CACAGAACCACACATACTATGACACTTTTGTGATCCAGACATTGGAGACTGTGCTGAATGCAA  
GGGTGCCCCAAGCCATGGTCTTTTGGCTACCAGATGAAGATCGGGCTAATGTCCAACGACGGG  
CACCTGGAATGCGCCAGATATATGGACGTCAGGGAGGCAACAGAACGGAGAGGGCCCCAGTTTC  
TTAACCTCCCCTATCAAGATCTGCCACTATTGGATATCAAGGCATTGCATAAGGATAATGTCT  
CGGTGAACCTATTTGTAGTGAACAAGCCCTGGCTCTTCTCTCTGCTTTGGTGTGCAGGGGTG  
ATTCGGTCACCACCAACGACTGCCAGCTGCTGCAGCAGATGCGTTACCCTATCTGGCTTATTA  
CCCCTCAAACCTACCTAATCATATGGGTCATTACCAATTGTGTTTCCACCATGCTGCTTTTGT  
GGACCTTCCTCCTCCAAAGGAGATTTGTTAAGAAGAGAGGGGAAAAGTGGCTTAGAAACAGCAG  
TGCTGCTGACAAGGATCAACAATTTTCATGATGGAG**TGA**ATGCCCTGCCCTGCTTCCCCACCCA  
AGCCAGTCTACATTGCCCAAACAGCAAGGGTTGGAGAGTGGCTTAAGTGGAATGCTTCAGGGG  
TGGTGGGTTGCAAGTGGGGGGAGCTTTGCCAACAGGAGGTTTTGAACCATGAGGGCCCTCTGC  
CCAGGTGATGGGCATTCCCTAAGCTGCTATGGAATCTGCTCCCTTTGGGGTTTTGACCTGAGA  
TGTTTGGGAAGAGAGTGAGTAATGAGAAGTTTCTCCTCAAATGAACTAGAACAGAGGAAGTA  
AAAGGGAGATTGCTCGGA

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**FIGURE 140**

MAESPGCCSVWARCLHCLYSCHWRKCPREERMQTSKDCIWFGLLFLTFLLSLSWLYIGLVLLN  
DLHNFNEFLFRRWGHWMDSLAFLLVISLLVTYASLLLVLALLLRRCRQPLHLHSLHKVLLLL  
IMLLVAAGLVGLDIQWQQEWHSRLRVSLQATAPFLHIGAAAGIALAWPVADTFYRIHRRGPKI  
LLLLLFFGVVLVIYLAPLCISSPCIMEPRDLPPKPGLVGHRGAPMLAPENTLMSLRKTAECGA  
TVFETDVMVSSDGVFPLMHDEHLSRTTNVASVFPTRIHSSDFSWTELKRLNAGSWFLERRP  
FWGAKPLAGPDQKEAESQTVPALEELLEEEAAALNLSIMFDLRRPPQNHTYYDTFVIQTLETVL  
NARVPQAMVFWLPDEDRAVQRRAPGMRQIYGRQGGNRTERPQFLNLPYQDLPLLDIKALHKD  
NVSVNLFVFNKFWLFSLLWCAGVDSVTTNDCQLLQQMRYPIWLITPQTYLIWVITNCVSTML  
LLWTFLLQRRFVKKRGKTGLETAVLLTRINNFMMME

**Important features of the protein:****Transmembrane domains:**

amino acids 38-60, 83-107, 122-138, 156-173, 189-210, 484-506

**N-glycosylation sites.**

amino acids 349-353, 362-366, 415-419, 442-446

**N-myristoylation sites.**

amino acids 163-169, 413-419, 523-529

**Leucine zipper pattern.**

amino acids 93-115, 109-131

**Glutamine amidotransferases class-II active site.**

amino acids 1-13



GCCGCGCGCCCGGGCTGGAGCCGAGCGCAGCAGCCACCGCGCGCGCGCCGAGAAAGTTTGGGTTGAACCGGAGC  
TGC CGGGAGGAAACTTTTTCTTTTTTCCCTCCTCCCGGGAGGAGGAGGAGGAGGAGGAGGGGAAGCTGCCG  
CGCGCGCCAAGGCTCGTGGGCTCGGGGTCGGCGCGGCCCGCAGAAGGGGCGGGGGCTCGCCCCGCGAGGGGAGG  
CGCGCCCCGGGGGCCCCGAGAGGGGCGGTGAGGACCGCGGGGTGCTGGTGC GCGCGCGCGCGCGCGCTGTGCCCG  
CGCAGGGGAGGGGCGCCGCCCCGCTCCCGGCCCGGCTGCGAGGAGGAGGCGCGCGCGCGCGCAGGAGGAGTGTACTT  
GGTGGCGGGGGACAGGGGGTTGGCCGGCTGCGGGCACCTCCTGGTCTCGCTGCTGGGCTGCTGCTGCTGGC  
GCGCTCCGTCACCCGGGCGCTGGTCTGCTGCCCTGTGACAGTCCAAGTGC GAGGCCAGGAACCTGCCCGGG  
GAGCATCGTGACGGGCTGCGGGCTGCTGCTACACGTGCGCGCAGCCAGAGGAACGAGAGCTGCGGCGGCACCTT  
CGGATTTACGGAACCTGCGACCGGGGGCTGCGTTGTGTATCCGCCCCCGCTCAATGGCGACTCCCTACCGA  
GTACGAAGCGGGCGTTTGCGAAGATGAGAAGTGGACTGATGACCAACTGCTTGGTTTTAAACCATGCAATGAAAA  
CCTTATTGCTGGCTGCAATATAATCAATGGGAAATGTGAATGTAACACCATTGCAACCTGCAGCAATCCCTTTGA  
GTTTCCAAGTCAGGATATGTGCCCTTTCAGCTTTAAAGAGAATTGAAGAAGAGAAGCCAGATGCTCCAGGCCG  
CTGTGAAGTCCAGTTCTCTCCACGTTGTCTGAAGATCTGTTCTGAGTGCAGGGTTATGCTCCTCCTGGGGAGTG  
CTGTCCCTTACCCAGCGCTGCGTGTGCAACCCCGCAGGCTGTCTGCGCAAAGTCTGCCAGCCGGGAACCTGAA  
CATACTAGTGTCAAAGCCTCAGGGAAGCCGGGAGAGTGTGTGACCTCTATGAGTGCAAACAGTTTTTCGGCGT  
GGACTGCAGGACTGTGGAATGCCCTCCTGTTGAGCAGACCGCGTGTCCCCCGGACAGCTATGAAACTCAAGTCAG  
ACTAAGTGCAGATGGTTGCTGTACTTTGCCAACAAGATGCGAGTGTCTCTCTGCGTTATGTGGTTTCCCGTGTG  
TGAGGTGGGATCCACTCCCCGATAGTCTCTCGTGGCAGTGGGACACCTGGAAGTGTGCTGATGTCTTTGAATG  
TGTTAATGATACAAAGCCAGCCTCGTATTTAAACAATTGGAATATTATGATGGAGACATGTTTCGAATGGACAA  
CTGTGGTTCTGTGATGCCAAGGGGGCTTGCCATCTGCTTCACTGCCAGTGTGGTGAGATAAACTGCGAGAG  
GTACTACGTGCCCGAAGGAGAGTGTGCCAGTGTGTGAAGATCCAGTGTATCCTTTAATAATCCCGCTGGCTG  
CTATGCCAATGGCCTGATCCTTGCCACGAGACCGGTGGCGGGAAGACGACTGCACATTTCTGCCAGTGGCTCAA  
CGGTGAACGCCACTGCGTTGCGACCGTCTGCGGACAGACCTGCACAACCCCTGTGAAGTGCCTGGGGAGTGTG  
CCCTGTGTGCGCAAGAAACCAACCATCACAGATGTATCCACTGCATGTGGGGAGTTATCAAAGTGCATCTGAC  
AGGGAAGGACTGCAATTAATGTTTCAAACGCGATACAATGGTTGTGCGACCTGTGAGTGCATAAACACCGAGGA  
ACTATGTTCAGAACGTAACAAGGCTGCACCTTGAAGTGTCCCTTCGGTTTCTTACTGATGCCCAAAGTGTGA  
GATCTGTGAGTGCCGCCCCAAGGCCCAAGAAGTGCAGACCCATAATCTGTGACAAGTATTGTCCACTTGGATTGCT  
GAAGAATAAGCACGGCTGTGACATCTGTGCTGTGAAGAAATGTCCAGAGCTCTCATGCAAGATGCTGCCCTT  
GGGTTTTCCAGCAGGACAGTACCGGCTGTCTTATCTGCAAGTGCAGAGGCTCTGCTTACGTGGGCGACCCCAT  
CCTGTGCGGCACCTGTCTCACCGTGGATGGTATCATATAAAATGAGGAGAGCTGGCAGCATGGGTGCCGGGA  
ATGCTACTGTCTCAATGGACGGGAAATGTGTGCCCTGATCACTGCCCGGTGCTGCTGTGGCAACCCACCAT  
TCACCCCTGGACAGTGTGCCCATCATGTGCAGATGACTTTGTGGTGCAGAAGCCAGAGCTCAGTACTCCCTCCAT  
TTGCCACGCCCCCTGGAGGAGAATACTTTGTGAAGGAGAAACCTGGAACATTGACTCCTGTACTCAGTGCACCTG  
CCACAGCGGACGGGTGCTGTGTGAGACAGAGGTGTGCCACCCTGCTCTGCCAGAACCCCTCAGCAGCCACGGA  
TTCTGTCTGCCACAGTGTACAGATCAACCTTTTCGGCTTCTTGTCCGCAATAACAGCGTACCTAATTACTG  
CAAAATGATGAAGGGGATATATTCCTGGCAGCTGAGTCTGGAAGCTGACGTTTGTACCAGCTGCATCTGCAT  
TGATAGCTGTAAATAGCTGTTTCTCTGAGTCTGCTTCTGTATCCTGTGAAAGACCTGTCTTGAGAAAAGGCCA  
GTGTTGTCCCTACTGCATAGAAGACACAATTCAAAGAAGGTGGTGTGCCACTTCAGTGGGAAGGCCTATGCCGA  
CGAGGAGCGGTGGGACCTTGACAGCTGACCCACTGCTACTGCCTGCAGGGCCAGACCCCTCTGCTCGACCTCAG  
CTGCCCCCTCTGCCCTGTGTTGAGCCCATCAACGTGGAAGGAAGTGTGCTGCCAATGTGCCAGAATGTATGT  
CCCAGAACCAACCAATATACCCATTGAGAAGACAACCATCAGGAGAGGTTGACCTGGAGGTTCCCTGTGGCC  
CAGCTAGTGAAGAAATGATATCGTCCATCTCCCTAGAGATATGGGTCACTCCAGGTAGATTACAGAGATAACAG  
GCTGCAACCTAAGTGAAGATTCTTCACTGGACTCCATTGCCTCAGTTGTGGTTCCCATATTATATGCTCTCTAT  
TATAATAGCATTCTATTATCATCAATCAGAAGAAACAGTGGATACCACTGCTTTGCTGGTATCGAACACCAACTAA  
GCCTTCTTCTTAAATAATCAGCTAGTATCTGTGGACTGCAAGAAAGGAACAGAGTCCAGGTGGACAGTTCCCA  
GAGAATGCTAAGAAATTGCAGAACCAGATGCAAGATTCACTGGCTTCAAGCATGCAAAAACAGAACCATCTACA  
GGCAGACAAATTTCTACCAACACAGTGTGAAGAAAGGCAACTAGGATGAGGTTTCAAAGACGGAGACGACTAAAT  
CTGCTCTAAAAAGTAAACTAGAATTTGTGCACTTGCTTAGTGGATTGTATTGGATTGTGACTTGATGTACAGCGC  
TAAGACCTTACTGGGATGGGCTCTGTCTACAGCAATGTGCAGAACAAGCATTCCCACTTTTCTCAAAAAA

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**FIGURE 142**

MYLVAGDRGLAGCGHLLVSLGLLLLLLARSSTRALVCLPCDESKCEEPRNCPGSIVQGVCGCC  
 YTCASQRNESC GGTFGIYGTCDRGLRCVIRPPLNGDSLTEYEAGVCE DENWTDQLLGFKPCN  
 ENLIAGCNI INKGCECNTIRTC SNPF EFPSQDMCLSALKRIEE EKPDCKARCEVQFS PRCP  
 DSVLIEGYAPPGECCPLPSRCVCNPAGCLRKVCQPGNLN LVSKASGKPGECCLYECKPVFG  
 VDCRTVECPVQQTACPPDSYETQVRLTADGCCTLPTRCECLSGLCGFPVCEVGSTPRIVSRG  
 DGTPGKCCDVFE CVNDTKPACVFNNVEYYDGMFRMDNCRFCRCQGGVAICFTAQCGEINCE  
 YYVPEGECCPVCEDPVYPFNNPAGCYANGLILAHGDRWREDDCTFCQCVNGERHCVATVCGQT  
 CTNPVKVPGECPPVCEPTIITVDPPACGELSNTLTGKDCINGFKRDHNGCR TCQCINTEEL  
 CSERKQGCTLNC PFGLTDAQNCEICECRPRPKKRPIICDKYCPLG LLKNKHGCDICRCKKC  
 PELSCSKICPLGFQQDSHGCLICKCREASASAGPPILSGTCLTVDGHHHKNEESWHDGCRECY  
 CLNGREMCALITCPVPACGNPTIHPGQCCPSCADDFVQKPELSTPSICHAPGGEYFVEGETW  
 NIDSCTQCTCHSGRVLCETEVCPPLLQNPSTQDSCCPQCTDQPFPSLSRNNSVPNYCKND  
 EGDIFLAAESWKPDVCTSCICIDSVISCFSESCPSVSCERPVL RKGQCCPYCIEDTIPKKVVC  
 HFSGKAYADEERWDLDSCTHCYCLQGQTLCTVSCPPLPCVEPINVEGSCCPMCPEMYVPEPT  
 NIPIEKTNHRGEVDLEVPWPPTSENDIVHLPRDMGHLQVDYRDNRLHPSEDSSLDSIASVVV  
 PIIICLSIIIAFLFINQKKQWIPLLCWYRTPTKPSLNNQLVSVDCCKGTRVQVDSSQRM LRI  
 AEPDARFSGFYSMQKQNLQADNFYQTV

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 940-962

**N-glycosylation sites.**

amino acids 71-75, 113-117, 330-334, 474-478, 746-750

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 992-996

**N-myristoylation site.**amino acids 9-15, 58-64, 61-67, 75-81, 79-85, 362-368, 402-408, 407-413,  
439-445, 492-498, 511-517, 551-557, 558-564, 586-592, 606-612, 625-631,  
845-851**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 52-63, 844-855

**Cell attachment sequence.**

amino acids 314-317

**Leucine zipper pattern.**

amino acids 3-25

**Eukaryotic thiol (cysteine) proteases cysteine active site.**

amino acids 57-69

**VWFC domain proteins.**

amino acids 448-456, 382-390

**C-terminal cystine knot proteins**

amino acids 60-86

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**FIGURE 143**

GACGTCTGGCCGGCTCCCGGCGAAGGGCAGCGGAGGAGCGGCCAGAGCGCGCAGCTAGGGCA  
CTGGCGAAACCCCGGGACAGTCCCTCTCCGTGCGGGGGCGGCGCAGAGCAGTCCCATCCCCG  
GGTCCCGGGCGCGGCTGACTGCCGGCTGGTTCCCTGCGCGCAGTAGCTCCCCGAGCCGGGCTG  
CACCGGAGGCGGCGAGATGGTGCGCGCGCTCGGCCTCCTGCTGCGCGCCCTGCAGCTGCTACT  
GTGGGGCCACCTGGACGCCCAGCCCGCGGAGCGCGGAGGCCAGGAGCTGCGCAAGGAGGCGGA  
GGCATTTCCTAGAGAAGTACGGATACCTCAATGAACAGGTCCCCAAAGCTCCCACCTCCACTCG  
ATTACGCGATGCCATCAGAGCGTTTCAGTGGGTGTCCCAGCTACCTGTCAGCGGCGTGTGGA  
CCGCGCCACCCTGCGCCAGATGACTCGTCCCCGCTGCGGGGTACAGATACCAACAGTTATGC  
GGCCTGGGCTGAGAGGATCAGTGACTTGTTTGCTAGACACCGGACCAAAATGAGGCGTAAGAA  
ACGCTTTGCAAAGCAAGGTAACAAATGGTACAAGCAGCACCTCTCCTACCGCCTGGTGAAGTG  
GCCTGAGCATCTGCCGGAGCCGGCAGTTCGGGGCGCCGTGCGCGCCGCCTTCCAGTTGTGGAG  
CAACGTCTCAGCGCTGGAGTTCTGGGAGGCCCCAGCCACAGGCCCGCTGACATCCGGCTCAC  
CTTCTTCCAAGGGGACCACAACGATGGGCTGGGCAATGCCTTTGATGGCCCAGGGGGCGCCCT  
GGCGCACGCCTTCCTGCCCCGCGCGGCGAAGCGCACTTCGACCAAGATGAGCGCTGGTCCCT  
GAGCCGCCGCGCGGGCGCAACCTGTTTCGTGGTGCTGGCGCACGAGATCGGTCACACGCTTGG  
CCTCACCCACTCGCCCGCGCCGCGCGCGCTCATGGCGCCCTACTACAAGAGGCTGGGCCGCGA  
CGCGCTGCTCAGCTGGGACGACGTGCTGGCCGTGCAGAGCCTGTATGGGAAGCCCCTAGGGGG  
CTCAGTGGCCGTCCAGCTCCCAGGAAAGCTGTTCACTGACTTTGAGACCTGGGACTCCTACAG  
CCCCAAGGAAGGCGCCCTGAAACGCAGGGCCCTAAATACTGCCACTCTTCCTTCGATGCCAT  
CACTGTAGACAGGCAACAGCAACTGTACATTTTTAAAGGGAGCCATTTCTGGGAGGTGGCAGC  
TGATGGCAACGTCTCAGAGCCCCGTCCACTGCAGGAAAGATGGGTCTGGGCTGCCCCCAACAT  
TGAGGCTGCGGCAGTGTCATTGAATGATGGAGATTTCTACTTCTTCAAAGGGGGTCGATGCTG  
GAGGTCCGGGGCCCCAAGCCAGTGTGGGGTCTCCACAGCTGTGCCGGGCAGGGGGCCTGCC  
CCGCCATCCTGACGCCGCCCTCTTCTCCCTCCTCTGCGCCGCCTCATCCTCTTCAAGGGTGC  
CCGCTACTACGTGCTGGCCCCAGGGGGACTGCAAGTGGAGCCCTACTACCCCCGAAGTCTGCA  
GGACTGGGGAGGCATCCCTGAGGAGGTCAGCGCGCCCTGCCGAGGCCCGATGGCTCCATCAT  
CTTCTTCCGAGATGACCGCTACTGGCGCCTCGACCAGGCCAACTGCAGGCAACCACCTCGGG  
CCGCTGGGCCACCGAGCTGCCCTGGATGGGCTGCTGGCATGCCAACTCGGGGAGCGCCCTGTT  
CTGAAGGCACCTCCTCACCTCAGAACTGGTGGTGCTCTCAGGGCAAATCATGTTCCCCACC  
CCCGGGGCAGAACCCTCTTAGAAGCCTCTGAGTCCCTCTGCAGAAGACCGGGCAGCAAAGCC  
TCCATCTGGAAGTCTGTCTGCCTTTGTTCTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 144**

MVARVGLLLRALQLLLWGHLDQAERGGQELRKEAEAFLEKYGYLNEQVPKAPTSTRFSDAI  
RAFQWVSQLPVSGVLD RATLRQMTRPRCGVTD TNSYAAWAERISDLFARHRTKMRRKKRFAKQ  
GNKWKQHL SYRLVNWPEHLPEPAVRGAVRAAFQLWSNVSALEFWEAPATGPADIRLTFFQGD  
HNDGLGNAFDGPGGALAHAF LPRRGEAHFDQDERWSLSRRRGRNLFVFLAHEIGHTLGLTHSP  
APRALMAPYYKRLGRDALLSWDDVLAVQSLY GKPLGGSVAVQLPGKLFTDFETWDSYSPQGRR  
PETQGPKYCHSSFDAITVDRQQQLYIFKGS HFWEVAADGNVSEPRPLQERWVGLPPNIEAAAV  
SLNDGDFYFFKGGRCWRFRGPKPVWGLPQLCRAGGLPRHPDAALFFPPLRRLILFKGARYYVL  
ARGGLQVEPYYP RSLQDWGGIPEEVSGALPRPDGSIIFRDDR YWRLDQAKLQATTSGRWATE  
LPWMGCWHANSGSALF

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 164-168, 355-359

**N-myristoylation sites.**amino acids 92-98, 153-159, 193-199, 202-208, 288-294, 368-374,  
509-515**Amidation site.**

amino acids 312-316

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 237-247

**Matrixins cysteine switch**

amino acids 231-262, 271-284

**Hemopexin domain protein**

amino acids 66-108, 231-262

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**FIGURE 145**

GCCGGCTAGGGCGCCGGAGCCGCACGCAGCCGCGGGGCTCCGAGAGGCGCGCACTGGGGCTGGGACTGCGCGGCG  
CCGCCGCTGCGAGCGCCACTGAGCGGTGCGCGCAACTTCGGAGGCACAGCGCCGGAGCCAGGCGAGCGCTCAGAGA  
CCCGGAGCCAGAGGGGCGCGCCGGAGCCTCGTTCGAGAGCCGGCGCCAGGCACCCACCGCGCTCCGAGTGCCAGG  
CGGCCCTCCGCGCAGCGTGGCTTCCGCTGCCCCACGGAAGGCACGGGCTGGCGCTGCCGGGCGCCGGGGAGGAC  
GGCGAGGAGGAGGCGGCGGCGGCGGAGACGGCGGCGGCGAGACTGGGGCCAGGGAGACAGCCCTGGGGGAGAGGC  
GCCCCAACCAGGCGCGGGAGC**ATG**GGGGCCCGAGCGGAGCTCGGGGCGCGCTGCTGCTGGCACTGCTGCTCTG  
CTGGGACCCGAGGCTGAGCCAAGCAGGCACTGATTCTGGCAGCGAGGTGCTCCCTGACTCCTTCCCGTCAGCGCC  
AGCAGAGCCGCTGCCCTACTTCTGTCAGGAGCCACAGGACGCGCTACATTGTGAAGAACAAGCCTGTGGAGCTCCG  
CTGCCGCGCCTTCCCCGCCACACAGATCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTCAC  
ACAGGAAGGCCTGGATGAGGCCACCGGCTGCGGGTGCAGGAGTGCAGATCGAGGTGTGCGGCGCAGCAGGTGGA  
GGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCCTGGCTGGAGCTCCGCGAGGCACCAAGAGTCGCGG  
AGCCTAGCTCCGCATCGCCTACCTGCGCAAGAACTTCGATCAGGAGCCTCTGGGCAAGGAGGTGCCCTGGACCA  
TGAGGTTCTCTGCACTGCGGCCCGCGGAGGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAAATGAGGATGT  
CTCGACCCACCCAGGACACCAACTTCTGCTCACCATCGACCAACCTCATCATCGCCAGGCGCGCTGTGTC  
GGACACTGCCAACTATACCTGCGTGGCCAAAGACATCGTGGCCAAACGCCGGAGCACCCTGCCACCGTCATCGT  
CTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCACCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAA  
GCGCACCCGACCTGCACCAACCCCGCTCCACTCAACGGAGGGGCTTCTGCGAGGGCCAGGCATTCCAGAAGAC  
CGCCTGCACCACCATCTGCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTGAGTG  
TGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCAGAAACGGAGGCGGTGACTGCAGCGGGACGCTGCT  
CGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAAAATAAGAAAATCTAAGCGACCCCAACAGCCACCTGCT  
GGAGGCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTGGTCTGTGGCAATCCTCATGGC  
GGTGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAGACATCACTGACTCATCTGCTGCCCTGAC  
TGGTGGTTTCCACCCCGTCAACTTTAAGACGGCAAGGCCAGCAACCCGAGCTCCTACACCCCTCTGTGCCCTCC  
TGACCTGACAGCCAGCGCGGCATCTACCGCGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCCAT  
GACCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCACCACGGGCTCTGG  
GCCAGGCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCGGCTGGCACATACCCTAGCGATTTGCCCGGGA  
CACCCACTTCTGCACTGCGCAGCGCCAGCCTCGGTTCCAGCAGCTCTTGGGCTGCCCGAGACCCAGGGAG  
CAGCGTCAGCGGCACCTTTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGCGCAGGGGTGAGCTTGCTGGTGCC  
CAATGGAGCCATTCCCCAGGGCAAGTCTACGAGATGTATCTACTCATCAACAAGGCAGAAAGTACCCTCCGCT  
TTCAGAAGGGACCCAGACAGTATTGAGCCCTCGGTGACCTGTGGACCCACAGGCTCCTGCTGTGCCGCCCCGT  
CATCCTCACCCTGCCCCACTGTGCCGAAGTCACTGCCCCGTGACTGGATCTTTCAGCTCAAGACCCAGGCCACCA  
GGGCCACTGGGAGGAGGTGGTGACCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCAG  
GGCCTGTACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCCATTCCCGCTCAGCAGTCAA  
GCGGCTCCAGCTGGCCGTCTTCGCCCCCGCCTCTGCACCTCCCTGGAGTACAGCCTCCGGGTCTACTGCCTGGA  
GGACACGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAA  
ACCGCTAATGTTCAAGGACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCCATGCCATTGGAGGAG  
CAAGCTGCTGGCCAAATACCAGGAGATCCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGGCCCTCCACTGCAC  
TTTACCCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCAAGATCTGCGTGCGGCAAGTGGAAGGGGA  
GGGCCAGATATTCCAGCTGCATACCACTCTGGCAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCC  
TGGCAGCACTGTACCAACCCAGCTGGGACCTTATGCCTTCAAGATCCCACTGTCCATCCGCCAGAAGATATGCAA  
CAGCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTATGGACCGGTACCT  
GAATTACTTTGCCACCAAGCGAGCCCCACGGGTGTGATCCTGGACCTCTGGGAAGCTCTGCAGCAGGACGATGG  
GGACCTCAACAGCCTGGCGAGTGCCCTTGGAGGAGATGGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGG  
GGACTGCT**AG**ACCTCCTGGGACAGCGGGCTGGCAGGACTGGCAGGAGGCAGGTGCAGGGAGGCCTGGGGCAGCC  
TCCTGATGGGGATGTTTGGCCTCTGCTTCCCTCCAGTTCACAGCCAGAGTTGCCTCTCCTCCTCTCTTCCCCAA  
CCCCAGACCATGACCAGCCTTAGAAAATCCATGTAATCTGTTGTTAGAGGGCCAGAGTTCCTTCTCCACCCCC  
GCTCTCTCTCTTGGCCTGAGATCTCTGTGCAGGAACCAAGATGGGGCTGAAGCCTCTGGAGGCAGTTGGTTGG  
GGGCGGGCAGGAGGAGGCCCCCTCCCTCCACCCCCCACCCTCAGCCCGGCAACTTCTGGGTTCCGTGGGTTTAG  
TTCCGTTCTCGTTTCTTCTTCCGTTATTGATTCTCCTTTCTCCCTAAGCCCCCTCTGCTTCCACGCCCTTT  
TCCTCTTTGAAGAGTCAAGTACAATTACAGACAACTGCTTTCTCCTGTCCAAAAGCAAAAAGGCAAGGAAAGAA  
AGAAAGCTTCAGACCGCTAGTAAGGCTCAAAGAAGAAAGAAAACACCAAAACCAAGGGAAAAGAAAACCCAG  
TTTCTTAGGAAACGCAACGATTTATTATCCAGATTATTTGGATAAGTCCTTTTAAAA

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**FIGURE 146**

MGARSGARGALLLALLLCWDPRLSQAGTDSGSEVL PDSFPSAPAEPLPYFLQEPQDAYIVKNK  
 PVELRCRAFPATQIYFKCNGEWSQNDHVTQEGLDEATGLRVREVQIEVSROQVEELFGLEDY  
 WCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPEGVPVAEVEWLK  
 NEDVIDPTQDTNFLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRSTTATVIVYVNGGWSSW  
 AEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQAFQKTACTTICPVDGAWTEWSKWSACS  
 TECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKKTLSDPNSHLLEASGDAALYA  
 GLVVAIFVVAAILMAVGVVVYRRNCRDFDITDSSAALTGGFHPVNFKTARPSNPQLLHPSV  
 PPDLTASAGIYRGPVYALQDSTDKIPMTNSPLLDPLPSLVKVYSSSTTGSGPGLADGADLLG  
 VLPPGTYPSPDFARDTHFLHLSASLGSQQLLGLPRDPGSSVSGTFCGLGGRLSIPGTGVSLLV  
 PNGAIPQKGKPYEMYLLINKAESTLPLSEGTQTVLSPSVTCGPTGLLLCRPVILTMPHCAEVSA  
 RDWIFQLKTOAHQGHWEVVTLDEETLNTPCYQCQLEPRACHILLDQLGTYVFTGESYSRSAVK  
 RLQLAVFAPALCTSLEYSRLVYCLEDTPVALKEVLELERTLGGYLVEEPKPLMFKDSYHNRL  
 SLHDLPHAHWRSKLLAKYQEI PFYHIWSGSQKALHCTFTLERHSLASTEITCKICVRQVEGEG  
 QIFQLHTTLAETPAGSLDTLCSAPGSTVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRM  
 LAQKLSMDRYLNYFATKASPTGVILDLWEALQDDGDLNSLASALEEMGKSEMLVAVATDGDC

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 374-395

**N-glycosylation sites.**

amino acids 222-225, 347-350

**Glycosaminoglycan attachment site.**

amino acids 492-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 233-236, 234-237

**Casein kinase II phosphorylation sites.**

amino acids 30-33, 87-90, 251-254, 341-344, 359-362, 629-632, 651-654, 706-709, 757-760, 827-830, 925-928, 941-944

**Tyrosine kinase phosphorylation sites.**

amino acids 216-223, 773-780

**N-myristoylation sites.**

amino acids 2-7, 6-11, 27-32, 96-101, 137-142, 179-184, 247-252, 281-286, 334-339, 379-384, 491-496, 495-500, 509-514, 542-547, 547-552, 550-555, 553-558, 560-565, 611-616, 785-790, 834-839, 844-849

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 541-551

**ATP/GTP-binding site motif A (P-loop).**

amino acids 926-933

**Growth factor and cytokines receptors family signature 2.**

amino acids 306-312

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**FIGURE 147**

GAGAGGGACAGAGGCTGGAGAAGGATGTATGGCCTGCCCTGGGCTTGTCTGTTCCCTCCTGAGCCTGAGCCCCTT  
ACCTTCTGACCCCATGAAGCACACACTGGCTCTGCTGGCTCCCCTGCTGGGCCTGGGCCTGGGGCTGGCCCTGA  
GTCAGCTGGCTGCAGGGGCCACAGACTGCAAGTTCCCTGGCCCCGAGAGCACCTGACATTACCCCCAGCAGCCA  
GGGCCCCGGTGGCTGGCCCCCTGAGTTCTGTGCGCCAGGACTCCTGGACTCCCTCTATGGCACCGTGCGCCGCTTCC  
TCTCGGTGGTGCAGCTCAATCCTTTCCCTTCAGAGTTGGTAAAGGCCCTACTGAATGAGCTGGCCTCCGTGAAGG  
TGAATGAGGTGGTGGGTACGAGGCGGGCTACGTGGTATGCGCTGTGATCGCGGGCCTCTACCTGCTGCTGGTGC  
CCTGTCGGGGCTTTGCTTCTGCTGCTGCCGCTGCCACCGCGCTGCGGGGACGAGTGAAGACAGAGCACAAAGG  
CGCTGGCCTGTGAGCGCGCGGCCCTCATGGTCTTCTGCTGCTGACCACCCTCTTGTGCTGATTGGTGTGGTCT  
GTGCCCTTTGTACCAACCAGCGCACGCATGAACAGATGGCCCCAGCATCGAGGCCATGCCTGAGACCCTGCTCA  
GCCTCTGGGGCCTGGTCTCTGATGTCCCCAAGAGCTGCAGGCCGTGGCACAGCAATTCTCCCTGCCCCAGGAGC  
AAGTCTCAGAGGAGCTGGATGGTGTGGTGTGAGCATTTGGGAGCGGATCCACACTCAGCTCAGGAGCTCCGTGT  
ACCCCTTGTGTCGGCGCCTGGGCGAGTTTGGGCCAGGTCTGCGAGTCTCCGTGCACCACCTGCAAACTTTGAATG  
CTACAGTGGTAGAGCTGCAGGCCGGGCAGCAGGAGATTGTGAGGGGCCCTGAGCTGGGCCCGCACCTGGAGCTGGGTG  
AGCTGCTGAGGAGGCCAGGTGCCAGGGAGATTGTGAGGGGCCCTGAGCTGGGCCCGCACCTGGAGCTGGGTG  
CTGACTTCAGCCAGGTGCCCTCTGTGGACCATGTCTGCACCAGCTAAAAGGTGTCCCCGAGGCCAACTTCTCCA  
GCATGGTCCAGGAGGAGAACAGCACCTTCAACGCCCTTCCAGCCCTGGCTGCCATGCAGACATCCAGCGTGGTGC  
AAGAGCTGAAGAAGGCAGTGGCCCCAGCAGCCGGAAGGGGTGAGGACACTGGCTGAAGGGTTCGCGGCTGGAGG  
CAGCTTCCCCGCTGGGCCAGGCACTGCAGGAGGTGGAGGAGAGCAGCCGCCCCCTACCTGCAGGAGGTGCAGAGAT  
ACGAGACCTACAGGTGGATCGTGGGCTGCGTGTCTGCTCCGTGGTCTTATTCGTGGTGTCTGCAACCTGCTGG  
GCCCAATCTGGGCATCTGGGGCCTGTCTGCCAGGGACGACCCCGACCCAGCAAGCCAAGGGCGAGGCTGGAG  
CCCCGCTTCTCATGGCAGGTGTGGGCCCTCAGCTTCTCTTTGCTGACCCCTCATCCTCCTGGTGTTCGCCACCT  
TCCTGGTGGGTGGCAACGTGCAGACGCTGGTGTGCCGGAGCTGGGAGAACGGCGAGCTCTTTGAGTTTGCAGACA  
CCCCAGGGAACCTGCCCCCGTCCATGAACCTGTGCAACTTCTTGGCCTGAGGAAGAATACAGCATCCACCAAG  
CCTATCAGCAGTGAAGGAAGGGGCAGCGCTCTGGACAGTCTGACCTACCTGAGCTCAACGACTCCTACGACCTGGAGGAGC  
ACCTGCTGAGCTCAGCCGCCCCGCGGGACCTGGAGGCCCTGCAGAGCAGTGGGCTTCAGCGCATCCACTACCCCG  
ACTTCTCGTTTCAGATCCAGAGGCCCGTGGTGAAGACCAGCATGGAGCAGCTGGCCCCAGGAGCTGCAAGGACTGG  
CCCAGGCCCAAGACAATTCTGTGCTGGGGCAGCGGCTGCAGGAGGAGGCCCAAGGACTCAGAAACCTTACCAGG  
AGAAGGTCTCCCCAGCAGAGCCTTGTGGCAAAGCTCAACCTCAGCGTCAGGGCCCTGGAGTCTCTGCCCCGA  
ATCTCCAGCTGGAGACCTCAGATGTCTAGCCAATGTACACTACCTGAAAGGAGAGCTGCCTGCCTGGGCAGCCA  
GGATCCTGAGGAATGTGAGTGAGTGTTCCTGGCCCCGAGAGATGGGCTACTTCTCCAGTACGTGGCCTGGGTGA  
GAGAGGAGTGACTCAGCGCATTTGCCACCTGCCAGCCCCCTCTCCGGAGCCCTGGACAACAGCCGTGTGATCCTGT  
GTGACATGATGGCTGACCCCTGGAATGCCTTCTGTTCTGCCTGGCATGGTGCACCTTCTTCTGATCCCCAGCA  
TCATCTTTGCGCTCAAGACCTCCAATACTTCCGTCTATCCGGAACGCCCTCAGCTCCACCAGCTCTGAGGAGA  
CTCAGCTCTTCCACATCCCCCGGGTTACCTCCCTGAAGCTGTAGGGCCTTGTGGGTGAGGTGACCTGAGGCTG  
CCTGTCTCTCCCTTTGATTTAGCCTGGGCCACAGGACTTCGGTAGCTCTTGCCCCAGAGCCCAGGCTGGCATCCA  
GGCCTGGACTGTCCCCAGTTCCGGCTTACCTGGCCCCACCTTGCCTGCTCCTTTCCACCCCTTTCTGCTCACGAC  
CCCCATCATTACGCTCAGAATCACATGGGACTTCTGTGCAGCTGCAGAGCCAGCAAGTCCCTACAGGTGTCAAC  
CGTTACCCCCATGCTGGTGGCATCCTCACAGGAAGAGCCTGTTCTCCACCTGCTGGAGCCTGGACCCTGGGGTGG  
GACAGAGGCCTCGTCCAACCCCACTCCCTTCCCGTGTGTCTTCCCCCTGCCAAGCCTCCCCCTGCCAAGCCTCC  
CCCTGCCCCCTCTCTGAGCCCCCTCGCCCCCACACCGTCTCATCTGGCCTCCCCCTGGCCCCCACTTCCCTCTT  
ATGCCCTTCTGGCCCTTGTCTTCTTCCCTTAGTCCCTCTTACCATATCTCCACTGCTACCTTGTGGCCCCA  
GAGACACCCCTGCCAACCACCACTCAGGTAACGCCACTAATCAGGCAGGGGCCACCATGGCCTAGGTCTGGG  
CTGGCTGCAGGCCCTGCCTCATGGCCTCTGAGCCCTCACTGCCCCAGGGCCTTGGGCCCTCTGCAGATCTCATC  
CAGGATTTATTGTTGTCCAGTGGGGTGGGGAGGCCCTGTCTGAAGGCCGAGCCTCCCTGCCTGCACCCAAGTTAG  
AAATGGGGGTACCAGCACTTAGCTTCTCTGTAGTGTGGCTQCCAAGGAAGGGACCTGGGACCTGGGCCACAGT  
GGGGGCTTGGCCTTACCTCTTCAAGGAAGCATCTTCCAGGCCCCCCACCAACTTCTTAGGAGTGATCTGGT  
GGCCAGAACAGGATTTGACGGCCCCCTTTTATCTGCGCATGTGGCCTAGGGTCATCCCCAGCCCATCCCTGTG  
TCAGCCCTGAGTGTCTGGACACTGCGTTCCAGAAATGAGGAAGAGGAGAGAGAAGAGATGGACAGACCTCAGATCC  
ATTAAAGTGTTCTCACTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 148**

MKHTLALLAPLLGLGLGLALSQLAAGATDCKFLGPAEHLTFTPAARARWLAPRVRAPGLL  
 DSLYGTVRRFLSVVQLNPFPSSELVKALLNELASVKVNEVVRYEAGYVVCVAVIAGLYLLL  
 PTAGLCFCCCRCHRRCGGRVKTEHKALACERAALMVFLLLTLLLLIGVVCAVVTNQRTH  
 EQMGPSIEAMPETLLSLWGLVSDVPQELQAVAQQFSLPQEQVSEELDGVGVSIGSAIHTQ  
 LRSSVYPLLAAGVSLGQVLQVSVHHLQTLNATVVELQAGQQDLEPAIREHRDRLELLQ  
 ARCQGDCAAGALSWARTLELGADFSQVPSVDHVLHQLKGVPEANFSSMVQEENSTFNALPA  
 LAAMQTSSSVQELKKAVAQQPEGVRTLAEGFPGLEAASRWAQALQVEESSRPYLQEVQR  
 YETRWIVGCVLCSVVLFFVLCNLLGLNLGIWGLSARDDPSHPEAKGEAGARTLMAGVGL  
 SFLFAAPLILLVFATFLVGGNVQTLVCRSWENGELFEFADTPGNLPPSMNLSQLLGLRKN  
 ISIHQAYQQCKEGAALWTVLQLNDSYDLEEHLDINQYTNKLRQELQSLKVDTSQSLDLLSS  
 AARRDLEALQSSGLQRIHYPDFLVQIQRPVVKTSMEQLAQELQGLAQADNSVLGQRLQE  
 EAQGLRNLHQEKVVPQQSLVAKLNLVRALESSAPNLQLETSDVLANVTYLGELPAWAA  
 RILRNVSECFLAREMGYFSQYVAWVREEVTQRIATCQPLSGALDNSRVILCDMMADPWNA  
 FWFCWCTFFLIPSIIFAVKTSKYFRPIRKRLSSTSSEETQLFHIPRVTSCLK

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 105-125, 153-173, 428-449, 476-500, 778-797

**N-glycosylation sites:**amino acids 270-273, 343-347, 352-356, 530-534, 540-546, 563-567,  
684-688, 707-711, 725-729**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 811-815

**Tyrosine kinase phosphorylation site.**

amino acids 95-103

**N-myristoylation sites.**amino acids 13-19, 15-21, 17-23, 26-32, 58-64, 124-130, 168-174,  
228-234, 230-236, 320-326, 338-344, 393-399, 429-435, 446-452,  
477-483, 500-506, 536-542, 644-650, 761-767**Phospholipase A2 histidine active site.**

amino acids 129-137

**4Fe-4S ferredoxins, iron-sulfur binding region signature.**

amino acids 126-138

**Mitochondrial energy transfer proteins signature.**

amino acids 80-89



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**FIGURE 149**

CACAGCTCCCTTCCCAGGACGTGAAAATCTGCCTTCTCACCATGAGGCTTCTAGTCCTTTCCA  
GCCTGCTCTGTATCCTGCTTCTCTGCTTCTCCATCTTCTCCACAGAAGGGAAGAGGCGTCCTG  
CCAAGGCCTGGTCAGGCAGGAGAACCAGGCTCTGCTGCCACCGAGTCCCTAGCCCCAACTCAA  
CAAACCTGAAAGGACATCATGTGAGGCTCTGTAAACCATGCAAGCTTGAGCCAGAGCCCCGCC  
TTTGGGTGGTGCCTGGGGCACTCCCACAGGTGTAGCACTCCCAAAGCAAGACTCCAGACAGCG  
GAGAACCTCATGCCTGGCACCTGAGGTACCCAGCAGCCTCCTGTCTCCCCTTTCAGCCTTCAC  
AGCAGTGAGCTGCAATGTTGGAGGGCTTCATCTCGGGCTGCAAGGACCCTGGGAAAGTTCCAG  
AACTCCACGTCCTTGTCTCAATTGTGCCATCAACTTTCAGAGCTATCATGAGCCAACCTCACC  
CCACAGGGCCTCAGTCGCCACCATGTGGGCCTCTCCAGTGCAAACCACCGAGCATTCCACCAT  
GACCGGTCACAGCTACAAATCCAGAGACCATCAATCCTGCTAGAGTGCAGGGTGGCAAGCACC  
CAAGGGTGGCTGACCAAGACTGCAGAGTCTCCTCCATCTTCAGGTCCATTAGCCTCCTGGCA  
TTTAACTACCAGCATCCAGTGGTCCCCAAGGAATCCCTTCCTAGCCTCCTGACATGAGTCTGC  
TGGAAAGAGCATCCAAACAAACAAGTAATAAATAAATAAATAAACTCA

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**FIGURE 150**

MRLLVLSLLCILLLCFSIFSTEGKRRPAKAWSGRRTRLCCHRVSPNSTNLKGHHVRLCKPC  
KLEPEPRLWVVP GALPQV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 48-52

**Amidation sites.**

amino acids 23-27, 33-37

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**FIGURE 151**

CACCGGAGGGACGCAGCTGACGGAGCTGCGCTGCGTTGCGCTCGTTTGCCTCGCGCCCTCCA  
CTGGAGCTGTTTCGCGCCTCCCGGCTCCCACCGCAGCCCACCGGCAGAGGAGTCGCTACCAGC  
GCCCAGTGGCTCTGTCACTCCGCAAACCTCCTTGCCGCCCCGCCCCGGGCTGGGCACCAAATAC  
CAGGCTACCA**ATGGT**CTACAAGACTCTCTTCGCTCTTTGCATCTTAACCTGCAGGATGGAGGGTA  
CAGAGTCTGCCTACATCAGCTCCTTTGTCTGTTTCTCTTCCGACAAACATTGTACCACCGACC  
ACCATCTGGACTAGCTCTCCACAAACACTGATGCAGACACTGCCTCCCCATCCAACGGCACT  
CACAACAACCTCGGTGCTCCCAGTTACAGCATCAGCCCCAACATCTCTGCTTCCTAAGAACATT  
TCCATAGAGTCCAGAGAAGAGGAGATCACCAGCCCAGGTTTGAATTGGGAAGGCACAAACACA  
GACCCCTCACCTTCTGGGTCTCTCGTCAACAAGCGGTGGAGTCCACTTAACAACCACGTTGGAG  
GAACACAGCTCGGGCACTCCTGAAGCAGGCGTGGCAGCTACACTGTCGCAGTCCGCTGCTGAG  
CCTCCACACTCATCTCCCCCAAGCTCCAGCCTCATCACCTCATCCCTATCAACCTCACCA  
CCTGAGGTCTTTTCTGCCTCCGTTACTACCAACCATAGCTCCACTGTGACCAGCACCCAACCC  
ACTGGAGCTCCAACCTGCACCAGAGTCCCCGACAGAGGAGTCCAGCTCTGACCACACACCCACT  
TCACATGCCACAGCTGAGCCAGTGCCCCAGGAGAAAACACCCCCAACAACTGTGTGAGGCAAA  
GTGATGTGTGAGCTCATAGACATGGAGACCACCACCACCTTTCCAGGGTGATCATGCAGGAA  
GTAGAACATGCATTAAGTTTCAAGCAGCATCGCCGCCATTACCGTGACAGTCATTGCCGTGGTG  
CTGCTGGTGTGGAGTTGCAGCCTACCTAAAAATCAGGCATTCTCCTATGGAAGACTTTTG  
GACGACCATGACTACGGGTCTGGGGAACTACAACAACCCTCTGTACGATGACTCC**TAACA**A  
TGGAATATGGCCTGGGATGAGGATTAACCTGTTCTTTATTTATAAGTGCTTATCCAGTAGAATT  
AATAAGTACCTGATGCGCATTTGAACGACAATCTTAAGCCCTGTTTTGTTGGTATGGTTGTTTT  
TGTTTTCTCTCCCTCTCCTCTGGCTGCTACAACTTCCCCTTTCTGGTACAAGAAGAACCATTCT  
TTAAAGGTGAGTGGAGGCTGATTTGCAGCTGAAGTGGGCCAGCCTTGACCAGCCAGGCCAGA  
CCACCATGGTGAAGGCTTCTTTCCCCACTGCAGGACCCACTTTGAGAAGGATCGAGGAGGAGG  
ATTTGGGTTGTTTTGTTAGGGGTTACTTTCAAGGGGAACATTTCAATTTGTGTTATTTCTTAAAC  
TTCTATTTAGGAAATTACATTAAGTATTAATGAGGGGAAAGGAAATGAGCTCTACGAGGATTT  
CACCTTGATGGGAGAGAGCAGGGTTTTCTCAGATTCTTTTAAATCTCTATTTATCTGGTTG  
TTTCTGACAGGATGCTGCCTGCTTGGCTCTACGAGCTGGAAAGCAGCTCTTAGCTGCCTAAT  
TAATGAAAGATGAAAATAGGAAGTGCCCTGGAGGGGGCCAGCAGGTACGGGGCAGAATCTCT  
CAGGTTGCTGTGGGATCTCAGTGTGCCCCTACCTGTTCTCCCCTCCAGGCCACCTGTCTCTGT  
AAAGGATGTCTGCTCTGTTCAAAAGGCAGCTGGGATCCCAGCCCACAAGTGATCAGCAGAGTT  
GCATTTCCAAAGAAAAAGGCTATGAGATGAGCTGAGTTATAGAGAGAAAGGGAGAGGCATGTA  
CGGTGTGGGGAAGTGGAAGAGAAGCTGGCGGGGGAGAAGGAGGCTAACCTGCACTGAGTACTT  
CATTAGGACAAGTGAGAATCAGCTATTGATAATGGCCAGAGATATCCACAGCTTGGAGGAGCC  
CAGAGACTGTTTGCTTTATACCCACACAGCAACTGGTCCACTGCTTTACTGTCTGTTGGATAA  
TGGCTGTAAATGTTTAAAAAC

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**FIGURE 152**

MVYKTLFALCILTAGWRVQSLPTSAPLSVSLPTNIVPPTTIWTSSPQNTDADTASPSNGTHNN  
SVLPVTASAPTSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVHLTTTLEEH  
SGTPEAGVAATLSQSAAPPTLISPQAPASSPSSLSTSPPEVFSASVTTNHSSTVTSTQPTGA  
PTAPESPTTESSSDHTPTSHATAEPVPQEKTPPTTVSGKVMCELIDMETTTTFPRVIMQVEH  
ALSSGSIAAITVTVIAVLLVFGVAAYLKIRHSSYGRLLDDHDYGSWGNYNPNPLYDDS

**Important features of the protein:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 258-278

**N-glycosylation sites.**

amino acids 58-61, 62-65, 80-83, 176-179

**Casein kinase II phosphorylation sites.**amino acids 49-52, 85-88, 95-98, 100-103, 120-123, 121-124, 141-  
144, 164-167, 191-194, 195-198, 200-203**Tyrosine kinase phosphorylation site.**

amino acids 289-296

**N-myristoylation sites.**

amino acids 59-64, 115-120, 128-133, 133-138, 257-262, 297-302

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**FIGURE 153**

[illegible]

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**FIGURE 154**

MLVHCVGLLLTGALLGLTLGAGALLASEPIYQPPSAWVPAGGLVGLALLGALLTLRWPRPFTV  
LGTTLGSAVLVACVDYFLEGLALGSWLGQRLQTLPALPSLC

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 38-55, 60-78

**N-myristoylation sites.**

amino acids 7-13, 12-18, 16-22, 22-28, 41-47, 50-56, 84-90, 88-94

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 67-78

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**FIGURE 155**

TGCAATTAAAGGAGTCGGGTCTCTAACTGTTGATCTGTTTTTTTCCCTTCTGAGCAATGGAGC  
TTACCATCTTTATCCTGAGACTGGCCATTTACATCCTGACATTTCCCTTGTACCTGCTGAACT  
TTCTGGGCTTGTGGAGCTGGATATGCAAAAAATGGTTCCCCTACTTCTTGGTGAGGTTCACTG  
TGATATACAACGAACAGATGGCAAGCAAGAAGCGGGAGCTCTTCAGTAACCTGCAGGAGTTTG  
CGGGCCCCCTCCGGGAAACTCTCCCTGCTGGAAGTGGGCTGTGGCACGGGGGCCAACTTCAAGT  
TCTACCCACCTGGGTGCAGGGTGACCTGTATTGACCCCAACCCCAACTTTGAGAAGTTTTTGA  
TCAAGAGCATTGCAGAGAACCGACACCTGCAGTTTGAGCGCTTTGTGGTAGCTGCCGGGGAGA  
ACATGCACCAGGTGGCTGATGGCTCTGTGGATGTGGTGGTCTGCACCCTGGTGCTGTGCTCTG  
TGAAGAACCAGGAGCGGATTCTCCGCGAGGTGTGCAGAGTGCTGAGACCGGGAGGGGCTTTCT  
ATTTTCATGGAGCATGTGGCAGCTGAGTGTTCGACTTGGAATTACTTCTGGCAACAAGTCCTGG  
ATCCTGCCTGGCACCTTCTGTTTGATGGGTGCAACCTGACCAGAGAGAGCTGGAAGGCCCTGG  
AGCGGGCCAGCTTCTCTAAGCTGAAGCTGCAGCACATCCAGGCCCCACTGTCCTGGGAGTTGG  
TGCGCCCTCATATCTATGGATATGCTGTGAAATAGTGTGAGCTGGCAGTTAAGAGCTGAATGG  
CTCAAAGAATTTAAAGCTTCAGTTTTACATTTAAATGCTAAGTGGGAGAAGAGAAACCTTTT  
TTTTGGGGGGCGGTTTTTTTTGGTTTTGTGTTGGTTTTTTTTTTTTTTTTTTGGCAGGAGAATCTC  
TTGAACCCAGAAGGCGAAGGTTGCAGTGAACCGAGATCATGCCATTGTACTCTAGCCTGGGTG  
ACAAGAGCAAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAGAAGTAGAGACAGGGAGAC  
GGGGTCTCACTGTGTTGCCTAGGCCGGTCTTGAACCTCCTGGGCTCAAGTGATTCTCCACCTT  
GACCTCCTAAATTGTTGGGATTACAGGTGTGAGACAGTGCACCTGGCCGAAATAGCTCAAGTT  
TCTGAAAAACAAATCTGAATCTATTTGTTATTCTTAGCGTCACTGGTCTGGCTTTCAGAATTA  
ACATACAAGGTTGCCACACCTAGTTCTGCCCAGCTTTATGTCTTTTATTCCAGTATTCCACCA  
AAGTTTGTTCCTGCATTCCAGTTCTCAAGTCTTAAGATAAAGATTGTAAGTTGACAGTTTAG  
TATATCCATAAACTATTTGAGGTGGTTAAGGTTCTTGGGTTCAATTTTCCTTAATACTTTGCT  
GAATATTGTAGATTGTAGGCAATGAAAAAGTCTACTAAATTAGGAAAACCTTGAATAATTAGG  
TATCCTAGGTAAGAGCCCCCTAAACATCAAGCAATCTGTGAGTCTGTAAAGAAATAAATATTTT  
TTGGATTATTCTTATCTAATTCCACCCCTGTTGGAAGATGATTTCTTTGTTCTTTGCAACTAT  
GGAAGCTGTGAAAATCATCACAAGTGCCTCTGAAAGCGAGTGTTAGGTTGGTTAGAGGGTTTA  
ATATTTTCTGCAATGGTTTGTAGGAATTTTAATAAATGTAGTATATTTTCTGAGATGATTTTG  
TAAAAGTACTATTTTAAATATCAAATCAACCAATAAATTCACATTTGTGTTAGGAACAAAA

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**FIGURE 156**

MELTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFPYFLVRFTVIYNEQMASKKRELFSLNQ  
EFAGPSGKLSLLEVGCCTGANFKFYPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAA  
GENMHQVADGSVDVVVCTLVLCVKNQERILREVCRLRPGGAFYFMEHVAAECSTWNYFWQQ  
VLDPAWHLLFDGCNLTRESWKALERASFSLKLQHIQAPLSWELVRPHIYGYAVK

**Signal peptide:**

amino acids 1-29

**N-glycosylation site.**

amino acids 203-207

**N-myristoylation sites.**

amino acids 78-84, 80-86, 91-97, 201-207



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**FIGURE 157**

CCGCTGAGATGTACGAACTTCCGGTTCTCCGGGCAGCTGCCACTGCTGTAGCTTCTGCCACCT  
GCCACGACCGGGCCTCTCCCTGGCGTTTGGTCACCTCTGCTTCATTCTCCACCGCGCCTATGG  
TCCCTCTTGAGCCAGCGTGGCGGGCCTGGCGGCTCCCGGGTGGTGAGAGAGCGGTCCGGGAA  
CGATGAAGGCCTCGCAGTGCTGCTGCTGTCTCAGCCACCTCTTGGCTTCCGTCCTCCTCCTGC  
TGTTGCTGCCTGAACTAAGCGGGCCCCCTGGCAGTCTTGCTGCAGGCAGCCGAGGCCGCGCCAG  
GTCTTGGGCCTCCTGACCCTAGACCACGGACATTACCGCCGCTGCCACCGGGCCCTACCCCTG  
CCCAGCAGCCGGGCGGTGGTCTGGCTGAAGCTGCGGGGCCGCGGGGCTCCGAGGGAGGCAATG  
GCAGCAACCCTGTGGCCGGGCTTGAGACGGACGATCACGGAGGGAAGGCCGGGGAAGGCTCGG  
TGGGTGGCGGCCTTGCTGTGAGCCCCAACCTGGCGACAAGCCCATGACCCAGCGGGCCCTGA  
CCGTGTTGATGGTGGTGAGCGGCGCGGTGCTGGTGTACTTCGTGGTCAGGACGGTCAGGATGA  
GAAGAAGAAACCGAAAGACTAGGAGATATGGAGTTTTGGACACTAACATAGAAAATATGGAAT  
TGACACCTTTAGAACAGGATGATGAGGATGATGACAACACGTTGTTTGATGCCAATCATCCTC  
GAAGATTAGAATGTGCCTTTTGATGAAAGAACTTTATCTTTCTACAATGAAGAGTGGAATTC  
TATGTTTAAGGAATAAGAAGCCACTATATCAATGTTGGGGGGGTATTTAAGTTACATATATTT  
TAACAACCTTTAATTTGCTGTTGCAATAAATACCGTATCCTTTTATTATATCTTTATATGTAT  
AGAAGTACTCTATTAATGGGCTCAGAGATGTTGGGGATAAAGTATACTGTAATAATTTATCTG  
TTTGAAAATTACTATAAAACGGTGTTTTCTGGTCGGTTTTTGTTCCTGCTTACCATATGATT  
GTAAATTGTTTTATGTATTAATCAGTTAATGCTAATTATTTTGCTGATGTCATATGTTAAAG  
AGCTATAAATTCCAACAACCAACTGGTGTGTAAAAATAATTTAAATTTCCCTTTACTGAAAGG  
TATTTCCCATTTTTGTGGGGAAAAGAAGCCAAATTTATTACTTTGTGTTGGGGTTTTTAAAT  
ATTAAGAAATGTCTAAGTTATTGTTTGCAAAACAATAAATATGATTTTAAATTCTCTTAAAA  
AAAAA

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**FIGURE 158**

MKASQCCCCLSHLLASVLLLLLLPELSGPLAVLLQAAEAAPGLGPPDPRPRTLPLPPGPTPA  
QQPGRGLAEAAGPRGSEGGNGSNPVAGLETDDHGGKAGEGSVGGGLAVSPNPGDKPMTQRALT  
VLMVVSGAVLVYFVVRTVRMRRNRKTRRYGVLDNIENMELTPLEQDDEDDNTLFDANHPRR

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 124-140

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 69-75, 78-84, 81-87, 97-103, 103-109, 106-112,  
157-160

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**FIGURE 159**

GCTGCAGGCGGGCGACGGCTACACCA**ATG**GGCCGGCTGCTGCGGGCCGCCGGCTGCCGCCGCTG  
CTTTTCGCCGCTGCTGCTTCTGCTGGTTGGGGGAGCGTTCTGGGTGCCTGTGTGGCTGGGTCT  
GATGAGCCTGGCCCAGAGGGCCTCACCTCCACCTCCCTGCTAGACCTCCTGCTGCCACTGGC  
TTGGAGCCACTGGACTCAGAGGAGCCTAGTGAGACCATGGGCCTGGGAGCTGGGCTGGGAGCC  
TCTGGCTCAGGCTTCCCCAGCGAAGAGAATGAAGAGTCTCGGATTCTGCAGCCACCACAGTAC  
TTCTGGGAAGAGGAGGAAGAGCTGAATGACTCAAGTCTGGACCTGGGACCCACTGCAGATTAT  
GTTTTTCTGACTTAACTGAGAAGGCAGGTTCATTGAAGACACTAGCCAGGCTCAAGAGCTG  
CCAAACCTCCCCTCTCCCTTGCCCAAGATGAATCTGGTTGAGCCTCCCTGGCATATGCCTCCC  
AGAGAGGAGGAAGAAGAGGAAGAGGAAGAGGAGGAGAGGGAGAAGGAAGAGGTAGAGAAACAA  
GAGGAGGAGGAAGAGGAGGAGCTGCTCCCTGTGAATGGATCCCAAGAAGAAGCCAAGCCTCAG  
GTCCGTGACTTTTCTCTCACCAGCAGCAGCCAGACCCAGGGGCCACCAAAAGCAGGCATGAA  
GACTCCGGGGACCAGGCCTCATCAGGTGTGGAGGTGGAGAGCAGCATGGGGCCCAGCTTGCTG  
CTGCCTTCAGTCACCCCAACTACAGTGACTCCGGGGGACCAGGACTCCACCAGCCAAGAGGCA  
GAGGCCACAGTGCTGCCAGCTGCAGGGCTTGGGGTAGAGTTCGAGGCTCCTCAGGAAGCAAGC  
GAGGAAGCCACTGCAGGAGCAGCTGGTTTGTCTGGCCAGCACGAGGAGGTGCCGGCCTTGCCCT  
TCATTCCCTCAAACCACAGCTCCCAGTGGGGCCGAGCACCCAGATGAAGATCCCCTTGCTCT  
AGAACCTCAGCCTCTTCCCCACTGGCCCCCTGGAGACATGGAAGTACACCTTCCTCTGCTACC  
TTGGGACAAGAAGATCTCAACCAGCAGCTCCTAGAAGGGCAGGCAGCTGAAGCTCAATCCAGG  
ATACCCTGGGATTCTACGCAGGTGATCTGCAAGGACTGGAGCAATCTGGCTGGGAAAACTAC  
ATCATTCTGAACATGACAGAGAACATAGACTGTGAGGTGTTCCGGCAGCACCGGGGGCCACAG  
CTCCTGGCCCTGGTGGAAGAGGTGCTGCCCCGCCATGGCAGTGGCCACCATGGGGCCTGGCAC  
ATCTCTCTGAGCAAGCCCAGCGAGAAGGAGCAGCACCTTCTCATGACACTGGTGGGCGAGCAG  
GGGGTGGTGCCCACTCAAGATGTCCTTTCCATGCTGGGTGACATCCGCAGGAGCCTGGAGGAG  
ATTGGCATCCAGAACTATTCCACAACCAGCAGCTGCCAGGCGCGGGCCAGCCAGGTGCGCAGC  
GACTACGGCACGCTCTTCGTGGTGCTGGTGGTCATTGGGGCCATCTGCATCATCATCATTGCG  
CTTGGCCTGCTCTACAACTGCTGGCAGCGCCGGCTGCCCAAGCTCAAGCACGTGTGCGACGGC  
GAGGAGCTGCGCTTCGTGGAGAACGGCTGCCACGACAACCCACGCTGGACGTGGCCAGCGAC  
AGCCAGTCGGAGATGCAGGAGAAGCACCCAGCCTGAACGGCGGGCGGGGCCCTCAACGGCCCCG  
GGGAGCTGGGGGGCGCTCATGGGGGGCAAGCGGGACCCCGAGGACTCGGACGTGTTGAGGAG  
GACACGCACCTG**TGA**GCGCAGCCGAGGCGCAGGCCGAGTGGGCCGCCAGGACCAAGCGAGGTG  
GACCCCGAAACGGACGGCCCCGGAGCCCCGACCAGCCCCGCGCCTACCCGGGGCGCCCCCGCGG  
CCTGGCCCTCGGCGCGGGCTCCTTCCCGCTTCCCCGACTTCACACGGCGGCTTCGGACCAAC  
TCCCTCACTCCCGCCCCGAGGGGCAGGCCTCAAAGCCCCGCTTGGCCCCGCTTCCCGCCCCCTG  
AACCCCGCCCCCGCGGGCGGGCGGGCGCTTCTGCGCCCCGGGACTCAATTAAACCCGCC  
GGAGACCACGCCGGGCCAGCAAAA

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**FIGURE 160**

MGRLLRAARLPPLLSPLLLLLLVGGAFLGACVAGSDEPGPEGLTSTSLDLLLPTGLEPLDSEE  
PSETMGLGAGLGASGSGFPSEENEESRILQPPQYFWEEEEELNDSSLDLGPTADYVFPDLTEK  
AGSIEDTSQAQELPNLPSPLPKMNLVEPPWHMPPREEEEEEEEEEREKEEVEKQEEEEEEEL  
LPVNGSQEEAKPQVRDFSLTSSSQTPGATKSRHEDSGDQASSGVEVESSMGPSSLLPSVTPTT  
VTPGDQDSTSQAEEATVLPAAAGLGVEFEAPQEASEEATAGAAGLSGQHEEVPALPSFPQTAP  
SGAEHPDEDPLGSRTSASSPLAPGDMELTPSSATLGQEDLNQQLLEGQAAEAQSRIPWDSTQV  
ICKDWSNLAGKNYIILNMTENIDCEVFRQHRGPQLLALVEEVLPRHGSGHHGAWHISLSKPSE  
KEQHLLMTLVGEQGVVPTQDVLSMLGDIRRSLEEIGIQNYSTTSSCQARASQVRSYGTLFVV  
LVVIGAICIIIIALGLLYNCWQRRPKLKHVSHGEELRFVENGCHDNPTLDVASDSQSEMQEK  
HPSLNGGGALNGPGSWGALMGGKRDPESDVFEEDTHL

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 499-521

**N-glycosylation sites.**

amino acids 106-110, 193-197, 395-399, 480-484

**Glycosaminoglycan attachment site.**

amino acids 77-81

**N-myristoylation sites.**amino acids 24-30, 28-34, 41-47, 69-75, 71-77, 73-79, 75-81,  
216-222, 327-333, 455-461, 519-525, 574-580, 581-587, 584-590**Amidation site.**

amino acids 588-592

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**FIGURE 161**

CCAGGGCGGAGCGCAGCTGCGCCGGGCTTGGGCGCCTGGGGCCGCGCTCCCCACCGTCGTTT  
TCCCCACCGAGGCCGAGGCGTCCCGGAGTCA**ATG**GCCGGCCTGAACTGCGGGGTCTCTATCGCA  
CTGCTAGGGGTTCTGCTGCTGGGTGCGGCGCGCCTGCCGCGCGGGGCAGAAGCTTTTGAGATT  
GCTCTGCCACGAGAAAGCAACATTACAGTTCTCATAAAGCTGGGGACCCCGACTCTGCTGGCA  
AAACCCTGTTACATCGTCATTTCTAAAAGACATATAACCATGTTGTCCATCAAGTCTGGAGAA  
AGAATAGTCTTTACCTTTAGCTGCCAGAGTCCTGAGAATCACTTTGTCATAGAGATCCAGAAA  
AATATTGACTGTATGTCAGGCCCATGTCCTTTTGGGGAGGTTTCTGCTTCTGACATCG  
TTGTTGCCTACCCCTCAACAGAACTTTCATCTGGGATGTCAAAGCTCATAAGAGCATCGGTTTA  
GAGCTGCAGTTTTCATCCCTCGCCTGAGGCAGATCGGTCCGGGTGAGAGCTGCCAGACGGA  
GTCCTCACTCCATCAGCGGCCGAATCGATGCCACCGTGGTCAGGATCGGAACCTTCTGCAGC  
AATGGCACTGTGTCCCGGATCAAGATGCAAGAAGGAGTGAAAATGGCCTTACACCTCCCATGG  
TTCCACCCCAGAAATGTCTCCGGCTTCTGAGCATTGCAAACCGCTCATCTATAAAACGTCTGTGC  
ATCATCGAGTCTGTGTTTGAGGGTGAAGGCTCAGCAACCCTGATGTCTGCCAACTACCCAGAA  
GGCTTCCCTGAGGATGAGCTCATGACGTGGCAGTTTGTTCGTTTCTGCACACCTGCGGGGCCAGC  
GTCTCCTTCCCTCAACTTCAACCTCTCCAACCTGTGAGAGGAAGGAGGAGCGGGTTGAATACTAC  
ATCCCGGGCTCCACCACCAACCCCGAGGTGTTCAAGCTGGAGGACAAGCAGCCTGGGAACATG  
GCGGGGAACCTTCAACCTCTCTCTGCAAGGCTGTGACCAAGATGCCCAAAGTCCAGGGATCCTC  
CGGCTGCAGTTCCAAGTTTGGTCCAACATCCACAAAATGAAAGCAGTGAG**TGA**GCCCCACTT  
TCCTTTTCTTCTCCTCCAGCACCTTCGTTGTTTCTGGGTAGTCTGCCTGGGTGAGGCTCC  
CTTCTGTTTCTCATCTGTGGCTTCTGAAACACTTAGACTCTGGACCCAGCAAGAGTTTTCAGG  
AAGTGGGTTGCTAGGCAGTTAGACAGGCTTGTGGTGAACACCCGGTATGTAGTTCCATTTCA  
GCACAATAAAAAGAAATCTTGCAATCAAGATGCTAAATTGTTTTTAACGAAA

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**FIGURE 162**

MAGLNCGVSIALLGVLLLGAARLPRGAFAFEIALPRESNITVLIKLGTPPTLLAKPCYIVISKR  
HITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMSGPCPFGEVQLQPSTSLPPTLNRTFI  
WDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSNGTVSRIKMQ  
EGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANYPEGFPEDELMTW  
QFVVPAPHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDKQPGNMAGNFNLSLQG  
CDQDAQSPGILRLQFQVLVQHPQNESSE

**Signal peptide:**

amino acids 1-29

**N-glycosylation sites.**amino acids 39-43, 122-126, 180-184, 205-209, 213-217, 270-274,  
310-314, 339-343**Tyrosine kinase phosphorylation site.**

amino acids 276-284

**N-myristoylation sites.**

amino acids 3-9, 7-13, 158-164, 175-181, 191-197, 303-309

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**FIGURE 163**

CAACCACACACCTGGGGAATTGCTGGCCTGACTTCTGACCCCTGACTCCTCATACCCTTCCTC  
CAGAGCATGACATTTGACCACCAACTGAAACCTGACCTCTGACCCAGACCACTGGCCCTTCC  
CCCGCCCTGTGGTGACTTCATAAAGTTACTAGCTTCTCCCCTGGCCTTGAGACCCACACGAT  
GGCCCTGCTGGCTCTGGCCAGTGCCGTCCCCCTCTGCCCTGCTGGCCCTGGCTGTCTTCAGGGT  
GCCCCCTGGGCCTGTCTCCTCTGCTTCACAACCTACTCTGAGCGCCTCCGCATCTGCCAGAT  
GTTTGTGGGATGCGGAGCCCCAAGCTTGAAGAGTGTGAGGAGGCCTTCACGGCCGCCTTCCA  
GGGCCTCTCTGACACCGAAATCAGTGAGGAGACCATCCACACTTCATCAGTGTCTTGGGGAAG  
GTGCAGAGGGAGGGCAGGAGAGGCCAGAGGGTCAGGCTGAGGGACAGACAGAGAGAAACAGT  
CAGAGGAGAAAGGCTCAAAGACCATGAGAACAACAGAGACTTAGGGACAGAGAGACACAGACA  
GGGGAAGACAGCAGGGCAAAGACTCAGAGAGGGGAGGATGGAGAGTCAGAGAGGGGAAGATGG  
AGACTCAGAGAGAGGGGAGGATGGAGACTCAGAGAGAGAGGAAGATGGAGACTCAGAGGGAAA  
GATGGAGACTCAGGAGTATGGAGAGTCAGAGAGGGGAGGATGGACACTCAGGGGAGGATGGAG  
AGTCAGGAGGATGGAGACTCATAGAAAGGGGAGGATGGAGAGTCAGGAGAGGTTGGAGACTGG  
AGAGGGAATAGAGACCCAGAAAGGGGAGGATGGAGACTCAGAGGGTGAAGATGGAGACTCAA  
AGAGGATGGAAACCCAGAGAGAGGAGGACAGAGATGAGGACAGAGACTAGGGGAAGCAGGATAG  
CGACTGGTCGGGGGCAGAGACTCAGGGAGGATAGAGACTCACAGAGAGGTGAGGATAGAGACT  
TGGGAGGGACTCAGGAAGCATAGCGACTGTGGGGCAAAGAGTCAGAGAGGGGAGGATACAGAC  
TTGGGAGGGCAGAGACTCAGAAACAGAATGTTTCGATTAGGGACATGGTGTTCGGGGAGCTG  
CCTCCCCCAGCCCTGCTCCCTCCCTCACCGCCAGACTATGATGAGAGAAGCCACCTGCATGA  
CACCTTCACCCAGATGACCCATGCCCTGCAGGAGCTGGCTGCTGCCCAGGGATCCTTTGAGGT  
TGCCTTCCCTGATGCTGCAGAGAAAATGAAGAAGGTCATTACACAGCTTAAAGAAGCCAGGC  
TTGCATCCCTCCCTGCGGTCTCCAGGAGTTCGCCCCGCGTTTCTCTGCAGCGGGTGCTACTC  
TAGGGTCTGCGACCTCCCGCTGGACTGCCCAGTTCAGGATGTGACAGTGAATCGGGGCGACCA  
GGCTATGTTTTCTTGATCGTAAACTTCCAGCTGCCAAAGGAGGAGATCACCTATTCCTGGAA  
GTTTCGAGGAGGAGGTCTCCGACTCAGGACTTGTCTTATTTCCGAGATATGCCGCGGGCCGA  
AGGATACCTGGCGCGGATCCGGCCGGCTCAGCTCACGCACCGCGGGACGTTCTCCTGCGTGAT  
CAAGCAAGACCAGCGCCCCCTGGCCCCGCTCTACTTCTTTCTTAACGTCCTCGGGGCCCTCGC  
ATCAGCGAGTGCGACAGTGTGGCGTGAGTTCTGGGGACTCCGGAGCCCCAGCATCTAGC  
TCCCCGCTGTCTCAGATCCCACCGAGAAGTCTGGGTCCCAGCAACCTCCAACCCAGGAGGAT  
GTTCTTTTCGATGGTACTGCAGTGGCAACTAACAAAGGTATCTTTCTCCTCCTTCCCTATCCTATT  
TCCATCCTGAAAATAAAGAATATATTTCAACTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAA

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**FIGURE 164**

MALLALASAVPSALLALAVFRVPAWACLLCFTTYSERLRICQMFVGMRSKPLEECEEAF  
TAAFQGLSDTEISEETIHTSSVSWGRCRGRAGEAQRVRLRDRQRETVRGERLKD  
HENNRLDLGTERHRQKTAGQRLREGRMESQRGEDGDSERGEDGDSEREEDGD  
SEGKMETQEYGESERGGWTLRGGWRVRRMETHRKGRMESQERLETGEG  
IETQKGEDGDSEGGRWRLKEDGNPERGGQR

**Signal peptide:**

amino acids 1-26

**N-myristoylation site.**

amino acids 65-71





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**FIGURE 166**

MELSDVTLIEGVGNEVMVVAGVVVLILALVLAWLSTYVADSGSNQLLGAIVSAGDTSVLHLGH  
VDHLVAGQGNPEPTELPHPSEGNDKAEAEAGEGRGDSTGEAGAGGGVEPSLEHLLDIQGLPKR  
QAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLNDTEELAVARPEDTVGALKSKYFPGQES  
QMKLIYQGRLQLQDPARTLRSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVGS  
LMVPVFVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLVFGMYGR

**Signal peptide:**

amino acids 1-36

**Transmembrane domains:**

amino acids 246-267, 275-301

**N-glycosylation sites.**

amino acids 162-166, 211-215

**N-myristoylation sites.**

amino acids 48-54, 105-111, 109-115, 129-135, 177-183, 247-253

**Cell attachment sequence.**

amino acids 97-100

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**FIGURE 167**

GGCGGCTGTGTGTCGCCGGAGCCGAAGCGCGCAGGCCCGTCCCGGTGGCCGGGAGCGGGCGGGTGGGGGCGCCA  
TGTGGTTTCATGTACCTGCTGAGCTGGCTGTGCTCTTTCATCCAGGTGGCCTTCATCACGCTGGCTGTGCGGGCTG  
GACTCTATTACCTGGCAGAACTGATAGAAGAATACACAGTGGCCACCAGCAGGATCATAAAATACATGATCTGGT  
TCTCCACCGCTGTACTGATTGGCCTCTACGTCTTTGAGCGCTTCCCCACCAGCATGATTGGAGTGGGCCTATTCA  
CCAACCTCGTCTACTTTGGCCTCCTCCAGACCTTCCCCCTTCATCATGCTGACCTCGCCTAACTTCATCCTGTGCT  
GTGGACTAGTGGTGGTGAATCATTACCTAGCATTTTCAGTTTTTTGCAGAAGAATATTATCCCTTCTCAGAGGTCC  
TGGCCTATTTCACTTTCTGCCTGTGGATAATTCCGTTTGGCTTTTGTGTCACTTTTCGGCCGGGAGAACGTCC  
TGCCCTCTACCATGCAGCCAGGAGATGATGTCGTCTCCAATTATTTACCAAAGGCAAGCGGGGCAAACGCTTAG  
GGATCCTGGTTGTCTTCTCCTTCATCAAAGAGGCCATTCTACCCAGTCGTCAGAAGATATACTGACCCCCATGCA  
GGCAGGATGTGGGGGCAAGATCAGGAGAGTCAGGCCCTGGGCCTCTATGCCAGGTGGGGACCAGAAGTCGGGA  
AGGCACCTACCACCTGCCCTGGCTTCTTCCCCCTCAACTCTGGAGCCCCATCCCCACCCTCCTTGGGGGGCTCAG  
CTTGGCTCAGATCTGATGCTTCAAGAGGCTGTAACCTCAGAGGGCACCAAGGAGGGTGGCAGAGCCTGCTTAGCC  
AGGAGGCCGAGGTCCCTCAGTCCTCCCCTGTCCCTTCCAAGTGGGTGAGGAGTTCTGGCCCCGCTGGGGCAGG  
CAGGGCAGGGTCTGTGAAGCTTAAGAGCAGATGGTGACAAGTTCTCTGGGCAGGTGGCCATGGGGAGGGGCCATG  
GCTTGGCATGTCCCAACAGAAATAGTTTTTGTCTGTTGAACGGTGATTTCTGTCCAAGTGCAGATTTCCGTTTGAAT  
AAAGCTTCGCTTCTAGGTGGCACTGTTTGCCTTAATACCCTGACAGTTCATCTTCTTCTTCTCCTGCTAACCTTC  
TGCTCTGGACTGGACTCACTTTTCTGCTCCAGGGACTCCTTTTCTGGGTTTGGGTCTTGGCCTTCCCAAGGGACT  
GTTCTTGTGGCCCTTAATGGGAAGGGGGCAGGGGTGAGGAGCTGAGCCTGCTCAAGGAGTGGGAAGTGGGGCTAT  
AGGCAGCCTCTCTGATGCACTCTCTTCCATCTCTTTCCCCAAGGCTCCGTGACTGTCAAAGTGGGAGTAGGAGAG  
GGGACAATTTAGGACTGGGCTAGATTTTCAGAAGAACATCTACAATATCCTATTTATAAATCTTCTCTGGGAAA  
AGGAGTGGTTTCTGGCTGAATACTATCTTAGGCTCAAGGAGAAACAAAATAAAATTAGCTTCCAGGCAGCCTGT  
TTTTAAAGAAATGGGACTAATGGGAGAAGCTGTTGTCACTCTAAGAGCATCCAAGCCCTGGCCCCGTCTGTGCAC  
TCTTGGCTCCTGGGGAGATATATCTGCCTTCTAAGAAGGCAGGCCAGGTCTTGGGCACAGACCTGCATTGTGGA  
CCTTGCACCTCAACTATAGTGCCCTTGCAAGTGCTCAACAGTACATATTGGAATGAAGTCCCTATGAGAGCCATTT  
CTGGCCATGTTCTATACCTCAAAGTGAGGCTGGCAGGTACAGAGATGAAGTGTACACATGTGATACATTTAAGCC  
ACTGGAAAAACCCCTGTGCTTGAAAATATTTCTCTATATCATGCCTGGAGTTCATCATAGCCCTTCATTTCTCT  
TGGCTTTAGCATTTACCTTCTCTTAAGAATACCAGCTTTCCCCTTTCCCTGAGAGGAAGAGCACATGTTGGTCTC  
CTCTTAGTGTGAACGAGATTGCCAGGCCCTTTTCTCCTATGCACACCAGGATAGACAAGGCAGGGGATACTGGCA  
GCCTGCATCATCTCCCATTGGGCTGACAGCTGGCCCTACTTTTCTCCTCTGCTGCTTGGTCCCTCACCTTGAT  
GATGTGGCTTCGCCCCCTCCACTCTACTGCCAGTGTTCTCCCAGGGGTTGCTAAATCCAGCAGACCCCTTTCTCTG  
TCTTACTAGATCTGGGCAGCATTTGACATGGCTGATCACCCCTTGCTTCTTGGATGGCACTTCCCTGGCACCTCT  
GTGGCTAGTTGTCTTACCTCCCTGGCTGTTTCTTTCAGGCTTCCGTGCAGGCTTCTCCACTTGCCCATGCACAGT  
AGGGTCTTTCAGGGTCTGCTGTGGGCTCCCTAGGGAAGCCCATCCATCTGGATGGTTTCAAGGATGGTGAGGAA  
TTTAGAGTTGACCTCCAGCCCCAACATCCTTCCCTGATCACCTGAACCACAGTTTGTGCTGCCCTCTAGGTGCACAG  
ACAATTCAGGTCCATGGCCAGATGGTACTTGCTGTCTTCTGCAAACCTGCCCTTCTGGGTACTTCCCTTGACC  
CCGAGATCACTCAGGAGCCAGACAGGAACTTATTCTATTCTGTTTTCTCTTTCTGCCCCACCACATCCAATCTC  
TCAAAACGGTCAGGTCTACCTTAACATCTCTTGATTGAGCCACTCCCACTGTCAATCAGCTTTACCTGGATTAT  
CGTGACAGCCTCCTACTGCTTCTCTATCATGTGGCCAGAGCTATCTTCTTAAATGCATTGCATAGTTGATCAAG  
TCACTCTCTGGCCTAAAACCTTCCCTTGGCTCCCTGCTGCCCTCAGGATAAAGTCTGGACCCCTCAGCATGGCTTG  
TGAGACTCATGGTGTCTTGTCCCTGCTCACCTCTCTGGTCTCATCACTTGCCTTCTTGCACTTGGGTCCGAGC  
CTCCTGTATCCAGAGATGCAGTGGCTCTCCATTGCCACTCTGATTCTCCTTCTTTTGGTCCACAGAGAAAGGT  
ACTTTCTCTGTCAAATCTCAACTTAGACTTGACTTCTCCCAAGGAGCTTTGGCTATACTCTCTCTCTCCCGACCCC  
CACCTTGGCATACTACACAGATCACTTGGGCTCACTTGCTGCCTAATGGTCATCTCCCCAGTAGACTGTAAGC  
TCCTTGAGGGCAAGGATTGTGTTGGAATTTTGTATTAAAGTGCCTGGCTTGGTGCCTGGCACCTAGAAAGCAC  
TCAATAAATGTTTGTTTAATGAA

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**FIGURE 168**

MWFMYLLSWLSLFIQVAFITLAVAAGLYYLAELIEEYTVATSRIIKYMIWFSTAVLIGLYVFE  
RFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCGLVVVNHYLAFQFFAEYYPFSEVL  
AYFTFCLWIIIPFAFFVSLSAGENVLPSTMQPGDDVVSNYFTKGKRGKRLGILVVFSFIKEAIL  
PSRQKIY

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 126-146

**Casein kinase II phosphorylation site.**

amino acids 145-148

**N-myristoylation sites.**

amino acids 73-78, 82-87

**Amidation sites.**

amino acids 168-171, 171-174

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 91-101

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**FIGURE 169**

CAAAGCCCTACCCTCACCATTACCAGGTCCCTGTGGGAAGAGCAGCGTGGAGGTGGGCTGAGG  
TTAGAAGGTGCAGAGCGTGAAGAAGATTGTGAGCTGAGTATTGGACATCTGTTCTTGAATAG  
TCCCTGGGCCTGCCATAGGAAAGGAAGTTCTCCAGGGTTACAGTTCTTATCCGCGTGAATACA  
**CATGG**CTCTGTTACGAAAAATTAATCAGGTGCTGCTGTTCTTCTGATCGTGACCCTCTGTGT  
GATTCTGTATAAGAAAGTTCATAAGGGGACTGTGCCAAGAATGACGCAGATGATGAATCCGA  
GACTCCTGAAGAACTGGAAGAAGAGATTCTGTGGTGATTTGTGCTGCAGCAGGGAGGATGGG  
TGCCACTATGGCTGCCATCAATAGCATCTACAGCAACACTGACGCCAACATCTTGTTCTATGT  
AGTGGGACTCCGGAATACTCTGACTCGAATACGAAAATGGATTGAACATTCCAAACTGAGAGA  
AATAAACTTTAAAATCGTGGAATTCAACCCGATGGTCCCTCAAAGGGAAGATCAGACCAGACTC  
ATCGAGGCCTGAATTGCTCCAGCCTCTGAACCTTGTTCGATTTTATCTCCCTCTACTTATCCA  
CCAACACGAGAAAGTCATCTATTTGGACGATGATGTAATTGTACAAGGTGATATCCAAGAACT  
GTATGACACCACCTTGCCCTGGGCCACGCGGCGGCTTTCTCAGATGACTGCGATTTGCCCTC  
TGCTCAGGACATAAACAGACTCGTGGGACTTCAGAACACATATATGGGCTATCTGGACTACCG  
GAAGAAGGCCATCAAGGACCTTGGCATCAGCCCCAGCACCTGCTCTTTCAATCCTGGTGTGAT  
TGTTGCCAACATGACAGAATGGAAGCACCAGCGCATCACCAAGCAATTGGAGAAATGGATGCA  
AAAGAATGTGGAGGAAAACCTCTATAGCAGCTCCCTGGGAGGAGGGGTGGCCACCTCCCCAAT  
GCTGATTGTGTTTCATGGGAAATATTCCACAATTAACCCCTGTGGCACATAAGGCACCTGGG  
CTGGAATCCAGATGCCAGATATTCGGAGCATTTTCTGCAGGAAGCTAAATTACTCCACTGGAA  
TGGAAGACATAAACCTTGGGACTTCCCTAGTGTTTACAACGACTTATGGGAAAGCTGGTTTGT  
TCCTGACCTGCAGGGATATTTAAACTCAATCACCATAGCT**TGAT**AATACTCTACCCTTAAAT  
ATTCCTGTATAGAAATGTGGAATTGTCCCTTTGTAGCCAACCTATAACATTGTTCTTTATGAA  
TATTACCTTTGATACATATGATCCACAATATAAAAACCAAAACTACTGTGTGCAAATTATAC  
CTTGGACCATATAGGCATTGATTAACCTTCTTTAAGTACATGTGATAACTATGGAAATCAAGAT  
TATGTGACTGAAAAACATAAAGGAAGAGACCCATCTAGATAACAGCAATCAACCTGCTTAATT  
CTGAATGACAATTATATCCACAAATTTTTAAACTTCTACATGTATTTTTTACATGAAGATCT  
CCTTAACAGGTTGCCAACCTTTTCTTTTATAAACTATTACATTTAAATATGGACGTCTGAA  
AAATAAAATATTCATCATTTTTTAAAA

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**FIGURE 170**

MALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESETPEELEEIPVVICAAAGRMG  
ATMAAINSIYSNTDANILFYVVGLRNTLTRIRKWIEHSLREINFKIVEFNPMVLKGKIRPDS  
SRPELLQPLNFVRFYLPLLIHQHEKVIYLDLDDVIVQGDIQELYDTTLALGHAAAFSDDCDLPS  
AQDINRLVGLQNTYMGYLDYRKKAIKDLGISPSTCSFNPGVIVANMTEWKHQIRITKQLEKWMQ  
KNVEENLYSSSLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFLQEAKLLHWN  
GRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 234-238

**Tyrosine kinase phosphorylation site.**

amino acids 253-261

**N-myristoylation sites.**amino acids 63-69, 86-92, 198-204, 218-224, 229-235, 265-271,  
266-272

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**FIGURE 171**

GCCAGAGGCTGCAGCTGGAGCCCAGAGCCCAAGATGGAGCCCCAGCTGGGGCCTGAGGCTGCC  
GCCCTCCGCCCTGGCTGGCTGGCCCTGCTGCTGTGGGTCTCAGCCCTGAGCTGTTCTTTCTCC  
TTGCCAGCTTCTTCCCTTTCTTCTCTGGTGCCCCAAGTCAGAACCAGCTACAATTTTGGAAGG  
ACTTTCCTCGGTCTTGATAAATGCAATGCCTGCATCGGGACATCTATTTGCAAGAAGTTCTTT  
AAAGAAGAAATAAGATCTGACAACTGGCTGGCTTCCCACCTTGGACTGCCTCCCGATTCCCTTG  
CTTTCTTATCCTGCAAATTACTCAGATGATTCCAAAATCTGGCGCCCTGTGGAGATCTTTAGA  
CTGGTCAGCAAATATCAAACGAGATCTCAGACAGGAGAATCTGTGCCTCTGCATCAGCCCCA  
AAGACCTGCAGCATTGAGCGTGCCTGCGGAAAACAGAGAGGTTCCAGAAATGGCTGCAGGCC  
AAGCGCCTCACGCCGGACCTGGTGCAGGACTGTCACCAGGGCCAGAGAGAACTAAAGTTCCTG  
TGTATGCTGAGATTAACACCAGTGAAAAAGCCTGGCATGGAGCCCAGCACTGAGAACTTCCAGA  
AAGTGTTAGCCTTCTCCCAACTGTGTTATACCAACCACATTTTCAAATAGTAATCATTAAAGA  
GGCTTCTGCATCAAA

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**FIGURE 172**

MEPQLGPEAAALRPGWLALLLWVSALSCSFSLPASSLSSLVPQVRTSYNFGRTFLGLDKCNAC  
IGTSICKKFFKEEIRSDNWLASHLGLPPDSLLSYPANYSDDSKIWRPVEIFRLVSKYQNEISD  
RRICASASAPKTCSIERVLRKTERFQWLQAKRLTPDLVQDCHQGQRELKFLCMLR

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 100-103

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 158-161

**N-myristoylation sites.**

amino acids 56-61, 65-70

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 18-28

**Prenyl group binding site (CAAX box).**

amino acids 179-182

**Leucine zipper pattern.**

amino acids 5-26



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**FIGURE 173**

GCTGGACTGCTCGCTGGCCGGCAGCGCACCGTTTTGAAGGTCCTAGCCACCTGGGCTGGCTC  
ACGCGCACGACTAGCCGCTCCCATACAGCACGCCCGGACTCTGTCTGCTGCTTAAGGCCACTCC  
TATTCTACGGCTGACCCCTGGTGGTCACGTGGATCTGTTTCGCCACGCAAGTCTGGGTCTTCG  
GCGATTGACCGGGGTCCTTGCTGTTTCGGGAGCCTCTCCTAAGCTGCCTGTTTCGCGCGAGAGTT  
TGGAGGGGCGGGTTTGGGGTCGGTGTCTGATTGGGGCTCGCACCGCAGCACGCTGGAGTCCCG  
CTTAGGTACCAGTTAGCGTCAGGGGAGCTGGGTTCAGGCGGTTCGCCGGGACACCCCGTGTGTGG  
CAGGCGGCGAAGCGCTCTGGAGAATCCCGGACAGCCCTGCTCCCTGCAGCCAGGTGTAGTTTC  
GGGAGCCACTGGGGCCAAAGTGAGAGTCCAGCGGTCTTCCAGCGCTTGGGCCACGGCGGGCGGC  
CCTGGGAGCAGAGGTGGAGCGACCCATTACGCTAAAGATGAAAGGCTGGGGTTGGCTGGCCC  
TGCTTCTGGGGGCCCTGCTGGGAACCGCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGAG  
CATGCAGGGCTCTGGTGGATGAACTAGAAATGGGAAATTGCCCAGGTGGACCCCAAGAAGACCA  
TTCAGATGGGATCTTTCCGGATCAATCCAGATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATG  
CCCGCTCAGAGGCCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATG  
GGGAACAGATTGATCCTTCCACCCATCGCAAGAACTACGTACGTGTAGTGGGCCGGAATGGAG  
AATCCAGTGAAGTGGACCTACAAGGCATCCGAATCGACTCAGATATTAGCGGCACCCCTCAAGT  
TTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTTTCCCGAGAGG  
CTGACAATGTTAAAGACAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACA  
TATCGCATGATGAGCTATGAACCACTGGAGCAGCCCACACTGGCTTGATGGATCACCCCCAGG  
AGGGGAAAATGGTGGCAATGCCTTTTATATATTATGTTTTTACTGAAATTAAGTAAAAATA  
TGAAACCAAAAAGT

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**FIGURE 174**

MKGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINPDGS  
QSVVEVPYARSEAHLTELEEICDRMKEYGEQIDPSTHRKNYVRVVGVRNGESSELDLQGIRID  
SDISGTLKFACESIVEEYEDELIEFFSREADNVKDKLCSKRTDLCDHALHISHDEL

**Signal peptide:**

amino acids 1-20

**N-myristoylation sites.**

amino acids 12-18, 16-22, 29-35

**Endoplasmic reticulum targeting sequence.**

amino acids 179-184

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**FIGURE 175**

CGCAGCGCGGCAGTCCTGATGGGCCCGGCATGGGTTACCGCTGCTGCCCCTGCTGTCGCTCCTG  
GTCGGCGCGTGGCTCAAGCTAGGAAATGGACAGGCTACTAGCATGGTCCAACTGCAGGGTGGG  
AGATTCTGATGGGAACAAATTCTCCAGACAGCAGAGATGGTGAAGGGCCTGTGCGGGAGGGC  
ACAGTGAAACCCTTTGCCATCGACATATTTCTGTGTCACCAACAAAGATTTTCAGGGATTTTGTC  
AGGGAGAAAAAGTATCGGACAGAAGCTGAGATGTTTGGATGGAGCTTTGTCTTTGAGGACTTT  
GTCTCTGATGAGCTGAGAAACAAAGCCACCCAGCCAATGAAGTCTGTACTCTGGTGGCTTCCA  
GTGGAAAAGGCATTTTGGAGGCAGCCTGCAGGTCCTGGCTCTGGCATCCGAGAGAGACTGGAG  
CACCCAGTGTTACACGTGAGCTGGAATGACGCCCGTGCCTACTGTGCTTGGCGGGGAAAACGA  
CTGCCCACGGAGGAAGAGTGGGAGTTTGCCGCCCGAGGGGGCTTGAAGGGTCAAGTTTACCCA  
TGGGGGAACTGGTTCCAGCCAAACCGCACCAACCTGTGGCAGGGAAAGTTCCCCAAGGGAGAC  
AAAGCTGAGGATGGCTTCCATGGAGTCTCCCCAGTGAATGCTTTCCCCGCCCAGAACAACCTAC  
GGGCTCTATGACCTCCTGGGGAACGTGTGGGAGTGGACAGCATCACCGTACCAGGCTGCTGAG  
CAGGACATGCGCGTCTCCGGGGGGCATCCTGGATCGACACAGCTGATGGCTCTGCCAATCAC  
CGGGCCCCGGGTACACCACAGGATGGGCAACACTCCAGATTGAGCCTCAGACAACCTCGGTTTC  
CGCTGTGCTGCAGACGCAGGCCGGCCGCCAGGGGAGCTGTAAGCAGCCGGGTGGTGACAAGGA  
GAAAAGCCTTCTAGGGTCACTGTCATTCCCTGGCCATGTTGCAAACAGCGCAATTCCAAGCTC  
GAGAGCTTCAGCCTCAGGAAAGAACTTCCCCTTCCCTGTCTCCCATCCCTCTGTGGCAGGCGC  
CTCTCACCAGGGCAGGAGAGGACTCAGCCTCCTGTGTTTTGGAGAAGGGGGCCCAATGTGTGTT  
GACGATGGCTGGGGGCCAGGTGTTTCTGTTAGAGGCCAAGTATTATTGACACAGGATTGCAAA  
CACACAAACAGTTGGAACAGAGCACTCTGAAAGGCCATTTTTTAAGCATTTTAAAATCTATTC  
TCTCCCCCTTTCTCCCTGGATGATTGAGGAAGCTGACATTGTTTCTCAAGGCAGAAATTTTCC  
TGGTTCTGTTTTCTCAGCCAGTTGCTGTGGAAGGAGAATGCTTTCTTTGTGGCCTCATCTGTG  
GTTTCGTGTCCCTCTGAAGGAACTAGTTTCCACTGTGTAACAGGCAGACATGTAACCTATTTA  
AAGCACAGTTCAGTCTAAAGGGTCTGGGAGAACCAGATGATGTACTAGGTGAAGCATTGCA  
TTGTGGGAATCACAAAGCAAATAGTACTCCAGAAAGACAAATATCAGAAGCTTCCTATTCTTT  
TTTTTTTTTTTTTTTTTTTTTTTTTGGAGACAGGGTCTTTCTCTGTTGCCCAGGCTAGAGTGCACTG  
GTGATCACGGCTCACTCTAGCCTTGAATTCCTGGGCCCCAAGCAATTCTCCACCTCAGCCTCC  
TGAGTAGCTGGGACTACAAGTGTGCACCACCATGCCTGGCTAATTTTTTGAATTTTTGTAGTG  
ATGGGATCTCGCTCTGTTGCCCAGGGTGGTCTCGAACTCCTGGCCTCAAGCGATCCTCCCACC  
TCGACCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCTCGCCTGGGCCCCCTTCTCCATA  
TGCCTCCAAAAACATGTCCCTGGAGAGTAGCCTGCTCCACACTGTCACTGGATGTGATGGGG  
CCAATAAAATCTCCTGCAATTGTGTATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAA

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**FIGURE 176**

MARHGLPLLPLLSLLVGAWLKLGNQGQATSMVQLQGGREFLMGTNSPDSRDGEGPVREATVKPFA  
IDIFPVTNKDFRDFVREKKYRTEAMFGWSFVFEDFVSDELNRNKATQPMKSVLWWLPVEKAFW  
RQPAGPGSGIRERLEHPVLHVSWNDARAYCAWRGKRLPTEEEWEFAARGGLKGQVYPWGNWFQ  
PNRTNLWQGKFPKGDKAEDGFHGVSPVNAFPAQNNGLYDLLGNVWEWTASPYQAAEQDMRVL  
RGASWIDTADGSANHRARVTTRMGNTPDSDNLGFRCAADAGRPPGEL

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 191-195

**N-myristoylation sites.**

amino acids 23-29, 25-31, 175-181

**Amidation site.**

amino acids 159-163

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**FIGURE 177**

GCCTTCTCGCGCCTGACCATGCACCCCTGCATCTTCCTGCTGGGCCACAGGCGAGCGCTTTAT  
TTCTGGAGCTGAGGGCTAAACCTTTTTTGACTTTTCTTCTCCTCAACATCTGAATC**ATG**CCAT  
GTGCCCAGAGGAGCTGGCTTGCAAACCTTTCCGTGGTGGCTCAGCTCCTTAACTTTGGGGCGC  
TTTGCTATGGGAGACAGCCTCAGCCAGGCCCGGTTTCGCTTCCCGGACAGGAGGCAAGAGCATT  
TTATCAAGGGCCTGCCAGAATACCACGTGGTGGGTCCAGTCCGAGTAGATGCCAGTGGGCATT  
TTTTGTCATATGGCTTGCACTATCCCATCACGAGCAGCAGGAGGAAGAGAGATTTGGATGGCT  
CAGAGGACTGGGTGTACTACAGAATTTCTCACGAGGAGAAGGACCTGTTTTTTAACTTGACGG  
TCAATCAAGGATTTCTTTCCAATAGCTACATCATGGAGAAGAGATATGGGAACCTCTCCCATG  
TTAAGATGATGGCTTCCTCTGCCCCCTCTGCCATCTCAGTGGCACGGTTCTACAGCAGGGCA  
CCAGAGTTGGGACGGCAGCCCTCAGTGCCTGCCATGGACTGACTGGATTTTTCCAACCTACCAC  
ATGGAGACTTTTTTCAATTGAACCCGTGAAGAAGCATCCACTGGTTGAGGGAGGGTACCACCCGC  
ACATCGTTTACAGGAGGCAGAAAGTTCCAGAAACCAAGGAGCCAACCTGTGGATTAAAGGGTA  
TTGTGACTCACATGTCCTCCTGGGTTGAAGAATCTGTTTTGTTCTTTTGG**TAG**TTTTATTAA  
ACATGACCTATTCTTACTCAAGTCTCTTATCTCCTCTGTATTCTTTTTTTTTTAATATCTTCA  
TGACATTCAAATCTCTTCTGTATTCTCTTGCCAGAAAGTGATACATTCTTTTGGCTTGATAAA  
CCCTTTCACCTGTC

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**FIGURE 178**

MPCAQRSWLANLSVVAQLLNFGALCYGRQPQPGPVRFPDRRQEHFIKGLPEYHVVG PVRVDAS  
GHFLSYGLHY PITSSRRKRDLDGSEDWVYYRISHEEKDLFFNLTVNQGFLSNSYIMEKRYGNL  
SHVKMMASAPLCHLSGTVLQQGTRVGTAALSACHGLTGFFQLPHGDFFIEPVKKHPLVEGGY  
HPHIVYRRQKVPETKEPTCGLKGIVTHMSSWVEESVLFFW

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 11-15, 105-109, 125-129

**N-myristoylation site.**

amino acids 149-155

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**FIGURE 179**

CAGATTTAAAAAGAAAACCTTTACTGAATCAGCTGAGTGTTAATAATACGAATTCCTTTTCT  
TGCCAATTCTGATCTGAACAGAAAATCCAAGAACAGGGATATGTGTGGATTACAGTTTTCTCT  
GCCTTGCTACGACTGTTTCTGGTTGTTACCTGTTATCTTTTATTATTACTCCACAAAGAAAT  
ACTTGGATGTTCTGCTGTTTGTCTGAGCTCTGCACTGGGAGACAAATTAAGTCCGTAACCTTAGG  
CCTTTCGAGTATTCCTAAGAATTTTCCTGAAAGTACAGTTTTTCTGTATCTGACTGGGAATAA  
TATATCTTATATAAATGAAAGTGAATTAACAGGACTTCATTCTCTTGTAGCATTGTATTTGGA  
TAATTCTAACATTCTGTATGTATATCCAAAAGCCTTTGTTCAATTGAGGCATCTATATTTTCT  
ATTTCTAAATAATAATTTTCATCAAACGCTTAGATCCTGGAATATTTAAGGGACTTTTAAATCT  
TCGTAATTTATATTTACAGTATAATCAGGTATCTTTTGTTCCGAGAGGAGTATTTAATGATCT  
AGTTTCAGTTCAGTACTTAAATCTACAAAGGAATCGCCTCACTGTCCTTGGGAGTGGTACCTT  
TGTTGGTATGGTTGCTCTTCGGATACTTGATTTATCAAACAATAACATTTTGAGGATATCAGA  
ATCAGGCTTTCAACATCTTGAAAACCTTGCTTGTTTGTATTTAGGAAGTAATAATTTAACAAA  
AGTACCATCAAATGCCTTTGAAGTACTTAAAGTCTTAGAAGACTTTCTTTGTCTCATAATCC  
TATTGAAGCAATACAGCCCTTTGCATTTAAAGGACTTGCCAATCTGGAATACCTCCTCCTGAA  
AAATTCAGAATTAGGAATGTTACTAGGGATGGGTTTAGTGGAATTAATAATCTTAAACATTT  
GATCTTAAGTCATAATGATTTAGAGAATTTAAATTCTGACACATTCAGTTTGTTAAAGAATTT  
AATTTACCTTAAGTTAGATAGAAACAGAATAATTAGCATTGATAATGATACATTTGAAAATAT  
GGGAGCATCTTTGAAGATCCTTAATCTGTCAATTAATAATCTTACAGCCTTGCATCCAAGGT  
CCTTAAGCCGTTGTCTTCATTGATTCATCTTCAGGCAAATCTAATCCTTGGGAATGTAAGT  
CAAATTTTGGGCCCTTCGAGACTGGCTAGCATCTTCAGCCATTACTCTAAACATCTATTGTCA  
GAATCCCCCATCCATGCGTGGCAGAGCATTACGTTATATTAAACATTACAAATTGTGTTACATC  
TTCAATAAATGTATCCAGAGCTTGGGCTGTTGTAAATCTCCTCATATTCATCACAAGACTAC  
TGCGCTAATGATGGCCTGGCATAAAGTAACCACAAATGGCAGTCCTCTGGAAAATACTGAGAC  
TGAGAACATTACTTTCTGGGAACGAATTCCTACTTCACCTGCTGGTAGATTTTTTCAAGAGAA  
TGCCTTTGGTAATCCATTAGAGACTACAGCAGTGTTACCTGTGCAAATACAACTTACTACTTC  
TGTTACCTTGAACCTTGGAATAAACAGTGCTCTACCGAATGATGCTGCTTCAATGTCAGGGAA  
AACATCTCTAATTTGTACACAAGAAGTTGAGAAGTTGAATGAGGCTTTTGACATTTTGCTAGC  
TTTTTTCATCTTAGCTTGTTGTTTAAATCATTTTTTTGATCTACAAAGTTGTTTCAGTTTAAACA  
AAAATAAGGCATCAGAAAATCAAGGGAAAATAGACTTGAATACTACAGCTTTTATCAGTC  
AGCAAGGTATAATGTAAGTGCCTCAATTTGTAACACTTCCCCAAATTCTCTAGAAAGTCCTGG  
CTTGGAGCAGATTCGACTTCATAACAAATTGTTCTGAAAATGAGGCACAGGTCAATCTTTT  
TGAACATTCTGCTTTATAACTCAACTAAATATTGTCTATAAGAACTTCAGTGCCATGGACAT  
GATTTAAACTGAAACCTCCTTATATAATTATATACTTTAGTTGGAAATATAATGAATTATATG  
AGGTTAGCATTATTAAATATGTTTTTTNTTAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 180**

MCGLQFSLPCLRLFLVVTCTYLLLLLHKEILGCSSVCQLCTGRQINCRNLGLSSIPKNFPPESTV  
FLYLTGNNISYINESELTGLHSLVALYLDNSNILYVYPKAFVQLRHLYFLFLNNNFIKRLDPG  
IFKGLLNLRNLYLQYNQVSFVPRGVFNDLVSQYLNLRNRLTVLGSGTFVGMVALRILDLSN  
NNILRISESGFQHLENLACLYLGSNNLTKVPSNAFEVLKSLRRLSLSHNPIEAIQPFQFKGLA  
NLEYLLLKNSRIRNVTRDGFSGINNLKHLILSHNDLENLNSDTFSLLKNLIYKLDRNRIISI  
DNDTFENMGASLKILNLSFNNLTALHPRVLKPLSSLIHLQANSNPWECNCKLLGLRDWLASSA  
ITLNIYCQNPPSMRGRALRYINITNCVTSSINVSRAWAVVKSPIHHKTTALMMAWHKVTTNG  
SPLENTETENITFWERIPTSPAGRFFQENAFGNPLETTAVLPVQIQLTTSVTNLNLEKNSALPN  
DAASMSGKTSLECTQEVEKLNEAFDILLAFFILACVLIIFLIYKVQFKQKLKASENSRENRL  
EYYSFYQSARYNVTASICNTSPNSLESPLGLEQIRLHKQIVPENEAQVILFEHSAL

**Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 530-547

**N-glycosylation sites.**amino acids 71-75, 76-80, 215-219, 266-270, 317-321, 331-335,  
336-340, 400-404, 410-414, 451-455, 579-583**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 231-235

**N-myristoylation sites.**

amino acids 3-9, 69-75, 126-132, 174-180

**ATP/GTP-binding site motif A (P-loop).**

amino acids 506-514



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**FIGURE 181**

GGCCTGGCGCGGCGCTCCGGTAAGGCGTGTGTGCGGCAGGGCGGGGACAGAACCGTCCTCTCG  
GGCTCTGGGCGTGTCCGAGACCGCGCTCCCCGCCGAAATCAAGCTCCGAGTCATCCGTGTGGG  
GCATTTCGTCCTCCCTGGCACAGTTGGCCTCTTTCCAGAAGCCCGTTTTGTTTGTTTTACGTCT  
AAATTCGCGTCGGTTCTTATTTCTCTCCCTGGCAAGGTCTGAAGACGGGTAGGAGAATAACCT  
GTGTCAGCGTGTATGATGCCGTCCCGTACCAACCTGGCTACTGGAATCCCCAGTAGTAAAGT  
GAAATATTCAAGGCTCTCCAGCACAGACGATGGCTACATTGACCTTCAGTTTAAGAAAACCC  
TCCTAAGATCCCTTATAAGGCCATCGCACTTGCCACTGTGCTGTTTTTGATTGGCGCCTTTCT  
CATTATTATAGGCTCCCTCCTGCTGTCAGGCTACATCAGCAAAGGGGGGCGAGACCGGGCCGT  
TCCAGTGCTGATCATTGGCATTCTGGTGTTCCTACCCGGATTTTACCACCTGCGCATCGCTTA  
CTATGCATCCAAAGGCTACCGTGGTTACTCCTATGATGACATTCCAGACTTTGATGACTAGCA  
CCCACCCCATAGCTGAGGAGGAGTCACAGTGGAAGTGTCCCAGCTTTAAGATATCTAGCAGAA  
ACTATAGCTGAGGACTAAGGAATTCTGCAGCTTGAGATGTTTAAGAAAATAATGGCCAGATT  
TTTTGGGTCCCTCCCAAAGATGTTAAGTGAACCTACAGTTAGCTAATTAGGACAAGCTCTATT  
TTTCATCCCTGGGCCCTGACAAGTTTTTCCACAGGAATATGTATCATGGAAGAATAGAGGTTA  
TTCTGTAATGGAAAAGTGTGCTGCCACCACCCTCTGTAGAGCTGAGCATTCTTTTAAATA  
GTCTTCATTGCCAATTTGTTCTTGTAGCAAATGGAACAATGTGGTATGGCTAATTTCTTATTA  
TTAAGTAGTTTATTTTAAAAATATCTGAGTATATTATCCTGTACACTTATCCCTACCTTCATG  
TTCCAGTGGAAGACCTTAGTAAAATCAAAGATCAGTGAGTTCATCTGTAATATTTTTTTTACT  
TGCTTTCTTACTGACAGCAACCAGGAATTTTTTTATCCTGCAGAGCAAGTTTTTCAAATGTAA  
ATACTTCCTCTGTTTAACAGTCCTTGGACCATTCTGATCCAGTTCACCAGTAGGTTGGACAGC  
ATATAATTTGCATCATTTTGTCCCTTGTAATCAAGATGTTCTGCAGATTATTCCTTTAACGG  
CCGGACTTTTGGCTGTTTCCTAATGAAACATGTAGTGGTTATTATTAGAGTTTATAGCCGTA  
TTGCTAGCACCTTGTAGTATGTCATCATTCTGCTCATGATTCCAAGGATCAGCCTGGATGCCT  
AGAGGACTAGATCACCTTAGTTTGATTCTATTTTTTAGCTTGCAAAAAGTGACTTATATTCCA  
AAGAAATTAAATGTTGAAATCCAAATCCTAGAAATAAAATGAGTTTNNNTCCAAAAA  
AAA

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## **FIGURE 182**

MMPSRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIALATVLFLLIGAFLLIIG  
SLLLSGYISKGGADRAVPVLLIIGILVFLPGFYHLRIAYYASKGYRGYSYDDIPDFDD

**Transmembrane domains:**

amino acids 45-66, 79-95

**N-myristoylation sites.**

amino acids 11-17, 75-81

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**FIGURE 183**

CTAAAAAATACAAAAATTAGCTGGGCGTGGTGTACGTGTAATCCCAGCTACTCAAGAGGCTGAGGCAGGA  
GAATCGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCAAGATTAAAGTCACTGCACTCCAGCCTGGGTGACAGA  
GCAAGACTCTGTATCAAAATAAAATAAAGTACAACCTCTGGATGGGCATGGTGGCTTATGCTGTAAATCCCAG  
CACTTTGGGAACCTTGAGGCGGGTAGATTGCTTGAGTCCGGGAGTTTGAGACCAGTCTGGGTAATATGGTAACCTT  
GTCTACCAAAAAATACAGGTATTAGCCAGTCTCATAACTCGGTCTCAAAATAAATAAATACATACATACATAGATG  
AAAATTTAAAAATAAAGTCCAACCTCAGCGGTTTTTACAGATATTACAGAGTTGTACAATCTTCACCACTATCTA  
ATTTCAGAACATTTTCATCACCCCCAAAAGAAACCTAACCCATTGACTATCTCTCCATTTCTCCCTCTCCCTAG  
CCTCTGGCAACCACTAATCTCTTTTTTGTCTCTATAGATTGCTTATTTTGACAGTTTATATACAAGGAATCAT  
ACCATGATAGCCTTTTGTGTCCGGCTTCTTTGATTAAATAGATGTTTTCAAGGCTCATCTATGCTGTAGCCTGT  
ATCAGCACTTCATTCTTTCTATGGCTGAATAATAGTCCACTGTAGGGATGTGCCATGTTTTTCCACTAGCTGAT  
GGACATTTGGGTTGTTTTCCACCTTCTGGCTATTATAAATATTGCTGCTATAAATATTCACCTACAAGTTTTTGTG  
TGGACATATGTTTTTATTTCTTCTGGTATATCCTTCGGAGTGGAACCTGCTGGATCAGGTGGTAACCTTAGGTCTA  
ACCTGGCAGTTAAACAGAATCCTATGCTGCTGTAGTCCATGAGTTGAAATAAACACTTGACCCATAGTAAGTGC  
CAGATCATCTTCATTTTCACAGCAACCAGTAATTTACAGATGAGGAAATGAAGGCTCCAGAGGTGAAGTGGCTT  
TTCCCATTTGAGCAGTTCCAAGTCAGACAGTTAAAAAGTGGCAGGACCTGGAAGAGAAGCTAGTTCTTTTACCCT  
GGCATTACAGGGCTGCCTCCTGGGCTACGGGGCTGGCATTTAGAATAGAGCTAAGGTCTGCTGCCAAGGCAGGTGC  
CCCAGTCTGCCTCCTCTGTGTCTTATTCCACTTTCTCTGCAGCCCTCCAGGGGACCCCTCTCTCAGCCACCCCTC  
TCTCTGGTGAATGTACAGTGCTGCCGGAAGATCAAAGATACGGTGCAGAACTGGCTTCGGACCATTAAGGACATT  
CACAGCAGTGTATCCCGAGTGGGCAAAGCCATTGACAGGAACCTTCGACTCTGAGATCTGTGGTGTGTGTGTCAGAT  
GCGGTGTGGGACGCGCGGGAACAGCAGCAGCAGATCCTGCAGATGGCCATCGTGGAACACCTGTATCAGCAGGGC  
ATGCTCAGCGTGGCCGAGGAGCTGTGCCAGGAATCAACGCTGAATGTGGAATTTCAAGCAGCCTTTTCTTA  
GAGTTGAATCGAATCCTGGAAGCCCTGCACGAACAAGACCTGGGTCTGCGTTGGAATGGGCCGTCTCCACAGG  
CAGCGCCTGCTGGAACCTCAACAGCTCCCTGGAGTTCAAGCTGCACCGACTGCACTTCATCCGCTCTTGGCAGGA  
GGCCCCGCGAAGCAGCTGGAGGCCCTCAGCTATGCTCGGCACTTCAGCCCTTTGCTCGGCTGCACCAAGCGGGAG  
ATCCAGGTGATGATGGGCAGCCTGGTGTACCTGCGGCTGGGCTTGGAAGAAGTCACCTACTGCCACCTGCTGGAC  
AGCAGCCACTGGGCAGAGATCTGTGAGACCTTTACCCGGGACGCTGTTCCTGCTGGGGCTTTCTGTGGAGTCC  
CCCCTTAGCGTCAGCTTTGCCTCTGGCTGTGTGGCGCTGCCTGTGTTGATGAACATCAAGGCTGTGATTGAGCAG  
CGGCAGTGCAGTGGGGTCTGGAATCACAGGACGAGTTACCGATTGAGATTGAAGTAGGCATGAAGTGTGGTAC  
GCTCATCTGTGGCCATGTTATCTCCCGAGATGCACTCAATAAGCTCATTAAATGGAGGAAACACTCCGTGTTCGCT  
TGCCCCATCCTCCGCCAGCAGACGTGAGATTTCAACCCCTCCCATCAAGCTGAAGTGTCCCTACTGTCCCATGGAG  
CAGAACC CGGCAGATGGGAAACGCATCATATTCTGATTCTTACCTGGAAGGAATTTTGTGAAAGGGGTTTTTAC  
CTGTGAGCCTTGGTCTGTCTCGGTAGGGTGGTCAACTTCAGTGGACTGTGGTTGGTTTCAGAGCGCCTGGCTGAG  
GAGTTCCACTGAGGGGAGCACTGGAGCAGCCCTTTGGCAGAGGCTGAGGAGGGAGATGGACCAGCCACGCTGG  
CACCTGGCTCCATGGCATAAGGAAAGGGAGATGCTGGCCTCTGTGCTCCTGCTGTCTTTTCTGTGTTTGC  
GTTTGACTTAGTAGCAACCGACAGAGTGGCAAGGGATTGGTCTTCAGCAGTAGACATCTTCCACCCCTGCCCT  
CAGCCAAGTCTCTTGCTGCCATGCCAATGCTATGTCCACCCTTGCCCTCGGCCCCAAGAGTGTCCAGCGGTGGCC  
CACCTCTTCTCCCACTACAGCCTCAACAGTATGTACCATCTCCACTGTAAATAGTCCAGTTAGAACGGAATG  
CCGTTGTTTTATAACTTTGAACAAATGTATTTACTGCCCTTCTCAAAA

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**FIGURE 184**

QCCRKIKDTVQKLASDHKDIHSSVSRVGKAIDRNFSEICGVVSDAVWDAREQQQQIILQMAIV  
EHLYQQGMLSVAEELCQESTLNVDLDFKQPFLELNRIEALHEQDLGPALEWAVSHRQRLEL  
NSSLEFKLHRLHFIRLLAGGPAKQLEALSARHFQPFARLHQREIQVMMGSLVYLRLGLEKSP  
YCHLLDSSHWAEICETFTRDACSLGLSVESPLSVSFASGCVALPVLNLIKAVIEQRQCTGVW  
NHNDELPIEIELGMKCWYHSVFACPILRQQTSDSNPPIKLCGHVISRDALNKLINGGKLKCP  
YCPMEQNPADGKRIIF

**Transmembrane domain:**

amino acids 222-241

**N-glycosylation site.**

amino acids 129-133

**Tyrosine kinase phosphorylation site.**

amino acids 151-159, 184-193

**Amidation site.**

amino acids 327-331

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 222-233

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**FIGURE 185**

GAGCGACGCTGTCTCTAGTCGCTGATCCCAAATGCACCGGCTCATCTTTGTCTACACTCTAAT  
CTGCGCAAACCTTTTGCAGCTGTCGGGACACTTCTGCAACCCCGCAGAGCGCATCCATCAAAGC  
TTTGCGCAACGCCAACCTCAGGCGAGATGACTTGTACCGAAGAGATGAGACCATCCAGGTGAA  
AGGAAACGGCTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAGGAACCTGCTCCTGAC  
ATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTTTGACAATCAGTTTGGATT  
AGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAAC  
CAGTACCATTATTAGAGGACGATGGTGTGGACACAAGGAAGTTCCTCCAAGGATAAAATCAAG  
AACGAACCAAATTAAAATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAA  
GATTTATTATTCTTTGCTGGAAGATTTCCAACCCGCAGCAGCTTCAGAGACCAACTGGGAATC  
TGTCACAAGCTCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCCTCTGAT  
TGCGGATGCTCTGGACAAAAAATTGCAGAATTTGATACAGTGGAAGATCTGCTCAAGTACTT  
CAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGG  
CAGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCG  
TTACAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCCAATGT  
GGTCTTCTTTCCACGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATTGTGGCTGTGGAAGTGT  
CAACTGGAGGTCTTGCACATGCAATTCAGGGAAAACCGTGAAAAAGTATCATGAGGTATTACA  
GTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCA  
GTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCACCTCGATTAAGAGAATGT  
GCACATCCTTACATTAAGCCTGAGAGAA

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**FIGURE 186**

MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDDLYRRDETIQVKNGYVQSPRF  
PNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDISETSTIIRGRWCG  
HKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASETNWESVTSSISGVSY  
NSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPRYRGRSYHDRKSKV  
DLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGNCGCGTVNWRSTCNSG  
KTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 270-274

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 262-266

**Tyrosine kinase phosphorylation site.**

amino acids 256-265

**N-myristoylation sites.**

amino acids 94-100, 186-192, 297-303, 298-304

**TonB-dependent receptor proteins signature 1.**

amino acids 1-56

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**FIGURE 187**

**CATG**CCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTG  
TGTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT  
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT  
CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG  
TGATCTTTCTGCTGAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG  
GGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCATCCTTTTTTTAGAAACACAAAT  
TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC  
AGAGAAGTGGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCT  
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA  
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTT  
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA  
TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT  
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA  
CCCAGCAAATTTGATTTTGAATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA  
AAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA  
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA  
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA  
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAG  
CAGAACAATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT  
TTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATT  
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCGAAACGTTACAGTACTCATACACCCC  
TCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA  
AGAGCCATCGACGACCCTGGTCGACTGGGATCCCCAACTGGCAGGCTGTGTATTCTTCCTCGCT  
GTCCAGCTTCGACCAGGATTAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA  
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC  
CTATCTCATGAATTCATGGAGGAATGGGGTTATATGTGCAGATGGAAAAC**TGA**TGCCAACA  
CTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA  
GTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTGAGTGTCTGTGAGAA

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**FIGURE 188**

MPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYF  
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQI  
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN  
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV  
FLFSVMGYSIYRYIHVGKEKHANLILYIGNEFDKRFFVPAEKIVINFITLNISSDDSKISHQD  
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGETSLTQQESLS  
RTIPDKTVIEYEYDVRTTDCAGPEEQELSLQEEVSTQGTLLSQALAVLGPQTLQYSYTP  
QLQDLPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDLGEE  
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 240-260

**N-glycosylation sites.**amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,  
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

**N-myristoylation sites.**

amino acids 53-58, 106-111, 368-373, 492-497

**Tissue factor**

amino acids 1-278



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**FIGURE 189**

**ATGT**GCTGCTGGCCGCTGCTCCTGCTGTGGGGGCTGCTCCCCGGGACGGCGGGGGGGGCTCG  
GGCCGAACCTATCCGCACCGGACCCTCCTGGACTCGGAGGGCAAGTACTGGCTGGGCTGGAGC  
CAGCGGGGACAGCCAGATCGCCTTCCGCCTCCAGGTGCGCACTGCAGGCTACGTGGGCTTCGGC  
TTCTCGCCCCACCGGGGCCATGGCGTCCGCCGACATCGTCTGGGCGGGGTGGCCCACGGGCGG  
CCCTACCTCCAGGATTATTTTACAAATGCAAATAGAGAGTTGAAAAAAGATGCTCAGCAAGAT  
TACCATCTAGAATATGCCATGGAAAATAGCACACACACAATAATTGAATTTACCAGAGAGCTG  
CATAATGTGACATAAATGACAAGAGTATAACGGATAGCACTGTGAGAGTGATCTGGGCCTAC  
CACCATGAAGATGCAGGAGAAGCTGGTCCCAAGTACCATGACTCCAATAGGGGCACCAAGAGT  
TTGCGGTTATTGAATCCTGAGAAAAGTAGTGTGCTATCTACAGCCTTACCATACTTTGATCTG  
GTAAATCAGGACGTCCCCATCCCAAACAAAGATACAACATATTGGTGCCAAATGTTTAAAGATT  
CCTGTGTTCCAAGAAAAGCATCATGTAATAAAGGTTGAGCCAGTGATACAGAGAGGCCATGAG  
AGTCTGGTGCACCACATCCTGCTCTATCAGTGCAGCAACAACCTTTAACGACAGCGTTCTGGAG  
TCCGGCCACGAGTGCTATCACCCCAACATGCCCGATGCATTCCCTCACCTGTGAAACTGTGATT  
TTTGCCTGGGCTATTGGTGGAGAGGGCTTTTCTTATCCACCTCATGTTGGATTATCCCTTGGC  
ACTCCATTAGATCCGCATTATGTGCTCCTAGAAGTCCATTATGATAATCCCACTTATGAGGAA  
GGCTTAATAGATAATTCTGGACTGAGGTTATTTTACAAATGGATATAAGGAAATATGATGCT  
GGGGTGATTGAGGCTGGCCTCTGGGTGAGCCTCTTCCATACCATCCCTCCAGGGATGCCTGAG  
TTCCAGTCTGAGGGTCACTGCACTTTGGAGTGCCTGGAAGAGGCTCTGGAAGCCGAAAAGCCA  
AGTGGAATTCATGTGTTTGCTGTTCTTCTCCATGCTCACCTGGCTGGCAGAGGCATCAGGCTG  
CGTCATTTTCGAAAAGGGAAGGAAATGAAATTACTTGCCTATGATGATGATTTTGACTTCAAT  
TTCCAGGAGTTTCAGTATCTAAAGGAAGAACAACAATCTTACCAGGAGATAACCTAATTACT  
GAGTGTGCTACAAACAGAAAGATAGAGCTGAGATGACTTGGGGAGGACTAAGCACCAGGAGT  
GAAATGTGTCTCTCATACCTTCTTTATTACCCAAGAATTAATCTTACTCGATGTGCAAGTATT  
CCAGACATTATGGAACAACCTTCAGTTCATTGGGGTTAAGGAGATCTACAGACCAGTCACGACC  
TGGCCTTTCATTATCAAAAAGTCCCAAGCAATATAAAAACCTTTCTTTCATGGATGCTATGAAT  
AAGTTTAAATGGACTAAAAAGGAAGGTCTCTCCTTCAACAAGCTGGTCCTCAGCCTGCCAGTG  
AATGTGAGATGTTCCAAGACAGACAATGCTGAGTGGTTCGATTCAAGGAATGACAGCATTACCT  
CCAGATATAGAAAGACCCTATAAAGCAGAACCTTTGGTGTGTGGCACGTCTTCTTCTCTTCC  
CTGCACAGAGATTTCTCCATCAACTTGCTTGTTTGCTTCTGCTACTCAGCTGCACGCTGAGC  
ACCAAGAGCTTG**TGA**TCAAATCTGTTGGACTTGACAATGTTTTCTATGATCTGAACCTGTC  
ATTTGAAGTACAGGTAAAGACTGTGTCCACTTTGGGCATGAAGAGTGTGGAGACTTTTCTTC  
CCCATTTTCCCTCCCTCCTTTTCCCTTTCCATGTTACATGAGAGACATCAATCAGGTTCTCTT  
CTCTTTCTTAGAAATACCTGATGTTATATATACATGGTCAATAAAAATAAACTGGCCTGACTT  
AAGATAACCATTTTAAAAAATTGGGCTGTCATGTGGGAATAAAAGAATTCTTTCTTCTTCTAA  
AAAAAAA

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**FIGURE 190**

MCCWPLLLLWGLLPGTAAGGSGRTYPHRTLDDSEGKYWLGWSQRGSQIAFRLQVRTAGYVGFG  
FSPTGAMASADIVVGGVAHGRPYLQDYFTNANRELKKDAQQDYHLEYAMENSTHTIIEFTREL  
HTCDINDKSITDSTVRVIWAYHHEDAGEAGPKYHDSNRGTKSLRLLNPEKTSVLSTALPYFDL  
VNQDVPIPNKDTTYWCQMFKIPVFQEKHHVIKVEPVIQRGHESLVHHILLYQCSNNFNDSVLE  
SGHECYHPNMPPDAFLTCTVIFAWAIGGEGFSYPHVGLSLGTPLDPHYVLLEVHYDNPTYEE  
GLIDNSGLRRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCTLECLEEALEAEKP  
SGIHVFAVLLHAHLAARGIRLRHFRKGKEMKLLAYDDDFDNFQEFQYLKEEQTILPGDNLIT  
ECRYNTKDRAEMTWGGLSTRSEMCLSYLLYYPRINLTRCASIPDIMEQLQFIGVKEIYRPVTT  
WPFIIKSPKQYKNLSFMDAMNKFKWTKKEGLSFNKLVLVSLPVNVRCSTDNAEWSIQGMTALP  
PDIERPYPKAEPLVCGTSSSSSLHRDFSINLLVCLLLLSTLSTKSL

**Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 56-73, 378-393, 583-602

**N-glycosylation sites.**

amino acids 114-118, 247-251, 476-480, 517-521

**N-myristoylation sites.**amino acids 11-17, 15-21, 20-26, 45-51, 68-74, 79-85, 290-296,  
316-322, 337-343, 342-348, 456-462, 534-540, 582-588**Copper type II, ascorbate-dependent monooxygenases proteins.**

amino acids 271-321, 422-474

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**FIGURE 191**

GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTTTTGTCTTTATAACAT  
TTTCTTCTGCATTTCCCTTAGTCCGGATGACGGAAAATGAAGAAAATATGCAACTGGCTCAGG  
CATATCTCAACCAGTTCTACTCTCTTGAAATAGAAGGGAATCATCTTGTTCAAAGCAAGAATA  
GGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTTTGGATTGACAGTGAAGTGGAA  
AACTGGACTCAAACACCCTTGAGATCATGAAGACACCCAGGTGTGGGGTGCCTGATGTGGGCC  
AGTATGGCTACACCCTCCCTGGGTGGAGAAAATACAACCTCACCTACAGAATAATAAACTATA  
CTCCGGATATGGCACGAGCTGCTGTGGATGAGGCTATCCAAGAAGGTTTAGAAGTGTGGAGCA  
AAGTCACTCCACTAAAATTACCAAGATTTCAAAGGGGATTGCAGACATCATGATTGCCTTTA  
GGACTCGAGTCCATGGTCCGTGTCCTCGCTATTTTGATGGTCCCTTGGGAGTGCTTGGCCATG  
CCTTTCCTCCTGGTCCGGGTCTGGGTGGTGACACTCATTTTGATGAGGATGAAAAGTGGACCA  
AGGATGGAGCAGGATTCAACTTGTTTCTTGTTGGCTGCTCATGAATTTGGTCATGCACTGGGGC  
TCTCTCACTCCAATGATCAAACAGCCTTGATGTTCCCAAATTATGTCTCCCTGGATCCCAGAA  
AATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGGAGGTCTGCCTAAGG  
TACCTGCTAAGCCAAAGGAACCCACTATACCCCATGCCTGTGACCCTGACTTGACTTTTGACG  
CTATCACAACCTTCCGCAGAGAAGTAATGTTCTTTAAAGGCAGGCACCTATGGAGGATCTATT  
ATGATATCACGGATGTTGAGTTTGAATTAATTGCTTCATTCTGGCCATCTCTGCCAGCTGATC  
TGCAAGCTGCATACGAGAACCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAAGTCTGGA  
TGATCAGAGGATATGCTGTCTTGCCAGATTATCCCAAATCCATCCATACATTAGGTTTTCCAG  
GACGTGTGAAGAAAATAGATGCAGCCGTCTGTGATAAGACCACAAGAAAAACCTACTTCTTTG  
TGGGCATTTGGTGCTGGAGGTTTGATGAAATGACCCAAACCATGGACAAAGGATTCCCGCAGA  
GAGTGGTAAACACTTTCCTGGAATCAGTATCCGTGTTGATGCTGCTTTCCAGTACAAAGGAT  
TCTTCTTTTTTTCAGCCGTGGATCAAAGCAATTTGAATACAACATTAAGACAAAGAATATTACCC  
GAATCATGAGAACTAATACTTGGTTTCAATGCAAAGAACCAAGAACTCCTCATTTGGTTTTG  
ATATCAACAAGGAAAAAGCACATTCAGGAGGCATAAAGATATTGTATCATAAGAGTTTAAGCT  
TGTTTATTTTTTGGTATTGTTTCAATTTGCTGAAAAACACTTCTATTTATCAATTAAATTCATAGAC  
CTAAAATAAACCTCAACAGGTCTTTTAATATAAATCTGCTTCAAATAGATAAAACCATTCT  
TTTAAACAAC

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**FIGURE 192**

MKRLLLLLFLFFITFSSAFPLVRMTENEENMQLAQAYLNQFYSLEIEGNHLVQSKNRSLLDDKI  
REMQAFFGLTVTGKLDSENTLEIMKTPRCGVPDVGQYGYTLPGWRKYNLTIRIINYTPDMARAA  
VDEAIQEGLEVWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLGVLGHAFPPGPGL  
GGDTHFDEDENWTKDGAGFNLFVAAHEFGHALGLSHSNDQTALMFPNYVSLDPRKYPLSQDD  
INGIQSIYGGLPKVPAKPKEPTIPHACDPDLTFDAITTFRREVMFFKGRHLWRIYYDITDVEF  
ELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGYAVLPDYPKSIHTLGFPGRVKKIDA  
AVCDKTTRKTYFFVGIWCWRFDEMTQTMKGFPQRVVKHFPGISIRVDAAFQYKGFFFFSRGS  
KQFEYNIKTKNITRIMRTNTWFQCKEPPKNSSFGFDINKEKAHSGGIKILYHKSLSLFIFGIVH  
LLKNTSIYQ

**Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 55-59, 110-114, 200-204, 452-456, 470-474, 508-512

**N-myristoylation site.**

amino acids 71-77, 205-211, 223-229

**Hemopexin domain signature.**

amino acids 171-202, 207-238, 318-334

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 213-223

**Matrixins cysteine switch.**

amino acids 89-97, 207-238

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**FIGURE 193**

CACAATCAGGTCCCATTCTATAGATGGGGAACTGAGGCTTGAGGTCACATAGGCGTCGTTCA  
AGGCTGGTATACCTGCACCCTCTCCCATGTGAACAACATGGTTCTGGGTAATGGGGGCTGTCA  
TCCAGTCTCCTCCCTGCCCCTGCTGGTGCACCTTCCTGCCTCTGCTGGTGCACCTTCTGCCCCCT  
ACTGGTATATTTGCTGCCTCTGCTGGGGCGCTTCCTGCCTCGGCTGGTGTATCTCCTGCCCCCT  
GCTGGTGCACCTTCTGCCCCCGCTGATGCACCTTCCTGCCTCTGCTGGTGCACCTTCCTGGCTCT  
GCTGGCACACTTCCTGCCTCTGCTGGTGCACCTTCCTGGCTCTGCTGGCGCACTTTCCTGCCCC  
TGCTGGTGTATTTCTGCCCCTGCTGGTGTACTTCCTTCCCCTGCTGGTGCACCTTCCTGCCTC  
TGCTGGCGCACTTCTTGCCTCTCCAGGCCCTACCTTAGCCTCTCCCTCTTATATATGGAAGTCT  
TCCCAGTTCACCTGACACTGGTAACAGGGACTCTGCTCTTGGTGTGCTGTCTGCCCTGGGGAT  
GGGCATCTGTGTCTTCCTTTACTACTGCTGGCTCAGGACCCAGAGCTTTGAAGCATGTCCAGA  
TGCAGGTCCGGGCACCAGAGTCTAAGGAGCCCCTACACCCACCAGGATTTTCCAATAAAGAGA  
TGTTACCA

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**FIGURE 194**

MVLGNGGCHPVSSLPLL VHFLPLL VHFLPLL VYLLPLL GRFLPRL VYLLPLL VHFLPPL MHFL  
PLL VHFLALL AHFLPLL VHFLALL AHFPAPAGVFPAPAGVLPSPAGALPASAGALLASPGPT

**Signal peptide:**

amino acids 1-39

**N-myristoylation sites.**

amino acids 4-10, 109-115, 116-122

**Leucine zipper pattern.**

amino acids 14-36, 16-38, 17-39, 21-43, 24-46, 28-50, 31-53,  
35-57, 38-60, 42-64, 45-67, 49-71, 52-74, 56-78, 59-81, 63-85,  
65-87, 66-88

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**FIGURE 195**

[illegible]

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**FIGURE 196**

MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPEVQTPKPSDADWDDLWDQFDERRYLN  
AKKWRVGDDPYKLYAFNQRESERISSNRAIPDTRHLRCTLVYCTDLPPTSIIITFHNEARST  
LLRTIRSVLNRTPTHLIREIILVDDFSNDPDDCKQLIKLPKVKCLRNNERQGLVRSRIRGADI  
AQGTTLTFLDSHCEVNRDWLQPLLHRVKEDYTRVVCVIDIINLDTFTYIESASELRGGFDWS  
LHFQWEQLSPEQKARRLDPTPIRTPIIAGGLFVIDKAWFDYLGKYDMDMDIWGGENFEISFR  
VWMCSSLEIVPCSRVGHVFRKKHPYVFPDGNANTYIKNTKRTAEVWMDYKQYYYAARPFAL  
ERPFGNVESRLDLRKNLRCQSFKWYLENIYPELSIPKESSIQGNIRQRQKCLESQRQNNQET  
PNLKLSPCAKVKGEDAKSQVWAFITYTQQILQEELCLSVITLFPVGVVLVLCCKNGDDRQQWTK  
TGSHEHIAHLCLDTDMFGDGTENGKEIVVNPCESSLMSQHWDMVSS

**Transmembrane domain:**

amino acids 475-493

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 2-6

**Tyrosine kinase phosphorylation sites.**

amino acids 68-75, 401-409

**N-myristoylation sites.**

amino acids 178-184, 186-192, 192-198, 346-352, 383-389, 526-532



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**FIGURE 197**

GCAGCTCACCTTCGCGAGCCGCGATGGGGGAAGACGACGCCGCGCTTCGGGCTGGCAGCAGGGGGCTCTCCGACC  
CGTGGGCAGACTCAGTGGGAGTGCGACCCCGCACCACGGAGCGCCACATCGCCGTACACAAGCGGCTTGTGCTGG  
CCTTCGCTGTGTCCCTCGTGGCATTGCTCGCGGTCACAATGCTCGCTGTGCTGCTCAGCCTGCGCTTCGACGAGT  
GCGGGGCGAGTGCCACGCCAGGCGCGGACGGTGGCCCCCTCAGGCTTTCGGGAGCGCGCGGCAACGGGAGCCTCC  
CTGGATCGGCCCCGGCGCAACCACCACGACGGCGGGGACTCCTGGCAGCCCCGAGGCGGGTGGGGTGGCCAGTCCGG  
GGACCACGTCCGCCCCAGCCGCCGTGGAGGAGGAGCGGGAGCCGCTGGAGCCGTGGACGAGCTGCGCCTGTGCG  
GCCACCTGAAGCCGCTGCACTACAATCTGATGCTCACCCTTCATGGAGAATTACCTTCTCCGGGGAGGTCA  
ACGTGGAGATCGCGTGCCGGAACGCCACCCGCTACGTAGTGCTGCACGCTTCCCGAGTGGCGGTGGAGAAAGTGC  
AGCTGGCCGAGGACCGGGCGTTCGGGGCTGTCCCTGTAGCCGTTTCTTCTACCCGCAAAACCCAGGTCTTAG  
TGGTGGTGTCTGAATAGGACACTGGACGCGCAGAGGAATTACAATCTGAAGATTATCTACAACGCGCTCATCGAGA  
ATGAGCTCCTGGGCTTCTTCGCGAGCTCCTATGTGCTCCACGGGGAGAGAAGATTCTTGGTGTACTCAGTTTT  
CGCTACACATGCCAGAAAGGCATTCTCTTGTGTTTGTAGGCCAATCTACAAGGCTACTTTCAAATCAGCATCA  
AGCATCAAGCAACCTATTTATCTTATCTAATATGCCAGTGGAACTTCCGTGTTTGAGGAAGATGGATGGGTTA  
CGGATCACTTTTACAGACCCCTCTCATGTCCACATATTATTTAGCCTGGGCAATTTGCAACTTCACATACAGAG  
AAACTACCACCAAGAGTGGGGTGTAGTAGCATTATATGAAGACCTGATGCTATCAGAAGAGGATCCGGGGACT  
ATGCTCTCCATATAACAAAGAGATTAAAGAAATTTTATGAAGACTACTTTAAAGTGCCCTATTCTTGCCAAAAC  
TAGATCTTTAGCTGTGCCTAAGCATCCGTATGCTGCTATGGAGAACTGGGGACTAAGTATTTTTGTGGAACAAA  
GAATACTGCTGGATCCCAGTGTTCATCTATTTCTTATTTGCTGGATGTCAACATGGTCATTGTTTCATGAGATAT  
GTCACCAAGTGGTTTGGTGACCTTGTGACGCTGTGTGGTGGGAAGACGTGTGGCTGAAGGAAGGGTTTGTCTACT  
ACTTTGAATTTGTTGGTACAGACTACCTCTATCTGGCTGGAACATGGAAGCAGAGGTTTCTGACCGATGTTT  
TGCATGAAGTGATGCTGCTGGACGGTTTGGCCAGTTCCTATCCAGTATCACAGGAAGTGTGACGGCAACAGATA  
TTGACAGGGTGTGACTGGATCGCATATAAAAGGGTGTGCTTTAATAAGAATGCTGGCTAATTTTATGGGCC  
ATTCAGTTTCCAGAGGGGTTTGCAAGATTATTTAAACATTCTAAGTATGGTAATGCAGCCAGAAATGATCTCT  
GGAATACATTATCGGAGGCTTTAAAAAGAAATGGGAAATATGTAATATACAAGAAGTAATGGATCAGTGGACAC  
TCCAGATGGGTTATCCTGTTATCACCATCTTGGGAAACACAACAGCAGAAAATAGAATAATAATTACCCAAACAGC  
ATTTTATCTATGATATCAGTGCTAAACTAAAGCACTTAAACTTCAGAATAACAGTTACCTGTGGCAGATTCCAT  
TAACTATTGTGGTAGGAAATAGAAGCCATGTGCTTCAGAAAGCAATTATTTGGGTGTCTAACAATCAGAGCACC  
ACAGAATAACTTATTTGGACAAAGGAAGCTGGCTGCTGGGGAACATCAATCAAAGTGGCTATTTTAGAGTCAACT  
ATGACCTAAGGAAGTGGAGATTATTAATTGATCAATTAATCCGGAATCATGAGGTCTTTCTGTGAGTAACCGAG  
CGGGCTTGATCGATGATGCCTTCAGCCTAGCCAGGGCTGGCTATTTGCCTCAGAATATTCTCTGGAGATTATCA  
GATACCTGTCTGAGGAGAAGGATTTTCTTCTTGGCATGCTGCCAGCCGAGCTCTTATCCTCTAGATAAATTAC  
TGGACCGCATGGAAACTACAACATTTTCAATGAATATATTTTAAAGCAAGTTGCAACAACATATATCAAGCTTG  
GGTGGCCGAAAAATAATTTAATGGATCTCTGTTCAGCATCCTACCAACATGAAGAACTACGTAGAGAAGTTA  
TAATGCTGGCCTGCAGTTTGGCAACAAGCACTGTCAACCAACAGGCATCAACACTTATTTAGATTGGATTCCA  
GCAACAGGAACAGAATACCACTAAATGTTAGAGACATCGTATACTGTACAGGAGTGTCACTACTGGATGAGGATG  
TCTGGGAATTCATATGGATGAAATTCATTCCACCACAGCAGTCTTCTGAGAAGAAAATATTATTGGAAGCCTTAA  
CTTGCAGTGATGACAGGAATTTATTAACAGGCTTCTAAATCTGTCACTGAATCTGAGGTGGTGTGCTGGATCAAG  
ATGCAATTGATGTCAATCCATGTAGCTCGAAATCCACATGGTTCGAGACCTTGCCCTGGAAGTTTTTCAGGGATA  
AATGGAAGATATTAAATACCAGGTATGGAGAAGCATTGTTATGTATTCCAACTCATCAGTGGTGTACAGAAT  
TTCTTAATACTGAAGGTGAAGTCAAGAGCTCAAGAACTCATGAAAACTATGATGGGTAGCTGCTGCTTCTT  
TCTCAGGAGCTGTGGAAGCTGTCGAAGCCAATGTGCGCTGGAAAATGCTTTACCAAGACGAGCTTTTCCAATGGT  
TAGGAAAAGCTCTAAGACACTAAATATATGTATCTTATAAACAAACAATTCAACTCAGAAGTTTATGAGAAGACAC  
GCTTTTTGTGGAATGAGGAAATGTACTACCTAGAAAATGGCCAGATTTTCAGTGTTAACGTGTGGGAGGAATTT  
TTTTTTTTTAGTTTTTATTTTTTGGTTTTGGGGGATATTTTTTATTTGTTTCATTCTGTTCTGTTCTCTAC  
TGGGTGTTCTCTCTAAAGAACTCTTGCAAGTGAACTAGCCATGATTGCTTCAGCTGTACATTCTTGTGTA  
CAGGACCAATATGATAGTGATGCTGTTGATGTTACAGTCAATTTGGAAGAAACATATTCAGAATATCTGTGCAT  
GGATATATTGCTGCTGTGTTCCAGCATGCTTATTTCAAACGTCCAGTGTGTTGTGTGAATATGTGTTACACC  
TAGGATGGGCATTATGCAAAAGCACAAAGATTATATGACAATCAGTATTGCAATGAAAGAAAACTAAAAACA  
GAAATGATATTCTCAATTTTGGGCAATGTGAGAGGTAAAATAGCCCTTGACATGATGAACATCACTTATTTTCAGC  
ACTTGGATTGTCTGGCAATGATTACTGTGTTGCTAACTCATTTTCTTTGAGTTAAAGCTGTGTATACATTTAAA  
AGGCATATAGATAGTGATGCATATGTATGTACATAGGGAAGCCCCATATGTATATAGTATGTTGATACATGC  
ACATGTACAAAGAAATGTCTTCAGATCAAAGAAAATTTATCTCTTTTATAAAGCTTAAAGACAGTTGCAAAAGGCT  
TCAAGGAATTTATCTCAACATTATTCTTCTATGTCTCACTAAATTTCTCAACTGTTATGAATTTTTCATCTAC  
TTCTTGACAGTGGTCTATTCTGCTACATGAAGATGAATACAAACAAAATTTTTGTATAAAGCTCCCAAAAAAAA  
AAAAA

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**FIGURE 198**

MGEDDAALRAGSRGLSDPWADSVGVRPRTTERHIAVHKRLVLAFVSLVALLAVTMLAVLLSL  
RFDECGASATPGADGGPSGFPERGGNGSLPGSARRNHHAGGDSWQPEAGGVASPGTTSAQPPS  
EEEREPEPWTQLRLSGHLKPLHYNLMLTAFMENFTFSGEVNVEIACRNATRYVVLHASRVAV  
EKVQLAEDRAFGAVPVAGFFLYPQTQVLVVVLNRTLDAQRNYNLKIIYNALIENELLGFFRSS  
YVLHGERRFLGVTQFSPTHARKAFPCFDEPIYKATFKISIKHQATYLSLSNMPVETSVFEEDG  
WVTDHFSQTPLMSTYYLAWAICNFTYRETTTKSGVVVRLYARPD AIRRGSGDYALHITKRLIE  
FYEDYFKVPYSLPKDLLAVPKHPYAAMENWGLSIFVEQRILLDPSVSSISYLLDVTMVIVHE  
ICHQWFGDLVTPVWWEDVWLKEGFAHYFEFVGTDYLYPGWNMEKQRFLTDVLHEVMLLDGLAS  
SHPVSQEV LQATDIDRVFDWIAYKKGAALIRMLANFMGHSVFQRLQDYLTIHKYGNAARNDL  
WNTLSEALKRNGKYVNIQEVMDQWTLQMGYPVITILGNTTAENRIIITQQHFIYDISAKTKAL  
KLQNNSYLWQIPLTIVVGNRSHVSSEAIWVSNKSEHHRITYLDKGSWLLGNINQTYFRVNY  
DLRNWRLLDQLIRNHEVLSVSNRAGLIDDAFSLARAGYLPQNIPLEIIRYLSEEKDFLPWHA  
ASRALYPLDKLLDRMENYNIFNEYILKQVATTYIKLGWPKNNFNGLVQASYQHEELRREVIM  
LACSFNGKHCHQQASTLISDWISSNRNRIPLNVRDIVYCTGVSLLEDVWEFIWMKFHSTTAV  
SEKKILLEALTCSDDRNLLNRLNLSLNSEVVLDQDAIDVIIHVARNPHGRDLAWKFFRDKWK  
ILNTRYGEALFMYSKLISGVTEFLNTEGELKELKNFMKNYDGVAAASFRAVETVEANVRWKM  
LYQDELFWLGKALRH

**Transmembrane domain:**

amino acids 44-63

**N-glycosylation sites.**amino acids 89-93, 160-164, 175-179, 222-226, 338-342, 605-609,  
634-638, 649-653, 663-667, 684-688, 800-804, 906-910**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 362-366

**Tyrosine kinase phosphorylation site.**

amino acids 520-528

**N-myristoylation sites.**amino acids 78-84, 87-93, 90-96, 118-124, 501-507, 604-610,  
825-831, 987-993**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 437-447

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**FIGURE 199**

GCGCCCGGCGCAGCTCGGCCAGAGCGACCGCGGGGCTGAGCGCGCGTCCGCCCAGGGGGCTCCGGAAGCTGCCCC  
GGCCCGCGGCTCCTCCCTCGCTCCCGCTTCCCCTTTCTCGCTACCGCCGCTCCTTCCCCAGCTCCCTCGCC  
GTCCGCCCCCCCCACAGCCAGCGGCTCCGCGCCCCCTGCAGCCACGATGCCCCGCGCCCGCGCCCGCGCGGG  
ACTCCGCGGGATCTCGCTGTTCTCGCTCTGCTCCTGGGGAGCCCGCGGCAGCGCTGGAGCGAGATGCTCTTCC  
CGAGGGAGATGCTAGCCCTTTGGGTCTTACCTCCTGCCCTCAGGAGCCCCGGAGAGAGGAGCTCCTGGCAAAGA  
GCACCTGAAGAGAGAGTGGTAACAGCGCCCCCAGTTCTCAGAGTCGGCGGAAGTGTGGGCGAGCTGGTGCT  
GGATGGGACCGCACCTCTGCACATCAGGACATCCCAGCCCTGTACCGCTGCTTCCAGAGGAGGCCGCCGCCAA  
GCACGCTTGCCCCCAAGAAGAACTGCCTTCGCTCAAGCAGGTGAACTCTGCCAGGAAGCAGCTGAGGCCCAA  
GGCCACCTCCGCAGCCACTGTCCAAAGGGCAGGGTCCCAGCCAGCGTCCCAGGGCCTAGATCTCCTCTCCTCCTC  
CACGGAGAAGCCTGGCCACCGGGGACCCGACCCATCGTGGCCTCCGAGGAGGCATCAGAAGTGCCCCCTTG  
GCTGGATCGAAAGGAGAGTGGGTCCCTACAACACCCGCACCCCTGCAAATCTCCCCCTTCACTTCGCAGCCCTA  
TGTGGCCACACACTCCCCAGAGGCCAGAACCCGGGGAGCCTGGGCCTGACATGGCCAGGAGGCCGCCAGGA  
GGACACCAGCCCCATGGCCCTGATGGACAAAGGTGAGATGAGCTGACTGGGTGAGCCTCAGAGGAGAGCCAGGA  
GACCACTACCTCCACCATTATCACCACCACGGTCATCACCACCGAGCAAGCACCAGCTCTCTGCAGTGTGAGCTT  
CTCCAACTCCTGAGGGGTACATTGACTCCAGCGACTACCCACTGCTGCCCTCAACAATTTCTGGAGTGCACATA  
CAACGTGACAGTCTACACTGGCTATGGGGTGGAGCTCCAGGTGAAGAGTGTGAACCTGTCCGATGGGGAAGTGT  
CTCCATCCGCGGGGTGGACGGCCCTACCCTGACCGTCTGGCCAAACCAGACACTCCTGGTGGAGGGGCAGGTAAT  
CCGAAGCCCCACCAACACCATCTCCGTCTACTTCCGGACCTTCCAGGACGACGGCCTTGGGACCTTCCAGCTTCA  
CTACCAGGCCTTCATGCTGAGCTGCAACTTTCCCCGCGGCTGACTCTGGGGATGTACGGTGATGGACCTGCA  
CTCAGGTGGGGTGGCCACTTTCCTGCCACCTGGGCTATGAGCTCCAGGGCGCTAAGATGCTGACATGCATCAA  
TGCCTCCAAGCCGCACTGGAGCAGCCAGGAGCCCATCTGCTCAGCTCCTTGTGGAGGGGCAGTGCACAATGCCAC  
CATCGGCCGCGTCTCTCCCCAAGTTACCCTGAAAACACAAATGGGAGCCAATTCTGCATCTGGACGATTGAAGC  
TCCAGAGGGCCAGAAGCTGCACCTGCACTTTGAGAGGCTGTTGCTGCATGACAAGGACAGGATGACGGTTACAG  
CGGGCAGACCAACAAGTCAGCTCTTCTTACGACTCCCTTCAAACCGAGAGTGTCCCTTTTGGGGCCTGCTGAG  
CGAAGGCAACACCATCCGCATCGAGTTCAGTCCGACCGGCCCGGCTCCACCTTCAACATCCGATTGGA  
AGCGTTTGAGAAAGGCCACTGCTATGAGCCCTACATCCAGAATGGGAACCTTCACTACATCCGACCCGACCTATAA  
CATTGGGACTATAGTGGAGTTCACCTGCGACCCCGGCCACTCCCTGGAGCAGGGCCCGGCCATCATCGAATGCAT  
CAATGTGCGGGACCCATACTGGAATGACACAGAGCCCTGTGCAGAGCCATGTGTGGTGGGGAGCTCTCTGCTGT  
GGCTGGGGTGGTATTGTCCCCAACTGGCCCGAGCCCTACGTGGAAGGTGAAGATTGTATCTGGAAGATCCACGT  
GGGAGAAGAGAAACGGATCTTCTTAGATATCCAGTTCCTGAATCTGAGCAACAGTGACATCTTGACCATCTACGA  
TGGCGACGAGGTGATGCCCCACATCTTGGGGCAGTACCTTGGGAACAGTGGCCCCCAGAACTGTACTCTCCAC  
GCCAGACTTAACCATCCAGTTCATTCCGACCCCTGCTGGCCTCATCTTTGGAAAGGGCCAGGGATTATCATGAA  
CTACATAGAGGTATCAAGGAATGACTCCTGCTCGGATTTACCCGAGATCCAGAATGGCTGGAAAACCACTTCTCA  
CACGGAGTTGGTGGGGGAGCCAGAATCACCTACCAGTGTGACCCCGCTATGACATCGTGGGGAGTGACACCT  
CACCTGCCAGTGGGACCTCAGCTGGAGCAGCGACCCCCATTTTGTGAGAAAATTATGTACTGCACCGACCCCG  
AGAGGTGGATCACTCGACCCGCTTAATTTCCGATCCTGTGCTGCTGGTGGGGACCACCATCCAATACACCTGCAA  
CCCCGTTTTGTGCTTGAAGGGAGTTCTCTTCTGACCTGTACAGCCGTGAAACAGGGACTCCCATCTGGACGTC  
TCGCCTGCCCCACTGCGTTTTCGGAGGAGTCCCTGGCATGTGACAACCCAGGGCTGCCTGAAAATGGATACCAAT  
CCTGTACAAGCGACTCTACCTGCCAGGAGAGTCCCTCACCTTCATGTGCTACGAAGGCTTTGAGCTCATGGGTGA  
AGTGACCATCCGCTGCATCCTGGGACAGCCATCCCACTGGAACGGGCCCCCTGCCCGTGTGTAAAGTTAATCAAGA  
CAGTTTTGAACATGCTTTAGAAGCAGAAGCGGCAGCAGAGACGTCGCTGGAAGGGGGGAACATGGCCCTGGCTAT  
CTTCATCCCGGTCCTCATCATCTCCTTACTGCTGGGAGGAGCCTACATTTACATCACAAGATGTCGCTACTATTC  
CAACCTCCGCTGCCTCTGATGTACTCCACCCCTACAGCCAGATCACCGTGGAAACCGAGTTTGACAACCCCAT  
TTACGAGACAGGGGAAACAGAGAGTATGAGGTTTCTATCTAAAGAGAGCTACACTTGAGAAGGGGACTTGTGAA  
CTCAACCACAATCTCCTCGAGACATTATCCAGAGACCATGTGGCACTTGATTGAAACCCAGAAATGTCGACTGT  
CTTTTGTAGACTCTTTATCAAAGTTTACTGTTTTCTTCCCTGTATTATTATATTTAAAGTGAAAAAAA  
AAAAAAA

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**FIGURE 200**

MPAARPPAAGLRGISLFLALLLGSPAAALERDALPEGDASPLGPYLLPSGAPERGSPGKEHPE  
ERVVTAPPSSSSQSAEVLGELVLDGTAPSAHHDIPALSPLLPEEARPKHALPPKKKLPSLKQVN  
SARKQLRPKATSAATVQRAGSQPASQGLDLLSSSTEKPGPPGDPDPDIVASEEASEVPLWLDRK  
ESAVPTTPAPLQISPFTSQPYVAHTLPQRPEPEGEPGPDMAQEAPQEDTSPMALMDKGENELTG  
SASEESQETTTSTIITTTVITTEQAPALCSVSFSNPEGYIDSSDYPLLPLNNFLECTYNVTVY  
TGYGVELQVKS VNLS DGELLSIRGVDGPTLTVLANQTLLEGGQVIRSPTNTISVYFRTFQDDG  
LGT FQLHYQAFMLSCNFPRRPDSGDVTVM DLHSGGVAHFHCHLGYELQGAKMLTCINASKPHW  
SSQEPICSAPCGGAVHNATIGRVLSPSYPENTNGSQFCIWTIEAPEGQKLHLHFERLLLHDKD  
RMTVHSGQTNKSALLYDSLQTESVPFEGLLSEGNTIRIEFTSDQARAASTFNIRFEAFEKGHC  
YEPYIQNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGPAIIECINVRDPYWNDTEPLCRAMCGG  
ELSAVAGVVLSPNWPEPYVEGEDCIWKIHVGEKRIFLDIQFLNLSNSDILTIYDGDEVMPHI  
LGQYLGNSGPQKLYSSTPDLTIQFHSDPAGLIFGKGQGFIMNYIEVSRNDSCSDLPEIQNGWK  
TTSHTELVRGARITYQCDPGYDIVGSDTLTCQWDLWSDDPPFCEKIMYCTDPGEVDHSTRLI  
SDPVLLVGTTIQYTCNPGFVLEGSSLLTCYSRETGTPIWTSRLPHCVSEESLACDNPGLPENG  
YQILYKRLLYPGESLTFMCYEGFELMGEVTIRCILGQPSHWNGPLPVCKVNQDSFEHALEAEA  
AAETSLEGGNMALAI FIPVLIISLLLGAYIYITRCRYYSNLRPLMYSHPYSQITVETEFDN  
PIYETGETREYEVS I

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 893-915

**N-glycosylation sites.**amino acids 311-315, 328-332, 350-354, 435-439, 458-462, 474-478,  
514-518, 576-580, 618-622, 674-678, 742-746**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 188-192

**N-myristoylation sites.**amino acids 23-29, 87-93, 146-152, 454-460, 475-481, 575-581,  
629-635, 695-701, 723-729, 766-772, 877-883, 953-959**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 383-394

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**FIGURE 201**

GATGGCTACGGCAGGGGGTGGCTCTGGGGCTGACCCGGAAGTCGGGGTCTCCTTCGCCTTCT  
GTCTTTCTGCGTCTACTAGCAGGTTTGTGTCAGGGGAACTCAGTGGAGAGGAAGATATATAT  
CCCCTTAAATAAAACAGCTCCCTGTGTTGCGCTGCTCAACGCCACTCATCAGATTGGCTGCCA  
GTCTTCAATTAGTGGAGACACAGGGGTTATCCACGTAGTAGAGAAAGAGGAGGACCTACAGTG  
GGTATTGACTGATGGCCCCAACCCCCCTTACATGGTTCTGCTGGAGAGCAAGCATTTTACCAG  
GGATTTAATGGAGAAGCTGAAAGGGGAGAACCAGCCGAATTGCTGGTCTTGCAGTGTCTTGAC  
CAAGCCCAGTCTGCTCAGGCTTCTCTCCTAGTGTACAGTGCCCAAATGATGGGTTTGGTGT  
TTACTCCAATTCTATGGGCCAGAGTTTGCTCACTGCAGAGAAATACAGTGGAATTGCTGGG  
CAATGGTTTGGCTTATGAAGACTTTAGTTTCCCCATCTTTCTTGAAGATGAAAATGAAAC  
CAAAGTCATCAAGCAGTGTATCAAGATCACAACTGAGTCAGAATGGCTCAGCACCAACCTT  
CCCCTATGTGCCATGCAGCTCTTTTACACATGCATGCTGTATCAGCACTGCCACCTGCAT  
GCGGCGCAGCTCCATCCAAAGCACCTTCAGCATCAACCCAGAAATCGTCTGTGACCCCTGTCT  
TGATTACAATGTGTGGAGCATGCTAAAGCCTATAAATACTGGGACATTAAAGCCTGACGA  
CAGGGTTGTGGTTGCTGCCACCCGGCTGGATAGTCGTTTCTTTTCTGGAATGTGGCCCCAGG  
GGCTGAAAGCGCAGTGGCTTCTTTGTACCCAGCTGGCTGCTGCTGAAGCTTTGCAAAAGGC  
ACCTGATGTGACCACCCTGCCCCGCAATGTCTGTTTGTCTTTTCAAGGGGAACTTTTGA  
CTACATTGGCAGCTCGAGGATGGTCTACGATATGGAGAAGGGCAAGTTTCCCGTGCAGTTAGA  
GAATGTTGACTCATTGTGGAGCTGGGACAGGTGGCCTTAAGAACTTCATTAGAGCTTTGGAT  
GCACACAGATCCTGTTTCTCAGAAAAATGAGTCTGTACGGAACCAGGTGGAGGATCTCCTGGC  
CACATTGGAGAAGAGTGGTGCTGGTGTCCCTGCTGTATCCTCAGGAGGCCAAATCAGTCCCA  
GCCTCTCCCACCATCTTCCCTGCAGCGATTTCTTCGAGCTCGAAACATCTCTGGCGTTGTTCT  
GGCTGACCACTCTGGTGCCTTCCATAACAATATTACCAGAGTATTTACGACACTGCTGAGAA  
CATTAAATGTGAGCTATCCCGAATGGCTGAGCCCTGAAGAGGACCTGAACTTTGTAACAGACAC  
TGCCAAGGCCCTGGCAGATGTGGCCACGGTGTGGGACGTGCTCTGTATGAGCTTGCAGGAGG  
AACCAACTTCAGCGACACAGTTTCAGGCTGATCCCCAACGGTTACCCGCTGCTCTATGGGTT  
CCTGATTAAAGCCAACAACATCATGGTTCCAGTCTATCCTCAGGCAGGACCTAAGGTCCTACTT  
GGGTGACGGGCTCTTCAACATTACATCGCTGTCTCCAGCCCCACCAACACCACTTATGTTGT  
ACAGTATGCCTTGGCAAATTTGACTGGCACAGTGGTCAACCTCACCCGAGAGCAGTGCCAGGA  
TCCAAGTAAAGTCCCAAGTGAACAAGGATCTGTATGAGTACTCATGGGTCCAGGGCCCTTT  
GCATTCTAATGAGACGGGACCGACTCCCCGGTGTGTGCGTTCTACTGCACGATTAGCCAGGGC  
CTTGTCTCCTGCCCTTTGAACTGAGTCAGTGGAGCTCTACTGAATACTCTACATGGACTGAGAG  
CCGCTGGAAAGATATCCGTGCCCCGATATTTCTCATCGCCAGCAAAGAGCTTGAGTTGATCAC  
CCTGACAGTGGGCTTCGGCATCCTCATCTTCTCCCTCATCGTCACCTACTGCATCAATGCCAA  
AGCTGATGTCCTTTTCATTGCTCCCCGGGAGCCAGGAGCTGTGTACATACTGAGGAGGACCCCCA  
GCTTTTCTTGCCAGNTCAGCAGTTCACCTTCTAGAGCATCTGTCCCACTGGGACACAACCACT  
AATTTGTCACTGGAACCTCCCTGGGCCTGTCTCAGATTGGGATTAACATAAAAGAGTGGAAC  
ATCCAAAAGAGACAGGGAGAAATAAATAAATTGCCTCCCTTCCCTCCGCTCCCTTTCCCATCA  
CCCCTTCCCATTTCCTCTTCTCTACTCATGCCAGATTTTGGGATTACAAATAGAAGCT  
TCTTGCTCCTGTTTAACTCCCTAGTTACCCACCCTAATTTGCCCTTCAGGACCCTTCTACTTT  
TTCTTCTGCCCCTGTACCTCTCTGCTCCTCACCCCCACCCCTGTACCCAGCCACCTTCCT  
GACTGGGAAGGACATAAAAGGTTTAAATGTCAGGGTCAAACCTACATTGAGCCCCCTGAGGACAGG  
GGCATCTCTGGGCTGAGCCTACTGTCTCCTTCCCACTGTCCTTTCTCCAGGCCCTCAGATGGC  
ACATTAGGGTGGGCGTGCTGCGGGTGGGTATCCACCTCCAGCCCACAGTGCTCAGTTGTACT  
TTTTATTAAGCTGTAATATCTATTTTTGTTTTTGTCTTTTTCCTTTATTCTTTTGTAAATAT  
ATATATAATGAGTTTCATTAAATAGATTATCCC

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**FIGURE 202**

MATAGGGSGADPGSRGLLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQIGCO  
SSISGDTGVIHVVEKEEDLQWVLTGDPNPPYMVLLSKHFTRDLMEKCLKGRTSRIAGLAVSLT  
KPSPASGFSPSVQCPNDGFGVYSNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLDENET  
KVIKQCYQDHNLSQNGSAPTFLCAMQLFSHMHAVISTATCMRRSSIQSTFSINPEIVCDPLS  
DYNVWSMLKPINTTGTLKPDDRNVVAATRLDSRSFFWNVAPGAESAVASFVTQLAAAEALQKA  
PDVTTLPRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVELGQVALRTSLELWM  
HTDPVSQKNESVRNQVEDLLATLEKSGAGVPAVILRRPNQSQPLPPSSLQRFRLARNISGVVL  
ADHSGAFHNKYYQSIYDTAENINVSYPEWLSPEEDLNFTVDTAKALADVATVLGRALYELAGG  
TNFSDTVQADPQTVTRLLYGFLIKANNSWFQSILRQDLRSYLGDGPLQHYIAVSSPTNTTYV  
QYALANLTGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLPRCVRSTARLARA  
LSPAFELSQWSSTEYSTWTESRWKDIRARIFLIASKELELITLTVGFGILIFSLIVTYCINAK  
ADVLFIAPREPGAVSY

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 671-692

**N-glycosylation sites.**

amino acids 45-49, 55-59, 187-191, 200-204, 204-208, 264-268,  
387-391, 417-421, 435-439, 464-468, 506-510, 530-534, 562-566,  
573-577, 580-584, 612-616

**Glycosaminoglycan attachment site.**

amino acids 404-408

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 232-236

**N-myristoylation site.**

amino acids 5-11, 6-12, 9-15, 29-35, 61-67, 120-126, 146-152,  
168-174, 205-211, 294-300, 438-444, 446-452, 504-510, 576-582

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**FIGURE 203**

GCTAGACCGAGCCCTGGGAGGCTACGGGCTCCCCGGAAACCCTGCCAGGGGAGCCGGGTTTT  
GAGCTCAGGCGCCTCTAGCGGCGGCCCCAGAAATCTGACTCGCGAGGCCAGAGTTGCAGGGA  
CTGAATAGCAAACCTGAGGCTGAGTAGGGAACAGACCATGAGGTCAGTGCAGATCTTCCTCTCC  
CAATGCCGTTTGTCTCTTCTACTAGTTCCGACAATGCTCCTTAAGTCTCTTGGCGAAGATGTA  
ATTTTTACCCCTGAAGGGGAGTTTGACTCGTATGAAGTCACCATTCCTGAGAAGCTGAGCTTC  
CGGGGAGAGGTGCAGGGTGTGGTCAGTCCCGTGTCTTACCTACTGCAGTTAAAAGGCAAGAAG  
CACGTCTCCATTTGTGGCCCAAGAGACTTCTGTTGCCCCGACATCTGCGCGTTTTCTCCTTC  
ACAGAACATGGGGAACCTGCTGGAGGATCATCCTTACATACCAAAGGACTGCAACTACATGGGC  
TCCGTGAAAGAGTCTCTGGACTCTAAAGCTACTATAAGCACATGCATGGGGGGTCTCCGAGGT  
GTATTTAACATTGATGCCAAACATTACCAAATTGAGCCCTCAAGGCCTCTCCCAGTTTTGAA  
CATGTCGTCTATCTCCTGAAGAAAGAGCAGTTTGGGAATCAGGTTTGTGGCTTAAGTGATGAT  
GAAATAGAATGGCAGATGGCCCCCTTATGAGAATAAGGCGAGGCTAAGGGACTTTCCTGGATCC  
TATAAACACCCAAAGTACTTTGGAATTGATCCTACTCTTTGATCAAAGTAGGTATAGGTTTGTG  
AACAACAATCTTTCTCAAGTCATACATGATGCCATTCTTTTACTGAGTGGGATTATGGACACCTAC  
TTTCAAGATGTTTCGTATGAGGATACACTTAAAGGCTCTTGAAGTATGGACAGATTTTAAACAA  
ATACGCGTTGGATATCCAGAGTTAGCTGAAGTTTTAGGCAGATTTGTAATATATAAAAAAGT  
GTATTAATGCTCGCCTGTCATCAGATTGGGCACATTTATATCTTCAAAGAAAATATAATGAT  
GCTCTTGTCATGGTCGTTTGGAAAAGTGTGTTCTCTAGAATATGCTGGATCAGTGAGTACTTTA  
CTAGATACAAATATCCTTGCCCCCTGCTACCTGGTCTGCTCATGAGCTGGGTCATGCTGTAGGA  
ATGTCACATGATGAACAATACTGCCAATGTAGGGGTAGGCTTAATTGCATCATGGGCTCAGGA  
CGCACTGGGTTTAGCAATTGCAGTTATATCTCTTTTTTAAACATATCTCTTCGGGAGCAACA  
TGCTAAATAATATCCCAGGACTAGGTTATGTGCTTAAGAGATGTGGAAACAAATTTGTGGAG  
GACAATGAGGAATGTGACTGTGGTTCCACAGAGGAGTGTGAGAAAGATCGGTGTTGCCAATCA  
AATTGTAAGTTGCAACCAGGTGCCAATGTAGCATTGGACTTTGCTGTGATGATTGTGCGGTTT  
CGTCCATCTGGATACGTGTGTAGGCAGGAAGGAAATGAATGTGACCTTGCAGAGTACTGCGAC  
GGGAATTCAGTTCTCTGCCCAAATGACGTTTATAAGCAGGATGGAACCCCTTGCAAGTATGAA  
GGCCGTTGTTTCAGGAAGGGGTGCAGATCCAGATATATGCAGTGCCAAAGCATTTTTGGACCT  
GATGCCATGGAGGCTCCTAGTGAGTGCTATGATGCAGTTAACTTAATAGGTGATCAATTTGGT  
AACTGTGAGATTACAGGAATTCGAAATTTTAAAAAGTGTGAAAGTGCAAATTCATATGTGGC  
AGGCTACAGTGTATAAATGTTGAAACCATCCCTGATTTGCCAGAGCATACGACTATAATTTCT  
ACTCATTTACAGGCAGAAAATCTCATGTGCTGGGGCACAGGCTATCATCTATCCATGAAACCC  
ATGGGAATACCTGACCTAGGTATGATAAATGATGGCACCTCCTGTGGAGAAGGCCGGGTATGT  
TTTAAAAAAATTTGCGTCAATAGCTCAGTCCTGCAGTTTGACTGTTGCCTGAGAAATGCAAT  
ACCCGGGGTGTGTTGCAACAACAGAAAAAAGTCCACTGCATGTATGGGTGGGCACCTCCATT  
TGTGAGGAAGTGGGGTATGGAGGAAGCATTGACAGTGGGCCTCCAGGACTGCTCAGAGGGGCG  
ATTCCTCGTCAATTTGGGTTGTGTCCATCATAATGTTTCGCCTTATTTTATTAATCCTTTCA  
GTGGTTTTTGTGTTTTTCCGGCAAGTGATAGGAAACCACTTAAACCCAAACAGGAAAAAATG  
CCACTATCCAAAGCAAAAAGTGAACAGGAAGAATCTAAAACAAAAAGTGTACAGGAAGAATCT  
AAAACAAAAAGTGGACAGGAAGAATCTGAAGCAAAAAGTGGACAGGAAGAATCTAAAGCAAAA  
ACTGGACAGGAAGAATCTAAAGCAACATTGAAAGTAAACGACCCAAAGCAAGAGTGTCAAG  
AAACAAAAAAGTAAACCGGGCAATCCATACTCATTAGTAACACAGGCTCATTATTTAAACCA  
GCTAATCATTTATCCAAAGGCTTTCATTCTTCTCCCAATATTTTTTACTTTAATTTTTCCC  
ACAAGTTTTGATCAGCAATAAACAGCATTCTTGTGTTTGGAAACAAAA

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**FIGURE 204**

MRSVQIFLSQCRLLLLLLVPTMLLKSLGEDVIFHPEGEFDSYEVTIPEKLSFRGEVQGVVSPVS  
YLLQLKGKKHVLHLWPKRLLLPRHLRVFSFTEHGELLEDHPYIPKDCNYMGSVKESLDSKATI  
STCMGGLRGVFNIDAKHYQIEPLKASPSFEHVYLLKKEQFGNQVCGLSDDDEIEWQMAPYENK  
ARLRDFPGSYKHPKYLELILLFDQSRVRFVNNNLSQVIHDAILLTGIMDTYFQDVRMRIHLKA  
LEVWTDNFNKIRVGYPELAEVLGRFVIYKKSVLNARLSSDWAHLYLQRKYNDALAWSFGKVCSL  
EYAGSVSTLLDTNILAPATWSAHELGHAVGMSHDEQYCQCRGLNCIMGSGRTGFSNCSYISF  
FKHISSGATCLNNIPGLGYVLKRCGNKIVEDNEECDCGSTEECQKDRCCQSNCKLQPGANCSI  
GLCCHDCRFRPSGYVCRQEGNECDLAEYCDGNSSSCPNDVYKQDGTCKYEGRCFRKGCRSRY  
MQCQSIFGPDAMEAPSECYDAVNLIQDQFGNCEITGIRNFKKCESANSICGRLQCINVETIPD  
LPEHTTIISTHLQAENLMCWGTGYHLSMKPMGIPDLGMINDGTSCGEGRVCFKKNCVNSSVLQ  
FDCLPEKCNTRGVCNNRNKCHCMYGWAPPFCEEVGYGGSIDSGPPGLLRGAIPSSIWVVSIIIM  
FRLILLILSVVFVFRQVIGNHLKPKQEKMPLSKAKTEQEESESKTKTVQEESESKTKTGQEESEAK  
TGQEESEKAKTGQEESEKANIESKRPKAKSVKKQKK

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 684-705

**N-glycosylation sites.**

amino acids 222-226, 372-376, 438-442, 473-477, 625-629

**N-myristoylation sites.**amino acids 131-137, 168-174, 235-241, 319-325, 364-370, 436-442,  
472-478, 609-615, 642-648, 668-674, 676-680, 680-686, 749-755,  
758-764, 767-773**Amidation site.**

amino acids 69-73

**Disintegrins proteins**

amino acids 429-479

**EGF-like domain proteins**

amino acids 650-662

**Neutral zinc metalloproteases, zinc-binding region proteins**

amino acids 335-345



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**FIGURE 205**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGGAAGGTTGAATGGGGTAGAAGGCCTG  
TTGTGGAGGGAAACCACCCATCCTCCTGCCTCCCACCACCACCATCATCCTGGCTGGACGGAG  
AGGGTGACGGGGGCTGGGAAGGGGCAGCTCATGTTTCAGGTTTCCAGGAGGGGCTACCTGTTGA  
CTGTCTTTGCAGGAAGAAGAAAACACCTGAGTGACCAGATGTCCCAGCTCCAGGTGCCTTGCC  
AGATGGCCAGAACCACACCTCTTGAAGAGTGACAGTGCTGTGGAGCATGGTTTCTGCACACCT  
GGAATGACTGGAACCCCAAAGACTCAAGAAGGAGCTAAAGATCTTGAAGTAGACATGAATAAA  
ACAGAAGGCTGTGGACCACCTGTCGAGATGGAGAAGTCCTTCTGAGGCTATCCAAACACGGAC  
CAGGCCATGAGACCCCGATGACCATCCCTGAATTTTTTTCGAGAGTCAGTCAACCGATTTGGAA  
CTTATCCAGCCCTCCCATCCAAGAATGGCAAAAAGTGGGAATTTCTGAATTTCAACCAGTACT  
ATGAGGCTTGTGCGAAGGCTGCAAAATCCTTGATCAAGCTGGGTTTGGAGCGTTTCCACGGAG  
TTGGTATCCTGGGGTTTAACTCTGCAGAGTGGTTTATCACTGCTGTTGGTGCCATCCTAGCCG  
GGGGTCTTTGTGTTGGTATTTATGCCACCAACTCTGCCGAGGCTTGTCAATATGTCATCACTC  
ATGCCAAAGTGAACATCTTGCTGGTTGAGAATGATCAACAGTTACAGAAAATCCTTTTCGATTC  
CACAGAGCAGCCTAGAGCCCCATAAAGCGATCATCCAGTACAGACTGCCAATGAAGAAGAACA  
ACAACCTTGTAATCTTGGGATGATTTTCATGGAACCTTGGCAGAAGTATCCCTGACACCCAACTGG  
AGCAGGTCATCGAGAGCCAGAAGGCGAATCAATGCGCAGTGCTCATCTACACTTCAGGGACCA  
CAGGCATACCCAAAGGGAGTGATGCTCAGTCATGACAACATCACGTGGATTGCAGGAGCAGTGA  
CAAAGGACTTTAACTGACAGACAAGCATGAGACGGTGGTTAGCTACCTCCCACTCAGCCATA  
TTGCAGCACAGATGATGGACATCTGGGTACCCATAAAGATTGGGGCGCTCACATACTTTGCTC  
AAGCAGATGCTCTCAAGGGCACCTTGGTAAGTACTCTAAAGGAGGTAACCTACTGTCTTCA  
TTGGAGTGCCTCAAATTTGGGAGAAGATACATGAGATGGTGAAGAAAAATAGTGCCAAGTCCA  
TGGGCTTGAAGAAGAAGGCATTTCGTGTGGGCAAGAAACATTGGCTTCAAGGTCAACTCAAAAA  
AGATGTTGGGGAAATATAATACTCCCGTGAGCTACCGCATGGCTAAGACTCTCGTGTTCAGCA  
AAGTCAAGACATCCCTTGGCTTGGATCACTGTCACTCTTTTATCAGTGGGACTGCGCCCCCTCA  
ACCAAGAGACTGCCGAGTTCTTTCTAAGCTTGGACATACCTATAGGCGAGTTGTATGGGTTGA  
GTGAGAGCTCGGGACCCACACGATATCCAACCAGAATAACTACAGGCTTCTAAGCTGTGGCA  
AGATCTTGACTGGGTGTAAGAATATGCTGTTCCAGCAGAACAAGGATGGCATTGGGGAGATCT  
GCCTCTGGGGTAGGCACATCTTCATGGGCTATCTGGAAAGTGAGACTGAACTACAGAGGCCA  
TCGATGATGAAGGCTGGCTACACTCTGGGGATCTGGGCCAGCTGGACGGTCTGGGTTTCTCTCT  
ATGTCACCGGCCACATCAAAGAAATCCTTATCACTGCTGGTGGTGAAAATGTGCCCCCATTC  
CTGTTGAGACCTTGGTTAAGAAGAAGATCCCCATCATCAGTAACGCCATGTTAGTAGGAGATA  
AACTGAAGTTTCTGAGCATGTTGCTGACGCTGAAGTGTGAGATGAATCAGATGAGCGGAGAAC  
CTCTGGACAAGCTGAACTTCGAGGCCATCAACTTCTGTGCGGGTCTGGGCAGCCAGGCATCCA  
CCGTGACTGAGATTGTGAAGCAGCAAGACCCCCCTGGTCTACAAGGCCATCCAGCAAGGCATCA  
ATGCTGTGAACCAGGAAGCCATGAACAATGCACAGAGGATTGAAAAGTGGGTCTCTTGGAGA  
AGGACTTTTCCATCTATGGTGGAGAGCTAGGTCCAATGATGAACTTAAGAGACATTTTGTAG  
CCCAGAAATACAAAAACAATTGATCACATGTACCCTGACTGCTTTGATGGAGCTGCTCTC  
AGCTGTTCTGATGCCTTCAGCAGGAAGACCTCATTGCAATAAGTGAAATGCTGCTCTAGGTAG  
AAGCTCTCCCTGCTGTTTTTAAGAAGCCACATTCCTCATTGGTCAGTTTCTTGATTGTTTCGTC  
TGTTGGAGAGGTGCTCCCTAGAAGAACCTGCCATACGTTTCAAAGCAATAAAATCACTGTATA  
TCTTTCTAAGGACCTTCAAGTCATGACTCCAGGGAAGCCTATTGGGAAGTCTACTAAAACTG  
CCTGATTTACAAGAAAGACCTGAACTTGTGGGCTCCCATTTGATTTTTTCTCCTCAGGGGAC  
TCAGACATTAGAAAGAAAAAGCCTCACAGATTTGAAGAACTGGACCCCCAAATCAACTCACCT  
GCCTGGAAGCAACTGGGAACCCCTTCCAATAAGTCCTGATAATAAGCACTTCAGGGTCCCAA  
AAAAAAAAAA

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**FIGURE 206**

MTIPEFFRESVNRFGTYPALPSKNGKKWEILNFNQYYEACRKAASLIKGLERFHGVGILGF  
NSAEWFITAVGAILAGGLCVGIYATNSAEACQYVITHAKVNILLVENDQQLOKILSIPQSSLE  
PLKAI IQYRLPMKKNNNLYSWDDFMELGRSIPDTQLEQVIESQKANQCAVLIYTSGTTGIPKG  
VMLSHDNITWIAGAVTKDFKLTDKHETVVSYLPLSHIAAQMMDIWVPIKIGALTYFAQADALK  
GTLVSTLKEVKPTVFIGVPQIWEKIHVMVKNSAKSMGLKKKAFVWARNIGFKVNSKKMLGKY  
NTPVSYRMAKTLVFSKVKTSGLDHCHSFISGTAPLNQETAFFLSLDIPIGELYGLSESSGP  
HTISNQNNYRLLSCGKILTGCKNMLFQQNKDGIGEICLWGRHIFMGYLESETETTEAIDDEGW  
LHSGDLGQLDGLGFLYVTGHIKEILITAGGENVPPIPVETLVKKKIPIISNAMLVGDKLKFLS  
MLLTLKCEMNQMSGEPLDKLNFEAINFCRGLGSQASTVTEIVKQQDPLVYKAIQQGINAVNQE  
AMNNAQRIEKWVILEKDFSIYGGELGPMMLKRHFVAQKYKKQIDHMYH

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 65-86

**N-glycosylation site.**

amino acids 196-200

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 282-286

**Tyrosine kinase phosphorylation sites.**

amino acids 547-555, 608-616

**N-myristoylation sites.**amino acids 15-21, 74-80, 80-86, 84-90, 185-191, 189-195,  
253-259, 337-343, 371-377, 448-454, 536-542**Amidation site.**

amino acids 24-28

**Putative AMP-binding domain signature.**

amino acids 177-189

**Putative AMP-binding domain proteins.**

amino acids 173-190

**FIGURE 207**

CCCACGCGTCCGCCCACGCGTCCGCGGACGCGTGGGGCCAGATCGCGGCCGGCGCCAGCGCA  
CCGTCCGGTCCACCCGCCAGCCCGCACAGCCGCGCCGCCGCGGAGCGTTTCGTGAGCGGCGCT  
CCGAGGATCAGGAATGGGGCTTCGGGCGCTGGGCGCGCTCCGAACCCGGCGCACGTAAGAGCC  
TGGGAGCGCCCGAGCCGCCCGGCTGCCCGGAGCCCCATCGCCTAGGACCGGGAGATGCTGGAA  
ATGCAACCGCCTGTTCCCCGAGGAGCCGCTGCCCCGGGACCCCCTGGCACTGTGCGACCCCT  
GGTCAGCAGCCCCCGGAGAAGACGGCGCCCCCAACGCCCCGACCGCGTGGCCGTGGCAGCGCC  
ACGCGAGCCCTCTAGGCGACCGCAGGGCCACAGCAGCTCAGCCGCCGGTGGCCCTCGGAAAC  
CATGACCCCCGGCGCGGGGCCCATGGAGCCATGGCCTATAGGGTCTTGGGCCGCGGGGCCAC  
CTCAGCCGCGGAGGGCGCGCAGGCTGCTCTTCGCCCTTACGCTCTCGCTCTCTGCACTTACC  
TGTGTTACAGCTTCTGTGCTGCTGCGACGACCTGGGTGCGAGCCGCCTCCTCGGCGCGCCTC  
GCTGCCTCCGCGGCCCCAGCGCGGGCGGCCAGAACTTCTCCAGAAGTCCCGCCCCCTGTGATC  
CCTCCGGGCGGACGCCCAGCGAGCCCGAGCGCTCCAGCGCGCCCGCCCGGTGCCCGCCC  
CTCGCTCTCCGGTTCACAACTCCTCGGCTCACCCAAAGCTGGGTACCAAGCGTTGCCCAAG  
CCCTCATTTGTGGGCGTGAAGAAGGGGGGACCCGGGCCGTGCTGGAGTTTATCCGAGTACACC  
CGGACGTGCGGGCCTTGGGCACGGAACCCCACTTCTTTGACAGGAACCTACGGCCGCGGGCTGG  
ATTGGTACAGGAGCCTGATGCCCAGGACCCCTCGAGAGCCAGATCACGCTGGAGAAGACGCCCA  
GCTACTTTGTCACTCAAGAGGCTCCTCGACGCATCTTCAACATGTCCCGAGACACCAAGCTGA  
TCGTGGTTGTGCGGAACCCGTGTGACCCGTGCCATCTCTGATTACACGCAGACACTCTCCAAGA  
AGCCCGACATCCCGACCTTTGAGGGCCTCTCCTTCGCAACCGCACCCCTGGGCCCTGGTGGACG  
TGTCATGGAACGCCATCCGCATCGGCATGTACGTGCTGCACCTGGAGAGCTGGCTGCAGTACT  
TCCCGCTAGCTCAGATTCACTTCGTGCTGCGAGCGACTCATCACTGACCCGGCCGGCGAGA  
TGGGGCGAGTCCAGGACTTCTTGGGCATTAAGAGATTTCATCACGGACAAGCACTTCTATTTC  
ACAAGACCAAAGGATTCCCTTGCTTGAAAAAAACAGAATCGAGCCTCCTGCCTCGATGCTTGG  
GCAAATCAAAGGGGAGAACTCATGTACAGATTGATCCTGAAGTGATAGACCAGCTCCGAGAAT  
TTTATAGACCGTATAATATCAAATTTTATGAAACCGTTGGGCAGGACTTCAGGTGGGAATAAG  
CCCACGAAAGGAAAGGGCTCTCAAGGGCTCTTCTGCTCATCTCTTCCGTGAGATTTGCTCCCA  
GACCCTCTGATCTCCCTCCAACAAACCTGGCTCCAGCCCCCTTCCCAACTTGAGTTGCATC  
ATCTTGGAACCAGGAAGCCAGCTAAAGCCAAGAGACCAGAGAGTCCCTGCCACTAGTTTTCA  
TCAGTCTGTTCAAGCAAAGTTGATCTGCTCCTGGCACGTCCAGTAAATTCAGAATCATTTCTC  
CTTTCTGCCATAAAGGGCCTTGAGAAATGCTTTAAGAAGAGTGAATGTTCCAATGATGATA  
GATATTATAAGCGATGATGGTTCTGTTGCTATGAACACAGCAGTCGGTCCCTGTGATTGTCCA  
CCCAGGAGTGGCCTTGTTAATTCCAAGTGGCATGTATCTTCCCTCTGAGCTTCATTTCTTCAA  
GATGCTCTGGGTGGTGGGATGGGAGACCATCCTCAGCCCTCCTCAGACCTTATCAATTCATTG  
AGAGATTGCAAAGCTGAAAGCACCTCCGGCCACTCCTGGGAGACAGACCCTTTGGTGATGAAA  
TAAACCACTGACTTCAGAGCCTATGGTCTCAACTGTGCTTGAAAAACACTGTCTCTGAAAAA  
ACTTTGTGATTCTCCCTGCTCCCTGTGGACAAAAGCACATAATTCTGCTGTTACGGGTACTTT  
GCTCATACGAGCTTTCATGTTGAGCATGCAATGGAATCATGCTTGTCCATGTGAAATAAATAT  
GGCTCTCTCGTGTCTTAATGCTGGGCTTTTCTCTGTAAGCTGGTTCGTGCAGCACAAATTCATT  
AATTAAACTTCTCCAGTGCAAGAAGGCAGCTGGTGCTGGGGGTGGTCTGGGGGGTCCAGGGAG  
GAGGGCAAGGACTACATGGGGCAGAGGCAAGGCGGTGGTGGAGATGAGGAAAGAAGTTCTTCT  
TGGCAGAAGCTGGGGCAGAAAGATCACATGAGATCTGTGGGGACACCCCTCTATCTGAAACATA  
AGTCTGTGTTTATTCTCTGCTTAGAAATTTTAGATCTGAAGTGCTACACTGAAGGTCCGAAGG  
TTGATGGGGCATCAGATATCTTTTTGGTTGGCCAGCATGATATTTTGAATAAAGTGTCAACAG  
TTAGAAACTGGGAGCATTCATATGTAAAAAATATGGATTTTCAGCTTCTTCTTAAAAA  
AAAAA

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**FIGURE 208**

MAYRVLGRAGPPQPRRARRLLFAFTLSLSCTYLCYSFLCCDDLGRSRLLGAPRCLRGPSAGG  
QKLLQKSRPCDPSGPTPSEPSAPSAPAAVAPARLSGNSHSGSPKLGTKRLPQALIVGVKKGG  
TRAVLEFIRVHPDVRLGTEPHFFDRNYGRGLDWYRSIMPRTLESQITLEKTPSYFVTQEAPR  
RIFNMSRDTKLIVVRNPVTRAISDYTQTLSSKPDIPTFEGLSFRNRTLGLVDVSWNAIRIGM  
YVLHLESWLQYFPLAQIHVSGERLITDPAGEMGRVQDFLGIKRFITDKHFYFNKTKGFCLK  
KTESSLLPRCLGKSKGRTHVQIDPEVIDQLREFYRPYNIKFYETVGQDFRWE

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 102-106, 193-197, 235-239, 306-310

**Tyrosine kinase phosphorylation site.**

amino acids 296-305

**N-myristoylation sites.**

amino acids 51-57, 100-106, 121-127, 125-131

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 20-31

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**FIGURE 209**

CTTTCCTTATCTGTGTGTA CTCTTATCTCACTGTTCTATTTTTTCTCCTCATTATATTA ACT  
CTTTCCTTACCTTTTTTCTGAACTTCTAGGCCTTCTCTTTCCAGAACTGGTGGAAGACAAATG  
AAACGGCCAAAGATGGTAAGAAACAAGCCGCATTTCTCCTTGGGGAGACTGATAATTTAAAGG  
TTTGTGTGTGTCAGAAACATTCCCAGCTTCATCACCAACCCTTTCCTTCCACCTCTGCCCCACTG  
GAGACCACTTACATCCCGAAGCGGACGCGGCAGCTGAAGTCAGGAAACCATGCATCACATTAG  
CAGGAGCCAACTGCAGACTTTAAACTCCGTTCAACATGTGGATGCGGCAGAGAAATGACCTGT  
CCAGACAAGCCGGGGCAGCTCATAAACTGGTTCATCTGCTCCCTGTGCGTCCCGCGGGTGCCT  
AAGCTCTGGAGCAGCCGGCGTCCAAGGACCCGGAGAAACCTTCTGCTGGGCACTGCGTGTGCC  
ATCTACTTGGGCTTCCTGGTGAGCCAGGTGGGGAGGGCCTCTCTCCAGCATGGACAGGCGGCT  
GAGAAGGGGGCCACATCGCAGCCGCGACACCGCCGAGCCATCCTTCCCTGAGATACCCCTGGAT  
GGTACCCTGGCCCCCTCCAGAGTCCCAGGGCAATGGGTCCACTCTGCAGCCCAATGTGGTGTAC  
ATTACCCTACGCTCCAAGCGCAGCAAGCCGGCCAATATCCGTGGCACCCTGAAGCCCAAGCGC  
AGGAAAAAGCATGCAGTGGCATCGGCTGCCCCAGGGCAGGAGGCTTTGGTCGGACCATCCCTT  
CAGCCGCAGGAAGCGGCAAGGGAAGCTGATGCTGTAGCACCTGGGTACGCTCAGGGAGCAAAC  
CTGGTTAAGATTGGAGAGCGACCCTGGAGGTTGGTGCGGGGTCCGGGAGTGCGAGCCGGGGGC  
CCAGACTTCCTGCAGCCCAGCTCCAGGGAGAGCAACATTAGGATCTACAGCGAGAGCGCCCCC  
TCCTGGCTGAGCAAAGATGACATCCGAAGAATGCGACTCTTGGCGGACAGCGCAGTGGCAGGG  
CTCCGGCCTGTGTCCTCTAGGAGCGGAGCCCGTTTGCTGGTGCTGGAGGGGGGCGCACCTGGC  
GCTGTGCTCCGCTGTGGCCCTAGCCCCCTGTGGGCTTCTCAAGCAGCCCTTGACATGAGTGAG  
GTGTTTGCTTCCACCTAGACAGGATCCTGGGGCTCAACAGGACCCTGCCGTCTGTGAGCAGG  
AAAGCAGAGTTCATCCAAGATGGCCGCCCATGCCCATCATTCTTTGGGATGCATCTTTATCT  
TCAGCAAGTAATGACACCCATTCTTCTGTAAAGCTCACCTGGGGAACCTTATCAGCAGTTGCTG  
AAACAGAAATGCTGGCAGAATGGCCGAGTACCCAAGCCTGAATCAGGTTGTACTGAAATACAT  
CATCATGAGTGGTCCAAGATGGCACTCTTTGATTTTTTGTACAGATTTATAATCGCTTAGAT  
ACAAATTGCTGTGGATTGAGACCTCGCAAGGAAGTGCCTGTGTACAGAATGGATTGAGGCCA  
AAATGTGATGACCAAGGTTCTGCGGCTCTAGCACACATTATCCAGCGAAAGCATGACCCAAGG  
CATTTGGTTTTTATAGACAACAAGGGTTTTCTTTGACAGGAGTGAAGATAACTTAAACTTCAA  
TTGTTAGAAGGCATCAAAGAGTTTCCAGCTTCTGCAGTTTCTGTTTTGAAGAGCCAGCACTTA  
CGGCAGAACTTCTTCACTCTCTGTTTCTGATAAAGTGTATTGGGAAAGTCAAGGAGGTAGA  
CAAGGAATTGAAAAGCTTATCGATGTAATAGAACACAGAGCCAAAATTCTTATCACCTATATC  
AATGCACACGGGGTCAAAGTATTACCTATGAATGAATGACAAAAGAATCTTCTGGCTAGGGTG  
TTAGATATATTTATGCATTTTTTGGTTTTTGTAAATCAAGCACATCAACCTCAAGCCCGTT  
TAGCAATGAGGCAGTGTAGATGAATACGTAAAATAAATGACTTTAACCAAGTAGCTATAAAGG  
GACTTAGCACTGTATGCATACTTAAAAAGGTTTTGAAAAACAACTACTTGAGAAATATTTGT  
TTATATTTTTCTCTAACATCATGCTATGTGTCAGTCTGAACATCTGACAACAGAAATTTTCACT  
TATTATTCTAGCTAAGTTTTGAAAACATTTGTCATGCTGTTTAAATAGAAAACCTGCAAACCAGA  
GATACTGACTCCATTAATAAACCATATTTTGTGCCGTTTTGACTGTTCTGACCAAATACTAAT  
GGGAACAATTCTTGACGTTTTTCTGTTGCTGATTGTTAACATAGAGCAGTCTCTACACTACCC  
TGAGGCAACTCTACATTGGAACACTGAGGCTTACAGCCTGCAAGAGCATCAGAGCTGACCATA  
CATTTAAACAGAAATGCTGGTTTTATTTGCAAAATCACCAGTATATTTTCTATTGTGTCTATAA  
AAAATCAGTCATTTAAGTACAAGAATCATATTTTCCATTCCTTTTTAGAAATTTATTTTGTG  
TCCCTATGGAAATCATTACATCTGACAATTTATATGTTAAAGAGTTTTACTCTCTCTATTTT  
GGTCCAATTTGTATCTAGTGGCTGAGAAATTAATAATTCTAAAGTATGAAGTTACCTATCTG  
AAAATGTACTTACAGAGTATCATTTTAAATGGATGTCTCTTTAAAAATTTTGTACTTTTAC  
CAACAATGTAATATAATTTATGTATATTTTATTAATAATAGTGAATTCCTTAAATTTGTCT  
ATGTACTTATATTTAATTTGATTTAATGGTTACTGCCCAGATATTGAGAAATGGTTCAAATAT  
TGAGTGTGTTTCAATAA

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**FIGURE 210**

MTC PDKPGQLINWFICSLCVPRVRKLWSSRRPRTTRNLLLGTACAIYLGFLVSQVGRASLQHG  
QAAEKGP HRSRD TAEP SFPEI PLDGT LAPPESQGN GSTLQPNVVYITLRSKR SKPANIRGTVK  
PKRRKKH AVASAA PGQEALVGPSLQPQEAA READAVAPGYAQGANLVKIGERP WRLV RGP GVR  
AGGPDFLQPSSRESNIRIYSESAPSWLSKDDIRMRLLADSAVAGLRPVSSRSGARLLVLEGG  
APGAVLR CGPSPCGLLKQPLDMSEVF AFHLD RILGLNRTLPSVSRKAEFIQDGRPCPIILWDA  
SLSSASNDTHSSVKLTWGTYQQLLKQKCWQNGRV PKPESGCTEIH HHEWSKMALFDLLQIYN  
RLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAA LAHI IQRKHDPRHLVFIDNKGFFDRSEDNL  
NFKLLEGIKEFPASAVSVLKSQHLRQKLLQSLFLDKVYWESQGGRQGIEKLIDVIEHRAKILI  
TYINAHGVKVLPMNE

**Transmembrane domain:**

amino acids 40-56

**N-glycosylation sites.**

amino acids 98-102, 289-293, 322-326

**N-myristoylation sites.**amino acids 8-14, 41-47, 97-103, 187-193, 251-257, 252-258,  
287-293, 484-490

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**FIGURE 211**

GTGGGGTGGTGAGCGCAGCGCCGAGGATGAGGAGGTGCAACAGCGGCTCCGGGCGCGCCGCTCGCTGCTGCTGC  
TGCTGCTGTGGCTGCTCGCGGTTCCCGGCGCTAACGCGGCCCCGCGGTGCGCGCTCTATTGCGCTTCCGACCCGC  
TGACGCTGCTGCAGGCGGACACGGTGCGCGCGCGGTGCTGGGCTCCCGCAGCGCCTGGGCGGTGGAGTTCTTCG  
CCTCTGGTGCGGCCACTGCATCGCCTTCGCCCCGACGTGGAAGGCGCTGGCCGAAGACGTCAAAGCCTGGAGGC  
CGGCCCTGTATCTCGCCGCCCTGGACTGTGCTGAGGAGACCAACAGTGCAGTCTGCAGAGACTTCAACATCCCTG  
GCTTCCCGACTGTGAGGTTCTTCAAGGCCTTTACCAAGAACGGCTCGGGAGCAGTATTTCCAGTGGCTGGTGCTG  
ACGTGCAGACGCTGCGGGAGAGGCTCATTGACGCCCTGGAGTCCCATCATGACACGTGGCCCCAGCCTGTCCCC  
CACTGGAGCCTGCCAAGCTGGAGGAGATTGATGGATTCTTTCGAGAAATAACGAAGAGTACCTGGCTCTGATCT  
TTGAAAAGGGAGGCTCCTACCTGGGTAGAGAGGTGGCTCTGGACCTGTCCAGCACAAAGGCGTGGCGGTGCGCA  
GGGTGCTGAACACAGAGGCCAATGTGGTGAGAAAGTTTGGTGTCAACGACTTCCCCCTCTTGCTACCTGCTGTTCC  
GGAATGGCTCTGTCTCCCGAGTCCCCGTGCTCATGGAATCCAGGTCTTCTATACCGCTTACCTGCAGAGACTCT  
CTGGGCTCACCAGGGAGGCTGCCAGACCACAGTTGCACCAACCACTGCTAACAGATAGCTCCCACTGTTTGA  
AATTGGCAGATCGCTCCAAGATCTACATGGCTGACCTGGAATCTGCACTGCACTACATCCTGCGGATAGAAGTGG  
GCAGGTTCCCGTCTCTGGAAGGGCAGCGCCTGGTGGCCCTGAAAAAGTTTGTGGCAGTGTGGCCAAGTATTTCC  
CTGGCCGCGCCTTAGTCCAGAATCTTCTGCACTCCGTGAATGAATGGCTCAAGAGGCAGAAGAGAAATAAAATTC  
CCTACAGTTTCTTTAAACTGCCCTGGACGACAGGAAAGAGGGTGCCGTTCTTGCCAAGAAGGTGAAGTGGATTG  
GCTGCCAGGGAGTGAGCCGATTTCCGGGCTTTCCCTGCTCCCTGTGGGTCTCTTCCACTTCTTGAGTCTG  
AGGCAGCTCGGCAAAATGTAGACCACTCACAGGAAGCAGCCAAGGCCAAGGAGGTCTCCAGCCATCCGAGGCT  
ACGTGCACTACTTCTTCGGCTGCCGAGACTGCGCTAGCCACTTCGAGCAGATGGCTGCTGCCTCCATGCACCGGG  
TGGGGAGTCCCAACGCGCTGTCTCTGGCTCTGGTCTAGCCACAACAGGGTCAATGCTCGCCTTGCAAGTGCCC  
CCAGCGAGGACCCCAAGTTCCCCAAGGTGCAGTGGCCACCCCGTGAACCTTGTCTGCTGCCACATGAACGCC  
TGGATGTGCCCGTGTGGGACGTGGAAGCCACCCTCAACTTCTCAAGGCCCACTTCTCCCCAAGCAACATCATCC  
TGGACTTCCCTGCAGCTGGGTGAGTGTCCCGGAGGGATGTGCAGAAATGTGGCAGCCGCCCCAGAGCTGGCGATGG  
GAGCCCTGGAGCTGGAAGCCGGAATCAACTCTGGACCCTGGGAAGCCTGAGATGATGAAGTCCCCACAAACA  
CCACCCACATGTGCCGGCTGAGGGACCTGAGGCAAGTCGACCCCGAAGCTGCACCCTGGCCTCAGAGCTGCAC  
CAGGCCAGGAGCTCCTGAGCACATGGCAGAGCTTCAGAGGAATGAGCAGGAGCAGCCGCTTGGGCAGTGGCACT  
TGAGCAAGCGAGACACAGGGGCTGCATTGCTGGCTGAGTCCAGGGCTGAGAAGAACCCTCTGGGGCCCTTTGG  
AGGTGAGGCGCGTGGGCCGAGCTCCAAGCAGCTGGTGCACATCCCTGAGGGCCAGCTGGAGGCCCCAGCTGGAC  
GGGGCCGAGGCGAGTGGCTGCAGGTGCTGGGAGGGGCTTCTCTTACCTGGACATCAGCCTCTGTGTGGGCTCT  
ATTCCCTGTCTTCATGGGCTGCTGGCCATGTACACCTACTTCCAGGCCAAGATAAGGGCCCTGAAGGGCCATG  
CTGGCCACCCTGCAGCTGTAACACCTGGGGAGGAGGCGGGAGAGGGAGCTGCCATCTCTAGGCACCTCAAGCCC  
CCTGACCCCATTCCTCCCCCTCCACCCCTTGCTCCTTGTCTGGCCTAGAAGTGTGGGAAATTGAGGAAACGAG  
TTGCTCCAGTGAAGCTTCTTGGGGTTGCTAGGACAGAGAGCTCCTTTGACACAAAAGACAGGAGCAGGGTCCAGG  
TTCCCTGCTGTGCAGGAGGGCAGCCCCGGGCGAGTGGGCATAGGGCAGCTCAGTCCCTGGCCTCTTAGCACCAC  
ATTCTGTTTTTCAGCTTATTTGAAGTCTGCTCATTTCTCACTGGAGCCTCAGTCTCTCTGCTTGGTCTTGGC  
CCTCAACTGGGGCAAGTGAAGCCAGAGGAGGTCCCCAGCTGGGTGGGCTGGAATGGAAGTCTCACTAGCTGC  
TGGGGCTCCGCCCCACCCTGCTCCCTTCCGGACAATGAAGAAGCCTTTGCACCCTGGGAGGAAGGACCACCCCGG  
CCCTCTATGCCTGGCCAGCCTCCAGCTCCTCAGACCTCCTGGGTGGGGTTTGGCTTCAGGGTGGGGTTTGAAGC  
TTCTGGAAGTCGTGCTGGTCTCCAGGTGAGGCAAGCCATGGTTGCTGGGCTGTAGGGTGAGTGGCTTGCTTGGT  
GGGACCTGACGAGTTGGTGGCATGGGAAGGATGTGGGTCTTAGTGCCTTGCCCTGGCTTAGCTGCAGGAGAAGA  
TGGCTGCTTTCACTTCCCCCATTGAGCTCTGCTCCCTCTGAGCCTGGTCTTTTGTCTTTTATTTTGGTCTC  
CAAGATGAATGCTCATCTTTGGAGGGTGCCAGGTAGAAGCTAGGGAGGGGAGTGTCTTCTCTCCAGGTTTCAC  
CTTCCAGTGTGCAGAAGTTAGAAGGGTCTGGCGGGGCGAGTGCCTTACACATGCTTGATTCCACGCTACCCCT  
GCCTTGGGAGGTGTGTGAATAAATTATTTTGTAAAGGCA

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**FIGURE 212**

MRRCSGSGPPPSLLLLLLWLLAVPGANAAPRSALYSPSDPLTLLQADTVRGAVLGSRSAWAV  
EFFASWCGHCIAFAPTWKALAEDVKAWRPALYLAALDCAEETNSAVCRDENIPGFPTVRFFKA  
FTKNGSGAVFPVAGADVQTLRERLIDALESHHDTWPPACPPLEPAKLEEIDGFFARNNEEYLA  
LIFEKGGSYLGREVALDLSQHKGVAVRRVLNTEANVVRKFGVTDFPSCYLLFRNGSVSRVPVL  
MESRSFYTAYLQRLSGLTREAAQTTVAPTANKIAPTVMWKLADRSKIYMADLESALHYILRIE  
VGRFPVLEGQRLVALKKFVAVLAKYFPGRPLVQNFLHSVNEWLKRQKRNKIPYSFFKTALDDR  
KEGAVLAKKVNWIGCQGSEPHFRGFPCSLWVLFHFLTQAAQNVVDHSQEAAKAKEVLPAIRG  
YVHYFFGCRDCASHFEQMAAASMRVGGSPNAAVLWLWSSSHNRVNARLAGAPSEDPOFPKVQWP  
PRELCSACHNERLDVPVWDVEATLNLKAFHSPSNIILDFFAAGSAARRDVQNVAAAPELAMG  
ALELESRNSTLDPGKPEMMKSPTNTTPHVPAGPEASRPPKLHPGLRAAPGQEPPEHMAELQR  
NEQEQPLGQWHLKRDGTGAALLAESRAEKNRLWGPLEVRRVGRSSKQLVDIPEGQLEARAGRG  
RGQWLQVLGGGFSYLDISLCVGLYSLSFMGLLAMTYTFQAKIRALKGHAGHPAA

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 705-728

**N-glycosylation sites.**

amino acids 130-134, 243-247, 575-579

**Glycosaminoglycan attachment site.**

amino acids 6-10

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 644-648

**N-myristoylation sites.**amino acids 52-58, 56-62, 196-202, 381-387, 392-398, 448-454,  
468-474, 684-690, 702-708**Cytochrome c family heme-binding site signature.**

amino acids 509-515

**Thioredoxin family proteins**

amino acids 62-78



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**FIGURE 213**

GCACGAGGCCGACTTCCAGACCATCTACAACTGCACGGCCTGGAACAGCTTCGGCTCCGACAC  
TGAGATCATCCGGCTCAAGGAGCAAGGTTTCGGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGA  
GTCTGTGCCGATGGCCGTCATCATTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCCTCGTCCT  
TATGGCAACCATCGTGGCGTTCGTGTGCCCCTTCCCAGAGAAATCTCAAAGGTGTTGTGTC  
AGCCAAAATGATATCCGAGTGGAAATTGTCCACAAGGAACCAAGCCTCTGGTCGGGAGGGTGA  
GGAGCACTCCACCATCAAGCAGCTGATGATGGACCGGGGTGAATTCCAGCAAGACTCAGTCCT  
GAAACAGCTGGAGGTCCTCAAAGAAGAGGAGAAAGAGTTTCAGAACCTGAAGGACCCACCAA  
TGGCTACTACAGCGTCAACACCTTCAAAGAGCACCCTCAACCCCGACCATCTCCCTCTCCAG  
CTGCCAGCCCGACCTGCGTCCTGCGGGTAAGCAGCGTGTGCCACAGGCATGTCCTTCACCAA  
CATCTACAGCACCCTGAGCGGCCAGGGCCGCTCTACGACTACGGGCAGCGGTTTGTGCTGGG  
CATGGGCAGCTCGTCCATCGAGCTTTGTGAGCGGGAGTTCAGAGAGGCTCCCTCAGCGACAG  
CAGTCCTTCCTGGACACGCAGTGTGACAGCAGCGTCAGCAGCAGCGGCAAGCAGGATGGCTA  
TGTGCAGTTCGACAAGGCCAGCAAGGCTTCTGCTTCCTCCTCCCACCACTCCCAGTCCTCGTC  
CCAGAACTCTGACCCCAGTCGACCCCTGCAGCGGCGGATGCAGACTCACGTCTTAAGGATCACA  
CACCGCGGGTGGGGACGGGCCAGGGAAGAGGTCAGGGCACGTTCTGGTTGTCCAGGGACGAGG  
GGTACTTTGCAGAGGACACCAGAATTGGCCACTTCCAGGACAGCCTCCCAGCGCCTCTGCCAC  
TGCCTTCCTTCGAAGCTCTGATCAAGCACAAATCTGGGTCCCCAGGTGCTGTGTGCCAGAGGT  
GGGCGGGTGGGGAGACAGACAGAGGCTGCGGCTGAGTGCCTGTGCTTAGTGCTGGACACCCG  
TGTCCCCGGCCCTTTCCTGGAGGCCCTCTACCACCTGCTCTGCCCACAGGCACAAGTGGCAG  
CTATAACTCTGCTTTCATGAACTGCGGTCCACTCTCTGGTCTCTCTGTGGGCTCTACCCCTC  
ACTGACCACAAGCTCTACCTACCCCTGTGCCTGTGCTCCCATACAGCCCTGGGGAGAAGGGGA  
TGACGTCTTCCCAGCACTGAGCTGCCCCAGAAACCCCGGCTCCCCACTGCTGCTCATAGCCCA  
TACCCTGGAGGCTGACAAGCCAGAAATGGCCTTGGCTAAAGGAGCCTCTCTCTCACCAGGCTG  
GCCGGGAGCCACCCCAATTTGTTTTGGTGTGTTTGTGTCCATACTCTTGCACTTCTGTCTTG  
GACTTGATGCCGCTGAACTCTGCGGTGGGACCGGTCCCGTCAGAGCCTGGTGTACTGGGGGA  
GGGAGGGAGGAGGGAGCCTGTGCTGACGGAGCACCTCGCCGGGTGTGCCCCCTCCTGGGCTGTG  
TGACCCAGCCTCCCCACCCACCTCCTGCTTTGTGTACTCCTCCCCTCCCCCTCAGCACAATC  
GGAGTTCATATAAGAAGTGCGGGAGCTTCTCTGGTCAGGGTTCTCTGAACACTTATGGAGAGA  
GTGCTTCCTGGGAAGTGTGGCGTTTGAAGGGGCTGGAGGGCAGGTCTTTAAGATGGCGAGACT  
GCCCTTCTCAGCTGATAAACACAAGAACGGCGATCCTGTCTTCAGTAAGGCTCCACGAGAAGA  
GAGGAAGTATATCTACACCTCAACCCCTCCTAGTCACCACCTGAAATAAATGTTAGGGAAAAAAA

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**FIGURE 214**

MAVIIGVAVGAGVAFLVLMATIVAFCCARSQRNLKGVVSAKNDIRVEIVHKEPASGREGEEHS  
TIKQLMMDRGEFQQDSVLKQLEVLKEEEKEFQNLKDPTNGYYSVNTFKEHHSTPTISLSSCQP  
DLRPAGKQRVPTGMSFTNIYSTLSGQGRLYDYGQRFVLGMGSSSIELCEREFQRGSLSDSSSF  
LDTQCDSSVSSSGKQDGYVQFDKASKASASSSHHSQSSSQNSDPSRPLQRRMQTHV

**Signal peptide:**

amino acids 1-28

**Glycosaminoglycan attachment site.**

amino acids 150-154

**N-myristoylation sites.**

amino acids 6-12, 10-16, 36-42, 139-145, 165-171

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 114-125

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**FIGURE 215**

CAGCCTTCCTCCCCAGCCTGAGTGA CTACTCTATTCCCTTGGTCCCTGCTATTGTCGGGGACG  
ATTGCAATGGGCTACGCCAGGAAAGTAGGCTGGGTGACCGCAGGCCTGGTGATTGGGGCTGGCG  
CCTGCTATTGCATTTATAGACTGACTAGGGGAAGAAAACAGAACAAAGGAAAAAATGGCTGAGG  
GTGGATCTGGGGATGTGGATGATGCTGGGGACTGTTCTGGGGCCAGGTATAATGACTGGTCTG  
ATGATGATGATGACAGCAATGAGAGCAAGAGTATAGTATGGTACCCACCTTGGGCTCGGATTG  
GGACTGAAGCTGGAACCAGAGCTAGGGCCAGGGCAAGGGCCAGGGCTACCCGGGCACGTCGGG  
CTGTCCAGAAACGGGCTTCCCCCAATTCAGATGATACCGTTTTGTCCCCTCAAGAGCTACAAA  
AGGTTCTTTGCTTGGTTGAGATGTCTGAAAAGCCTTATATTCTTGAAGCAGCTTTAATTGCTC  
TGGGTAACAATGCTGCTTATGCATTTAACAGAGATATTATTCGTGATCTGGGTGGTCTCCCAA  
TTGTCGCAAAGATTCTCAATACTCGGGATCCCATAGTTAAGGAAAAGGCTTTAATTGTCCTGA  
ATAACTTGAGTGTGAATGCTGAAAATCAGCGCAGGCTTAAAGTATACATGAATCAAGTGTGTG  
ATGACACAATCACTTCTCGCTTGAACCTCATCTGTGCAGCTTGCTGGACTGAGATTGCTTACAA  
ATATGACTGTTACTAATGAGTATCAGCACATGCTTGCTAATTCCATTTCTGACTTTTTTCGTT  
TATTTTCAGCGGGAAATGAAGAAACCAAACCTTCAGGTTCTGAAACTCCTTTTGAATTTGGCTG  
AAAATCCAGCCATGACTAGGGAACTGCTCAGGGCCCAAGTACCATCTTCACTGGGCTCCCTCT  
TTAATAAGAAGGAGAACAAAGAAGTTATTCTTAAACTTCTGGTCATATTTGAGAACATAAATG  
ATAATTTCAAATGGGAAGAAAATGAACCTACTCAGAATCAATTGCGTGAAGGTTCACTTTTTT  
TCTTTTTTAAAAGAATTTCAAGTGTGTGCTGATAAGGTTCTGGGAATAGAAAGTCACCATGATT  
TTTTGGTGAAAGTAAAAGTTGGAAAATTCATGGCCAACTTGCTGAACATATGTTCCCAAAGA  
GCCAGGAATAAACACCTTGATTTTGTAAATTTAGAAGCAACACACATTGTAAACTATTCAATTTT  
TCCACCTTGTTTATATGGTAAAGGAATCCTTTCAGCTGCCAGTTTTGAATAATGAATATCATA  
TTGTATCATCAATGCTGATATTTAACTGAGTTGGTCTTTAGGTTTAAAGATGGATAAATGAATA  
TCACTACTTGTCTGAAAACATGTTTGTTGCTTTTTATCTCGCTGCCTAGATTGAAATATTTT  
GCTATTTCTTCTGCATAAGTGACAGTGAACCAATTCATCATGAGTAAGCTCCCTTCTGTCATT  
TTCATTGATTTAATTTGTGTATCATCAATAAAATTGTATGTTAATGCTGGAAAGA

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**FIGURE 216**

MGYARKVGWVTAGLVIGAGACYCIYRLTRGRKQNKEMAEGGSGDVDDAGDCSGARYNDWSDD  
DDDSNESKSIVWYPPWARIGTEAGTRARARARARATRRARRAVQKRASPNSDDTVLSPQELQKV  
LCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKALIVLNN  
LSVNAENQRRLLKVYMNQVCDDTITSRLNSSVQLAGLRLLTNMTVTNEYQHMLANSISDFFRLF  
SAGNEETKLQVLKLLLNLAE NPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIFENINDN  
FKWEENEPTQNQFGEGSLFFFLKEFQVCADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPSQE

**Signal peptide:**

amino acids 1-20

**N-glycosylation sites.**

amino acids 68-72, 189-193, 217-221, 230-234

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-111

**N-myristoylation sites.**amino acids 13-19, 17-23, 19-25, 54-60, 83-89, 147-153, 255-261,  
290-296**Amidation site.**

amino acids 29-33



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**FIGURE 218**

MAIAQLATEYVFSDFLLKEPTEPKFKGLRLELAVDKMVTCTIAVGLPLLLISLAFQAQEISIGTQ  
ISCFSPSSFSWRQA AFVDSYCWA AVQQKNSLQSESGNLPLWLHKFFPYILLF AILLYLPPLF  
WRFAAAPHICSDLKFIMEELDKVYNRAIKA AKSARDLDMRDGACSVPGVTENLGQSLWEVSES  
HFKYPIVEQYLKTKKNSNNLI IKYISCRLLTLIIILLACIYLGYYFSLSSLSDEFVCSIKSGI  
LRNDSTVPDQFQCKLIAVGIFQLLSVINLVVYVLLAPVVVYTLFVPFRQKTDVLKVYEILPTF  
DVLHFKSEGYNDLSLYNLFLEENISEVKS YKCLKVLENIKSSGQGIDPMLLLTNLGMIMD VV  
DGKTPMSAEMREEQGNQTAE LQGMNIDSETKANNGEKNARQRLDSSC

**Transmembrane domains:**

amino acids 37-55, 108-126, 216-232, 273-290

**N-glycosylation sites.**

amino acids 255-259, 338-342, 394-398

**Glycosaminoglycan attachment site.**

amino acids 357-361

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 203-207

**N-myristoylation sites.**

amino acids 61-67, 174-180, 251-257, 393-399

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 218-229

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**FIGURE 219**

CTGTGAGTGACACACGCTGAGTGGGGTGAAGGGAAATGCTGGTGAATTTTCATTTTGAGGTGTG  
GGTTGCTGTTAGTCACTCTGTCTCTTGCCATTGCCAAGCACAAGCAATCTTCCTTCACCAAAA  
GTTGTTACCCAAGGGGAACATTGTCCCAAGCTGTTGACGCTCTCTATATCAAAGCAGCATGGC  
TCAAAGCAACGATTCCAGAAGACCGCATAAAAAATATACGATTATTA AAAAAGAAAACAAAAA  
AGCAGTTTATGAAAACTGTCAATTTCAAGAACAGCTTCTGTCCTTCTTCATGGAAGACGTTT  
TTGGTCAACTGCAATTGCAAGGCTGCAAGAAAATACGCTTTGTGGAGGACTTTCATAGCCTTA  
GGCAGAAATTGAGCCACTGTATTTCTGTGCTTCATCAGCTAGAGAGATGAAATCCATTACCA  
GGATGAAAAGAATATTTTATAGGATTGGAAACAAAGGAATCTACAAAGCCATCAGTGAAGTGG  
ATATTCTTCTTTCTGGATTAAAAAATTATTGGAAAGCAGTCAGTAAACCAAAGCCAAGTACA  
TTGATTTTACAGTTATTTTGAAATACAATAAGAACTGCTAGAAATATGTTTATAACAGTCTAT  
TTCTTTTAAAACTTTTAAACATAATACTGACGGCATGTTAGGTGATTCAGAATAGACAAGAA  
GGATTTAGTAAATTAACGTTTTGGATATAAGTTGTCACTAATTGCACATTTTCTGTGTTTTC  
AAATAATGTTTCCATTCTGAACATGTTTTGTCATTCACAAGTACATTGTGTCAACTTAATTTA  
AAGTATGTAACTGAATTAACCTCGTGTAAATATTTGTGTGTGGAGTGGGATGTGGGGGGTGGAG  
GGGGAATGACAGATTTCTGGAATGCAATGTAATGTTACTGAGACTTAAATAGATGTTATGTAT  
ATGATTGTCTGTTTAAGTGTGTTGAAAATTGTTAATTATGCCCAGTGTGAACTTAGTACTTAAC  
ACATTTTGATTTTAATTAAATAAATTGGGTTTCTCTCAAAAAAAAAAAAAAAAAAAAAA  
AAAAA

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**FIGURE 220**

MLVNFILRCGLLLVTLSLAIAKHKQSSFTKSCYPRGTL SQAVDALYIKA AAWLKATIPEDRIKN  
IRLLKKKTKKQFMKNCQFQEQLLSFFMEDVFGQLQLQGCKKIRFVEDFHSLRQKLSHCISCAS  
SAREMKSITRMKRIFYRIGNKGIYKAISELDILLSWIKKLESSQ

**Signal sequence:**

amino acids 1-21

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 68-71

**N-myristoylation site.**

amino acids 148-153

**Interleukin-10 proteins.**

amino acids 58-94, 74-102, 128-170



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**FIGURE 221**

GACCACGGCCCTGCGCCCCAGCCAGGCCTGAGGACATGAGGCGGCCGGCGGGTGCCGCTCC  
TGCTGCTGCTGTGTTTTGGGTCTCAGAGGGCCAAGGCAGCAACAGCCTGTGGTCGCCCCAGGA  
TGCTGAACCGAATGGTGGGCGGGCAGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTCAGCA  
TCCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAGTGGGTCTTGACGG  
CTGCGCACTGCTTCCGCAACACCTCTGAGACGTCCCTGTACCAGGTCTTGCTGGGGGCAAGGC  
AGCTAGTGCAGCCGGGACCACACGCTATGTATGCCCCGGTGAGGCAGGTGGAGAGCAACCCCC  
TGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGGTGGAGCTGGAGGCACCAGTGCCCT  
TCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCCCTCGGTGATCTTTGAGACGGGCATGA  
ACTGCTGGGTCACTGGCTGGGGCAGCCCCAGTGAGGAAGACCTCCTGCCCCGAACCGCGGATCC  
TGCAGAAACTCGCTGTGCCCATCATCGACACACCCAAGTGCAACCTGCTCTACAGCAAAGACA  
CCGAGTTTGGCTACCAACCCAAAACCATCAAGAATGACATGCTGTGCGCCGGCTTCGAGGAGG  
GCAAGAAGGATGCCTGCAAGGGCGACTCGGGCGGGCCCCCTGGTGTGCCTCGTGGGTCAAGTCGT  
GGCTGCAGGCGGGGGTGATCAGCTGGGGTGAGGGCTGTGCCCCGCCAGAACCGCCCAGGTGTCT  
ACATCCGTGTCACCGCCCCACCACAACCTGGATCCATCGGATCATCCCCAACTGCAGTTCCAGC  
CAGCGAGGTTGGGCGGCCAGAAGTGAGACCCCCGGGGCCAGGAGCCCCCTTGAGCAGAGCTCTG  
CACCAGCCTGCCCCGCCACACCATCCTGCTGGTCTCTCCAGCGCTGCTGTTGCACCTGTGAG  
CCCCACCAGACTCATTTGTAAATAGCGCTCCTTCCTCCCCTCTCAAATACCCTTATTTTATTT  
ATGTTTCTCCAATAAAAACCCAGCCTGTGTGCCAGCTGAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 222**

MRRPAAVPLLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFCGGS  
LIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSADVA  
LVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDTP  
KCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEG  
CARQNRPGVIYIRVTAHHNWIHRIIPKLQFQPARLGGQK

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 55-58, 79-82

**Casein kinase II phosphorylation sites.**

amino acids 121-124, 165-168, 167-170, 248-251

**Tyrosine kinase phosphorylation sites.**

amino acids 78-86, 197-203

**N-myristoylation sites.**

amino acids 16-21, 37-42, 56-61, 62-67, 118-123

**Amidation site.**

amino acids 219-222

**Serine proteases, trypsin family, histidine active site.**

amino acids 71-76

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**FIGURE 223**

CAAGATGTGGACAGCTCTTGTGCTCATTGATTTTCTCCTTGTCTTATCTGAAAGCCATGC  
GGCATCCAACGATCCACGCAACTTTGTCCCTAACAAAATGTGGAAGGGATTAGTCAAGAGGAA  
TGCATCTGTGGAAACAGTTGATAATAAAACGTCTGAGGATGTAACCATGGCAGCAGCTTCTCC  
TGTACATTGACCAAAGGGACTTCGGCAGCCCACCTCAACTCTATGGAAGTCACAACAGAGGA  
CACAAGCAGGACAGATGTGAGTGAACCAGCAACTTCAGGAGTTGCAGCTGATGGTGTGACCTC  
CATTGCTCCACGGCTGTGGCCTCCAGTACGACTGCGGCCTCCATTACGACTGCGGCCTCCAG  
TATGACTGTGGCCTCCAGTGCTCCACGACTGCAGCCTCCAGTACAACCTGTGGCCTCCATTGC  
TCCCACGACTGCAGCCTCCAGTATGACTGCGGCCTCCAGCACTCCCATGACACTTGCAGCTCCC  
CGCGCCACGTCCACTTCCACAGGGCGGACCCCGTCCACTACCGCCACTGGGCATCCATCTCT  
CAGCACAGCCCTCGCACAAAGTGCCAAAGAGCAGCGCGTTGCCAAGAACAGCAACCCTGGCCAC  
ATTGGCCACACGTGCTCAGACTGTAGCGACCACAGCAAACACAAGCAGCCCCATGAGCACTCG  
TCCAAGTCCTTCCAAGCACATGCCCAGTGACACCGCGGCAAGCCCTGTACCCCTATGCGTCC  
CCAAGCACAAGGTCCCATTAGCCAGGTGTCAGTGGACCAGCCTGTGGTTAACACAACAAATAA  
ATCCACACCCATGCCCTCAAACACAACCCAGAGCCCGCCCCACCCCCACAGTGGTGACCAC  
CACCAAGGCACAAGCCAGGGAGCCAACTGCCAGCCCAGTGCCAGTACCTCACACCAGCCCAAT  
CCCTGAGATGGAGGCCATGTCCCCACGACACAGCCAAGCCCCATGCCATATACCCAGAGGGC  
CGCTGGGCCAGGCACATCCCAGGCACCGGAGCAGGTAGAGACTGAAGCCACACCAGGTACTGA  
TTCCACTGGGCCAACACCCAGGAGCTCAGGGGGCACTAAGATGCCAGCCACGGACTCGTGCCA  
GCCCAGCACCCAAGGCCAGTACATGGTGGTCACCACTGAGCCCCTCACCCAGGCCTGGTAGA  
CAAACTCTCCTTCTGGTGGTGTGTTACTCGGGGTGACCCTTTTCATCACAGTCTTGGTTTT  
GTTTGCCCTGCAGGCCTATGAGAGCTACAAGAAGAAGGACTACACCCAGGTGGACTACTTAAT  
CAACGGGATGTATGCGGACTCAGAAATGTGAGGGGGGGCGGGGGCCTGGCGGGAGGCCTGGCCC  
CTTCCTCGTCCTTTCTTTTGCCCTTGAGACCAAACCAAGTGCTTCCAAATTCTTTTGGTGCA  
ATTGAGGAGATATGCCAGATGCTTAAACACATTTAATTGCTGTCAGATTAATTCCATGATCAC  
TAAAGAGTTGCTGCTTTTTTTCATATTTATTTTGTAAATGATTCTGTGCCAGGAGCAGCTGG  
GGGTTCCACCTCAGGGTGGGGCGGGCAGGACCCCGTCTCCCCAGGTGTCGGAGCCTGACCTGA  
ATTAAAGTACTGACTGCTCGCCA

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**FIGURE 224**

MWTALVLIWIFSLSLSESHAASNDPRNFVPNKMWGLVKRNASVETVDNKTS EDVTMAAASP  
V  
TLTKGTSAAHLNSMEVTTEDTSRTDVSEPATSGVAADGVTSIAPTAVASSTTAASITTAASSM  
TVASSAPTTAASSTTVASIAPTTAASSMTAASSTPMTLALPAPTSTSTGRTPSTTATGHPSLS  
TALAQVPKSSALPRTATLATLATRAQTVATTANTSSPMSTRPSPSKHMPSDTAASPVPMPRPQ  
AQGPISQVSVDQPVVNTTNKSTPMPSNTTPEPAPTPTVVTTTKAQAREPTASPVVPHTSPIP  
EMEAMSPTTQSPMPYTQRAAGPGTSQAPEQVETEATPGTDSTGPTPRSSGGTKMPATDSCQP  
STQGQYMVVTTEPLTQAVVDKTL LLLVLLLVLLGVTLFITVLVLFALQAYESYKKKDYTQVDYLIN  
GMYADSEM

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 396-420

**N-glycosylation sites.**

amino acids 41-44, 49-52, 222-225, 268-271, 271-274

**Casein kinase II phosphorylation sites.**

amino acids 14-17, 51-54, 80-83, 85-88, 280-283, 434-437

**N-myristoylation sites.**

amino acids 68-73, 354-359

**Aldo/keto reductase family putative active site signature.**

amino acids 195-210

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**FIGURE 225**

GGAAGGCGCTCAAGGTGCGCGGCCCGGGGCGCGCTACTGGGGGCGCCCTCCGCGGTGGGCAGC  
GCGCCAGGGATCGGCCTGGGCAGCCGCGGGGCGCGCGAAGGCTGCGCTTTCCCTACGGCCCCC  
CTCGCTTCCTCCGGCACGGCGGCAACGGAGATTTCTCTCGGGGAACTACGCGGATCCTTTT  
CGGGGATCCTCGCCCCGCCAGTTCTCCGCCCCCTCCCCTTTGCTGGGGCGCCTGGGCTGGC  
CCGCGCAGGGGAGGAGGCTCTGGCAGCCTGGGCAGGAGGCGGGGGGGCCGCGGAGCCGCT  
GGCCATCGATTCTCCCCGCCATGTGACGCCGTCTTAGCCCTGCGACCCCCAGCGGTCCCGG  
GCCTGCGCCTCCGCCCCGCCGCGCAGCGCACGATGCTTCTGCCGGGACGCGCACGCCAACCGC  
CGACGCCCCAGCCCGTGCAGCATCCCGGCCTCCGCCGGCAGGTAGAGCCGCCGGGGCAGCTCC  
TGCGCCTCTTCTACTGCACTGTCTGGTCTGCTCCAAAGAGATCTCAGCGCTCACCGACTTCT  
CTGGTTACCTAACCAAACCTCCTGCAAACACACCACCTATGCCTGTGATGGGGACTATTTGA  
ATCTACAGTGCCCTCGGCATTCTACGATAAGTGTCCAATCGGCATTTTATGGGCAAGATTACC  
AAATGTGTAGTTCCCGAAGCCTGCCTCCAGAGGGAAGACAGCTTAACCTGTGTGGCAGCCA  
CCACCTTCCAGAAGGTGCTGGACGAATGCCAGAACCAGCGGGCCTGCCACCTCCTGGTCAATA  
GCCGTGTTTTTGGACCTGACCTTTGTCCAGGAAGCAGTAAATACCTCCTGGTCTCCTTTAAAT  
GCCAACCTAATGAATTAAAAACAAAACCGTGTGTGAAGACCAGGAGCTGAAACTGCACTGCC  
ATGAATCCAAGTTCCTCAACATCTACTCTGCGACCTACGGCAGGAGGACCCAGGAAAGGGACA  
TCTGCTCCTCCAAGGCAGAGCGGCTCCCCCCTTTCGATTGCTTGTCTTACTCAGCTTTGCAAG  
TCCTATCCCGAAGGTGCTATGGGAAGCAGAGATGCAAAATCATCGTCAACAATCACCATTTTG  
GAAGCCCCTGTTTGCCAGGCGTGAAAAATACCTCACTGTGACCTACGCATGTGTTCCCAAGA  
ACATACTCACAGCGATTGATCCAGCCATTGCTAATCTAAACCTTCTTTGAAGCAGAAAGATG  
GTGAATATGGTATAAACTTCGACCCAAGCGGATCGAAGGTTCTGAGGAAAGATGGAATTCTTG  
TTAGCAACTCTCTGGCAGCCTTTGCTTACATTAGAGCCCACCCAGAGAGAGCTGCCCTGCTGT  
TCGTGTCCAGTGTCTGCATCGGCCTGGCCCTCACACTGTGCGCCCTGGTCATCAGAGAGTCCT  
GTGCCAAGGACTTCCGCGACTTGACAGCTGGGGAGGGAGCAGCTGGTGCCAGGAAGTGACAAGG  
TCGAGGAGGACAGCGAGGATGAAGAAGAGGAGGAGGACCCCTCTGAGTCTGATTTCCAGGGG  
AACTGTGGGGTTCTGTAGGACTTCATATCCTATATACAGTTCCATAGAAGCTGCAGAGCTCG  
CAGAAAGGATTGAGCGCAGGGAGCAAATCATTCAGGAAATATGGATGAACAGTGGTTTGGACA  
CCTCGCTCCCAAGAAACATGGGCCAGTTCTACTGAAAACACATGCATCTTGATGCGATCGCA  
CTTTCTGAAGAAGGAAGGATCCCAAATGCCCCCTCAGTTCTGGTTCACCTGTACCTTCTATGA  
AGGAGAATTCGTATGTCATTCAACACTCGTGAGGCCAGGAAGCTATTAAAGGGATGTTTCAA  
GCTGTTTCTAGCACATTCCAAAATAAATGAGGAGGGAGGAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

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**FIGURE 226**

MLLPGRARQPPTPQPVQHPGLRRQVEPPGQLLRLFYCTVLVCSKEISALTDGSGYLTKLLQNH  
TTYACDGDYLNLCQPRHSTISVQSAFYQGQDYQMCSSQKPASQREDSLTCVAATTFQKVLDECQ  
NQRACHLLVNSRVFGPDLCPGSSKYLVSFKCQPNELKNKTVCEDQELKLHCHESKFLNIYSA  
TYGRRTQERDICSSKAERLPPFDCLSYALQVLSRRCYGKQRCKIIVNNHHFGSPCLPGVKKY  
LTVTYACVPKNILTAIDPAIANLKPSLKQKDGEYGINFDPGSKVLRKDGILVSNLAAAFAYI  
RAHPERAALLFVSSVCIGLALTLCALVIRESCAKDFRDLQLGREQLVPGSDKVEEDSEDEEEE  
EDPSESDFPGELSGFCRTSYPIYSSIEAAELAERIERREQIIQEIWMNSGLDTSLPRNMGQFY

**Transmembrane domains:**

amino acids 32-49, 322-343

**N-glycosylation sites.**

amino acids 62-66, 165-169

**Tyrosine kinase phosphorylation site.**

amino acids 280-287

**N-myristoylation site.**

amino acids 302-308, 333-339, 428-434

**Amidation site.**

amino acids 191-195

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**FIGURE 227**

GGCACGAGGTGGAAGGGCTTTTACAAACAGATTGCTGGCCCCACCCCCAGAATTTCTCATCA  
GGAGTGGGCAAGACCAATCATTTGCATTTCTGACAAGTTCCCAGGAGCTGCAGCTGCTGGCCC  
TGGAACCACACTTTGAGAACCACTGCTTTAGACCAAACACCAAAGGAAGATGCAGCCACCCCTC  
CTTTACATGTACAAACGCTCAGGGTCCATGAGTACCTCAGGCTGTCCAGCTGAGCTCCACCTG  
CAGCAGCCGAGATTCCCGACTCGCTCCACCATTGGGGGCTAGGAGTGAAGCGTGTCAACCATGG  
TCAGCTCATGGCCAGCCAGGAAAGCCTCTCTGCTGTGCGTCTGTGCAGTTCTTGTTCTTCCCT  
GGAGGACTCTTGGATCGCCTGTGATCTTGGCCAGGAGACCAGGTGCCTGGGTCCCTTCCTGGA  
AGGGGACAAGTTACACACCCCGAGCCCCATTTTCCCACTTCTACATGCCTTGGGAGAACC  
TTCTACATGTTGGCTGCCCCCTTCCCCTATTTAGCAGTGCCCAGTCCTGCTTATAAACCTGA  
GGCCTGCTCCCCATACCTTCCCTGTGCAAGTGCCAGCCGTTATTCCAGGCAGCCCAATGTTGT  
TGAGGCCAGATGGATTCTGGAAGCAGCTGGCCCATGGATGTGAGTCAACAGTATTCTAGA  
AACAGAGAAGAGGTCTTAACCTAATGCGCATAGAGAAATTGTTCTCATTGTAAACATACCCCT  
GTCCTTAGCTGATCTAGGTGGAAGCCCAGCTTCATGTGCTAGGGGGCATGATAATGATAATAA  
AGGAATTGTATCTAGGACTAA

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**FIGURE 228**

MVSSWPARKASLLCVC AVL VLPWRTL GSPVILARRPGAWVPSWKGT SYTPQPHFPTNFYMPWE  
NLLHVGCPLPLFQQCPVLLINLRPAPHTFPVQVPAVIPGSPMLLRPDGFLEAAGPWM

**Signal peptide:**

amino acids 1-27

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 8-12



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**FIGURE 229**

GGGAAGGGATGCAAGGAAGCCCTCCGGCGCTGCGCTCCGAGGCGGGAGACAGCGTCCCGCTGA  
AAATGTGTGTCTGACATGCAAGCTCAGTGGGGCAGAGACCCGTGGATTGCTGTGCCCTGCCCT  
CCGGACCTGGATC**ATGA**AGGTGTTGGGAAGAAGCTTCTTCTGGGTGCTGTTTCCCGTCCTTCC  
CTGGGCGGTGCAGGCTGTGGAGCACGAGGAGGTGGCGCAGCGTGTGATCAAACCTGCACCGCGG  
GCGAGGGGTGGCTGCCATGCAGAGCCGGCAGTGGGTCCGGGACAGCTGCAGGAAGCTCTCAGG  
GCTTCTCCGCCAGAAGAATGCAGTCTGAACAACTGAAAACCTGCAATTGGAGCAGTGGAGAA  
AGACGTGGGCCTGTCGGATGAAGAGAACTGTTTCAGGTGCACACGTTTGAAATTTTCCAGAA  
AGAGCTGAATGAAAGTGAAGTCCGTTTTCCAAGCTGTCTACGGACTGCAGAGAGCCCTGCA  
GGGGGATTACAAAGATGTCGTGAACATGAAGGAGAGCAGCCGGCAGCGCCTGGAGGCCCTGAG  
AGAGGCTGCAATAAAGGAAGAAACAGAATATATGGAACCTTCTGGCAGCAGAAAAACATCAAGT  
TGAAGCCCTTAAAAATATGCAACATCAAAACCAAGTTTATCCATGCTTGACGAGATTCTTGA  
AGATGTAAGAAAGGCAGCGGATCGTCTGGAGGAAGAGATAGAGGAACATGCTTTTGACGACAA  
TAAATCAGTCAAGGGGGTCAATTTTGAGGCAGTTCTGAGGGTGGAGGAAGAAGAGGCCAATTC  
TAAGCAAAATATAACAAAACGAGAAGTGGAGGATGACTTGGGTCTTAGCATGCTGATTGACTC  
CCAGAACAACCAGTATATTTTGACCAAGCCCAGAGATTCAACCATCCCACGTGCAGATCACCA  
CTTTATAAAGGACATTGTTACCATAGGAATGCTGTCTTGCCTTGTGGCTGGCTATGTACAGC  
CATAGGATTGCCTACAATGTTTGGTTATATTATTTGTGGTGTACTTCTGGGACCTTCAGGACT  
AAATAGTATTAAAGTCTATTGTGCAAGTGGAGACATTAGGAGAATTTGGGGTGTTTTTTACTCT  
TTTTCTTGTTGGCTTAGAATTTTCTCCAGAAAAGCTAAGAAAGGTGTGGAAGATTTCCCTTACA  
AGGGCCGTGTTACATGACACTGTTAATGATTGCATTTGGCTTGCTGTGGGGGCATCTCTTGCG  
GATCAAACCCACGCAGAGCGTCTTCAATTCACGTGTCTGTCTTGTCAAGCACACCCCTCGT  
GTCCAGGTTCCCTCATGGGCAGTGTCTCGGGGTGACAAAGAAGGCGACATTGACTACAGCACCGT  
GCTCCTCGGCATGCTGGTGACGCAGGACGTGCAGCTCGGGCTCTTCATGGCCGTATGCCGAC  
TCTCATACAGGCGGGCGCCAGTGCATCTTCTAGCATTGTCTGTGGAAGTTCTCCGAATCCTGGT  
TTTGATTGGTCAGATTCTTTTTTCACTAGCGGCGGTTTTTCTTTTATGTCTTGTTATAAAGAA  
GTATCTCATTGGACCCTATTATCGGAAGCTGCACATGGAAAGCAAGGGGAACAAAGAAATCCT  
GATCTTGGGAATATCTGCCTTTATCTTCTTAATGTTAACGGTCACGGAGCTGCTGGACGTCTC  
CATGGAGCTGGGCTGTTTCCCTGGCTGGAGCGCTCGTCTCCTCTCAGGGCCCCGTGGTCACCGA  
GGAGATCGCCACCTCCATCGAACCCATCCGCGACTTCCTGGCCATCGTTTTCTTCGCCTCCAT  
AGGGCTCCACGTGTTCCCCACGTTTGTGGCGTACGAGCTCACGGTGCTGGTGTTTCTCACCTT  
GTCAGTGGTGGTGATGAAGTTTCTCCTGGCGGCGCTGGTCTGTCTCTCATTCTGCCGAGGAG  
CAGCCAGTACATCAAGTGGATCGTCTCTGCGGGGCTTGCCCAGGTGAGCGAGTTTTCTTTGT  
CCTGGGGAGCCGGGCGGAAGAGCGGGCGTCTCTCGGGAGGTGTACCTCCTTATACTGAG  
TGTGACCACGCTCAGCCTCTTGCTCGCCCCGGTGCTGTGGAGAGCTGCAATCACGAGGTGTGT  
GCCCAGACCGGAGAGACGGTCCAGCCTC**TGAT**GGCTCGGAGATGATGGACCGTGGAAGGGAAG  
CGTCTGTGGGGAGTGAGCGCTTAGATGGCCAGCAGTGTCTCTTCTGGGAAGCTCGCACCTTG  
GCAACAGAACAGCCCTCTAGCAGAGCGTCAGTGCAGTCGTGTTATCCCGGCTTTTACAGAATA  
TTCTTGTCCTATTTTAGAATTTTCCGGAGTAGTTTATTTGCAGTCTGTTGATTATGTGCAGTA  
GACCCGGGACACTGCGTTTTACCGATCACCTTGAATGTGGTGCCTGGATGTGCCTTTTTTTTT  
TTTCCCTGAAATTATTATTAATTTTCTATTGTGAGTTCATCAGTTCATAGTTTTTTTAGTAAA  
GAAGCAAAATTAAAAGGCTTTTAAAAATGTACAACCTTCAGAATTATAATCTGTTAGTCAAATA  
TTTGTTATTAAACATTTCTGTAATATGAAGTTGTAATCTGGCCGTGAGCTTGAAGCTTACT  
TTTGATTCTTAAAGCCTATGTTTTCTAAAATGAGACAAATACGGATGTCTATTTGCCTTTTTAT  
TGTAACCTTTAAATGAAATAATTTTCATGTCAATTTCTATTAGATATATCACTTAAATATTTG  
GTTTTAAATCACAAGAATATGTATTCTTTAATAAAGATAATTTATGATCATGGTAAAAA

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**FIGURE 230**

MKVLGRSFFWVLPVLPWAVQAVEHEEVAQRVIKLRGRGVAAMQSRQWVRDSCRKLSGLLRQ  
KNAVLNKLKTAIGAVEKDVGLSDEEKLQVHTFEIFQKELNESENSVFQAVYGLQRALQGDYK  
DVVNMKESSRQRLEALREAAIKEETEYMELLAAEKHQVEALKNMQHQNQSLSMLDEILEDVRK  
AADRLEEEIEEHAFDDNKSVMGVNFEAVLRVEEEEANSKQNTKREVEDDLGLSMLIDSQNNQ  
YILTKPRDSTIPRADHHFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLNSIK  
SIVQVETLGEFGVFFTLFLVGLFEFSPEKLRKVKISLQGPCYMTLLMIAFGLLWGHLLRIKPT  
QSVFISTCLSLSSSTPLVSRFLMGSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQA  
GASASSSIVVEVLRLILVLIGQILFSLAAVFLLCVVIKKYLIGPYRKLHMESSKGNKEILILGI  
SAFIFLMLTVTELLDVSMELGCFLAGALVSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHV  
FPTFVAYELTVLVFLTLVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQVSEFSFVLGSR  
ARRAGVISREVYLLILSVTTLSLLLAPVLWRAAITRCVPRPERRSSL

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**amino acids 282-304, 322-337, 354-370, 379-395, 445-474, 501-520,  
576-598, 641-660**N-glycosylation sites.**

amino acids 104-108, 174-178, 206-210, 230-234

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 55-59, 673-677

**Tyrosine kinase phosphorylation site.**

amino acids 407-414

**N-myristoylation sites.**amino acids 116-122, 327-333, 366-372, 401-407, 419-425, 429-435,  
442-448, 525-531, 530-536**Cell attachment sequence.**

amino acids 404-407

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**FIGURE 231**

GAGAAAAACAACAGGAAGCAGCTTACAACTCGGTGAACAACTGAGGGAACCAAACCAGAGAC  
GCGCTGAACAGAGAGAATCAGGCTCAAAGCAAGTGGAAGTGGGCAGAGATTCCACCAGGACTG  
GTGCAAGGCGCAGAGCCAGCCAGATTTGAGAAGAAGGCCAAAAGATGCTGGGGAGCAGAGCTG  
TAATGCTGCTGTTGCTGCTGCCCTGGACAGCTCAGGGCAGAGCTGTGCCTGGGGGCAGCAGCC  
CTGCCTGGACTCAGTGCCAGCAGCTTTCACAGAAGCTCTGCACACTGGCCTGGAGTGCACATC  
CACTAGTGGGACACATGGATCTAAGAGAAGAGGGAGATGAAGAGACTACAAATGATGTTCCCC  
ATATCCAGTGTGGAGATGGCTGTGACCCCCAAGGACTCAGGGACAACAGTCAGTTCTGCTTGC  
AAAGGATCCACCAGGGTCTGATTTTTTATGAGAAGCTGCTAGGATCGGATATTTTCACAGGGG  
AGCCTTCTCTGCTCCCTGATAGCCCTGTGGGCCAGCTTCATGCCTCCCTACTGGGCCTCAGCC  
AACTCCTGCAGCCTGAGGGTCACCACTGGGAGACTCAGCAGATTCCAAGCCTCAGTCCCAGCC  
AGCCATGGCAGCGTCTCCTTCTCCGCTTCAAATCCTTCGCAGCCTCCAGGCCTTTGTGGCTG  
TAGCCGCCCCGGTCTTTGCCCATGGAGCAGCAACCCTGAGTCCCTAAAGGCAGCAGCTCAAGG  
ATGGCACTCAGATCTCCATGGCCCAGCAAGGCCAAGATAAATCTACCACCCAGGCACCTGTG  
AGCCAACAGGTTAATTAGTCCATTAATTTTAGTGGGACCTGCATATGTTGAAAATTACCAATA  
CTGACTGACATGTGATGCTGACCTATGATAAGGTTGAGTATTTATTAGATGGGAAGGGAAATT  
TGGGGATTATTTATCCTCCTGGGGACAGTTTGGGGAGGATTATTTATTGTATTTATATTGAAT  
TATGTACTTTTTTCAATAAAGTCTTATTTTTGTGGCTAAAAAAAAAAAAA

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**FIGURE 232**

MLGSRAVMLLLLLPWT AQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHPLVGHMDLREEGDEE  
TTNDVPHIQCGDGC DPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSPVGQLHA  
SLLGLSQLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAAARVFAHGAATLSP

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Casein kinase II phosphorylation site.**

amino acids 64-67

**N-myristoylation sites.**

amino acids 25-30, 81-86, 122-127

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**FIGURE 233**

CCCACGCGTCCGGCCCTGTAACCAAGATACTGACTGAACATGGCTGGCGGACTCAGGCTGGGGTCTGCAGTGCAG  
CATTAAATGGGCGGCTGACATGAATATGGAGTAGTTTTCTCTAGCAAAGAGTAATGTTGGGCCATGGAGTCAAGGCCA  
CCTCCTCTGGGCTCTGCTGTTTCATGCAGTCTTGTGGCCTCAACTGACTGATGGAGCCACTCGAGTCTACTACCT  
GGGCATCCGGGATGTGCAGTGGAACTATGCTCCCAAGGGAAGAAATGTATCAGCAACCAGCCTCTGGACAGTGA  
CATAGTGGCTTCCAGCTTCTTAAAGTCTGACAAGAACCGGATAGGGGGAACCTACAAGAAGACCATCTATAAAGA  
ATACAAGGATGACTCATACACAGATGAAGTGGCCAGCCTGCCTGGTTGGGCTTCCCTGGGGCCAGTGTTCAGGC  
TGAAGTGGGGGATGTCATTCTTATTCACCTGAAGAATTTTGCCACTCGTCCCTATACCATCCACCCTCATGGTGT  
CTTCTACGAGAAGGACTCTGAAGGTTCCCTATACCCAGATGGCTCCTCTGGGCCACTGAAAGCTGATGACTCTGT  
TCCCCGGGGGGCAGCCATATCTACAACCTGGACCATTCCAGAAGGCCATGCACCCACCGATGCTGACCCAGCGTG  
CCTCACCTGGATCTACCATTCTCATGTAGATGCTCCACGAGACATTGCAACTGGCCTAATTGGGCTCTCATCAC  
CTGTAAAAGAGGAGCCCTGGATGGGAACCTCCCCTCCTCAACGCCAGGATGTAGACCATGATTCTTCTCCTCTT  
CAGTGTGGTAGATGAGAACCTCAGCTGGCATCTCAATGAGAACATTGCCACTTACTGCTCAGATCCTGCTTCAGT  
GGACAAGAAGATGAGACATTTTCAGGAGAGCAATAGGATGCATGCAATCAATGGCTTTGTTTTTGGGAATTTACC  
TGAGCTGAACATGTGTGCACAGAAACGCTGTGGCCTGGCACTTGTTCAGTGGCAATGAAATGATGTCCACAC  
AGCATTTTCCATGGACAGATGCTGACTACCCGTGGACACCACACTGATGTGGCTAACATCTTCCAGCCACCTT  
TGTGACTGCTGAGATGGTGGCCTGGGAACCTGGTACCTGGTTAATTAGCTGCCAAGTGAACAGTCACTTTCGAGA  
TGGCATGCAGGCACTCTACAAGGTCAAGTCTTGCTCCATGGCCCCCTCTGTGGACCTGCTCAGGCCAAAGTTCCG  
ACAGTACTTCATTGAGGCCCATGAGATTCAATGGGACTATGGCCGATGGGGCATGATGGGAGTACTGGGAAGAA  
TTTGAGAGAGCCAGGCAGTATCTCAGATAAGTTTTTCCAGAAGAGCTCCAGCCGAATTGGGGGCACTTACTGGAA  
AGTGGCATATGAAGCCTTTTCAAGATGAGACATTTCCAAGAGAAGATGCATTTGGAGGAAGATAGGCATCTTGGAA  
CCTGGGGCCAGTGATCCGGGCTGAGGTGGGTGACACCATTTCAGGTGGTCTTCTACAACCGTGCCTCCAGCCATT  
CAGCATGCAGCCCATGGGGTCTTTTATGAGAAAGACTATGAAGGCACTGTGTACAATGATGGCTCATCTTACCC  
TGGCTTGGTTGCCAAGCCCTTTGAGAAAGTAACATACCGCTGGACAGTCCCCCTCATGCCGGTCCCACTGCTCA  
GGATCCTGCTTGTCTCACTTGGATGTACTTCTGCTGCAGATCCCATAGAGACACAAATTCTGGCCTGGTGGG  
CCCCCTGCTGGTGTGCAGGGCTGGTGCCTTGGGTGCAGATGGCAAGCAGAAAGGGTGGATAAAGAATTCTTCT  
TCTCTTCACTGTGTGGATGAGAACAGAGCTGGTACAGCAATGCCAATCAAGCAGCTGCTATGTTGGATTTCCG  
ACTGCTTTTCAGAGGATATTGAGGGCTTCCAAGACTCCAATCGGATGCATGCCATTAATGGGTTTCTGTTCTCTAA  
CCTGCCCAGGCTGGACATGTGCAAGGGTGACACAGTGGCCTGGCACCTGCTCGGCCTGGGCACAGAGACTGATGT  
GCATGGAGTCATGTTCCAGGGCAACACTGTGCAGCTTCAAGGCGATGAGGAAGGGTGCAGCTATGCTCTTCTCA  
TACCTTTGTATGGCCATCATGCAGCCTGACAACCTTGGGACATTTGAGATTTATTGCCAGGCAGGCAGCCATCG  
AGAAGCAGGGATGAGGGCAATCTATAATGTCTCCAGTGTCTGGCCACCAAGCCACCCCTCGCCAACGCTACCA  
AGCTGCAAGAATCTACTATATCATGGCAGAAGAAGTAGAGTGGGACTATTGCCCTGACCGGAGCTGGGAACGGGA  
ATGGCACAACCAGTCTGAGAAGGACAGTTATGGTTACATTTTCTGAGCAACAAGGATGGGCTCCTGGGTTCGAG  
ATACAAGAAAGCTGTATTCAGGGAATACACTGATGGTACATTTCAGGATCCCTCGGCCAAGGACTGGACCAAGA  
ACACTTGGGAATCTTGGGTCCACTTATCAAAGGTGAAGTTGGTGATATCCTGACTGTGGTATTCAAGAATAATGC  
CAGCCGCCCCCTACTCTGTGCATGCTCATGGAGTGGTGAATCTACTACTGTCTGGCCACTGGCTGCTGAGCCTGG  
TGAGGTGGTCACTTATCAGTGGAAACATCCCAGAGAGGTCTGGCCCTGGGCCAATGACTCTGCTTGTGTTTCTTG  
GATCTATTATTCTGCAGTGGATCCCATCAAGGACATGTATAGTGGCCTGGTGGGGCCCTTGGCTATCTGCCAAA  
GGGCATCCTGGAGCCCCATGGAGGACGGAGTGACATGGATCGGGAATTTGCATTGTTGTTCTTGATTTTGTGAG  
AAATAAGTCTTGGTATTTGGAGGAAAATGTGGCAACCCATGGGTCCCAGGATCCAGGCAGTATTAACCTACAGGA  
TGAAACTTTCTTGGAGAGCAATAAAATGCATGCAATCAATGGGAAACTCTATGCCAACCTTAGGGGTCTTACCAT  
GTACCAAGGAGAACGAGTGGCCTGGTACATGCTGGCCATGGGCAAGATGTGGATCTACACACCATCCACTTTCA  
TGCAGAGAGAACTTCTCTATCGGAATGGCGAGAATACCGGGCAGATGTGGTGGATCTGTCCCAGGGACTTTTGA  
GGTTGTGGAGATGGTGGCCAGCAACCTGGGACATGGCTGATGCACTGCCATGTGACTGACCATGTCCATGCTGG  
CATGGAGACCCTCTTCACTGTTTTTCTCGAACAGAACCTTAAGCCCTCTCACCCTCATACCAAAGAGACTGA  
AAAAGTGGCCCCCAGAGACATTGAAGAAGGCAATGTGAAGATGCTGGGCATGCAGATCCCCATAAAGAATGTTGA  
GATGCTGGCCTCTGTTTTGGTTGCCATTAGTGTACCCCTTGTCTGCTGTTGTTCTGGCTCTTGGTGGAGTGGTTG  
GTACCAACATCGACAGAGAAAGCTACGACGCAATAGGAGGTCCATCCTGGATGACAGCTTCAAGCTTCTGTCTTT  
CAACACAGTAACTCGGAGCCTGGAGATATCCTCAGGAAGCACATCTGTAGTGCATCCCAGCAGGCCATGGACT  
AGTCACTAACCCACACTCAAGGGGCATGGGTGGTGGAGAAGCAGAAGGAGCAATCAAGCTTATCTGGATATTT  
CTTTCTTTATTTATTTTACATGGAAATAATATGATTTTCACTTTTCTTTAGTTTCTTTGCTCTACGTGGGCACCT  
GGCACTAAGGAGTACCTTATTATCTACATCGCAAATTTCAACAGCTACATTATATTTCTTCTGACCTTGGGA  
AGGTATTGAATTTCTAGAAATGTATCCTTCTCACAAGTAGAGACCAAGAGAAAACTCATTGATTGGGTTTCT  
ACTTCTTTCAAGGACTCAGGAAATTTCACTTTGAACTGAGGCCAAGTGAGCTGTTAAGATAACCCACACTTAAAC  
TAAAGGCTAAGAAATATAGGCTTGTGGGAAATTGAAGGTAGGCTGAGTATTGGGAATCCAAATTTGAATTTGATT  
CTCCTTGGCAGTGAATACTTTGAAGAAGTGGTCAATGGGTTGTTGCTGCCATGAGCATGTACAACCTCTGGAGC  
TAGAAGCTCCTCAGGAAAGCCAGTTCTCCAAGTTCTTAACCTGTGGCACTGAAAGGAATGTTGAGTTACCTCTTC  
ATGTTTTAGACAGCAACCCCTATCCATTAAAGTACTTGTAGACCAAAAAAAAAAAAAA

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**FIGURE 234**

MWAMESGHELLWALLFMQSLWPQLTDGATRVYYLGIRDVQWNYAPKGRNVITNQPLDSDIVASS  
FLKSDKNRIGGTYKKTIIYKEYKDDSYTDEVAQPAWLGFGLGPVLQAEVGDVILHLKNFATRPY  
TIHPHGVFYEKDSEGSLYPDGSSGPLKADDSVPPGGSHIYNWTIPEGHAPTDADPACLTWIIYH  
SHVDAPRDIATGLIGPLITCKRGALDGNSPQQRQDVHDFFLLFSVVDENLSWHLNENIATYC  
SDPASVDKEDETFOESNRMHAINGFVFGNLPPELNMCAQKRVAWHLFGMGNEIDVHTAFFHGM  
LTTRGHHTDVANIFPATFVTAEMVPWEPTWLI SCQVNSHFRDGMQALYKVKSCSMAPPVDLL  
TGKVRQYFIEAHEIQWDYGPMGHGSGTGKNLREPGSISDKFFQKSSSRIGGTYWKVRYEAFQD  
ETFQEKMHLEEDRHLGILGPVIRAEVGDITQVVFYNRASQPFMOPHGVFYEKDYEGTVYNDG  
SSYPGLVAKPFKVTYRWTVPFHAGPTAQDPACLTWMYFSAADPIRDTNSGLVGPLLVCRA  
LGADGKQKGV DKEFFLLFTVL DENKSWYSNANQAAAMLD FRLLEDIEGFQDSNRMHAINGFL  
FSNLPRLD MCKGDTVAWHLLGLGTETDVHGVFMFQGN TVQLQGM RKAAMLPHTFVMAIMQPD  
NLGTFEIYCQAGSHREAGMRAIYNVSQCPGHQATPRQRYQAARIYYIMAEVEWDYCPDRSWE  
REWHNQSEKDSYGYIFLSNKDGLLGSRYKKA VFREYTDGTFRI PRPRTGPEEHLGILGPLIKG  
EVGDILT VVFKNNASRPYSVHAHGVLESTTVWPLAAEPGEVVTYQWNIPERSGPGPNDSACVS  
WIIYS AVDPIKDMYSGLVGPLAICQKGILEPHGGRSDMDREFALLFLIFDENKSWYLEENVAT  
HGSQDPGSINLQDET FLESNKMHAINGKLYANL RGLTMYQGERVAWYMLAMQD VDLHTIHFH  
AESFLYRNGENYRADVVDLFPGT FEVVMVASNPGTWLMHCHVTDH VHAGMETLFTVFSRTEH  
LSPLTVITKETEKVPPRDIEEGNVKMLGMQIPIKNVEMLASVLVAISVTL LLVLALGGVVWY  
QHRQRKLRNRRSILDDSFKLLSFQ

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 1109-1130

**N-glycosylation sites.**amino acids 167-171, 239-243, 591-595, 717-721, 761-765, 832-836,  
876-880, 934-938**Glycosaminoglycan attachment site.**

amino acids 871-875

**Tyrosine kinase phosphorylation sites.**

amino acids 82-90, 137-145, 494-502, 513-521

**N-myristoylation sites.**amino acids 212-218, 313-319, 498-504, 566-572, 672-678, 778-784,  
843-849**Multicopper oxidases signature 1.**

amino acids 344-365, 696-717, 1043-1064

**Multicopper oxidases signature 2.**

amino acids 1048-1060

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**FIGURE 235**

GGAAAGAGTGCTGGTACTACAACCAGGAAGTGACAGATAATGTGCTTTAAACTACATTAGAAAAGCTTCTCATAG  
CAAAACTGAGAGATTGAAGCAGTGATTATTTTTACATAGTTGTCATTAAATATTTGGAGCTCTGCTGTGCATAGA  
GATGGCAACATACTTAGAATACACAGCTTTCTGGGCCAGAAATTGATCTTCTGACTTTTGAGCCTTATCTGATTA  
CTGCTTGGTTTCATCTTTATTTTGTAACTACTCTGTAGGCTGAAAGGGAGAGACTCTCCTTGGTTTGCAGAGCC  
TGACTAGACAGGAATTCTGGCAACTGCTCCAGCAGAAGTATGGCACTGAGCTAGGTTTAAATGCTGAGGAGATGG  
AAAACCTTGCTCACTGTGATTGAGGATGTGCAGCCAAGAAGTCCAGGAAGAAGCAGCTTGGATGACTCTGGGGAGA  
GAGATGAAAAATTATCCAAGTCAATCAGTTTTACCAGTGAATCAATTAGTCGGGTTTCAGAAACAGAGTCATTCTG  
ATGGAAATTCATCAAAAGGAGGATTAGGCAAAAGAGGAGTCCCAAAATGAGAAACAGACCAGGAGAGTCTCTTAC  
CAACTTTGGAAAAGAAGTTAACTAGAGTGCCATCAAAGTCACTGGACTTGAATAAAAATGAATATCTTCTCTGG  
ACAAAAGCAGCACTTCAGATTCTGTTGATGAAGAAAATGTTCTGAGAAAGATCTTCATGGAAGACTTTTTATCA  
ACCGTATTTTTCATATCAGTGCTGACAGAATGTTTGAATTGCTCTTACCAGTTACAGCTTTATGCAGAAATTTG  
CCAGTTCTAGAAATATAATAGATGTAGTATCTACCCCTTGGACTGCAGAACTTGGAGGTGATCAGCTGAGAACGA  
TGACCTACACTATAGTCCTTAATAGTCCACTTACTGGAAATGCACTGCTGCCACTGAAAAGCAGACACTGTATA  
AAGAAAGTCGGGAAGCAGATTTTATTTGGTAGATTTCAGAAGTACTGACACATGATGTCCCCTACCATGATTACT  
TCTATACCGTGAACAGATACTGTATCATCCGATCTTCAAACAGAAATGCAGGCTAAGAGTTTCCACAGATTTGA  
AATACAGAAAACAGCCATGGGGCCTTGTCAAATCTTTAATTGAAAAGAATTCCTGGAGTTCTTTGGAGGACTATT  
TCAAACAGCTTGAATCAGATTTGTTAATTGAAGAATCTGTATTAAATCAGGCCATTGAAGACCCCTGGAAAACCTA  
CTGGCCTACGAAGGAGAAGGCGAACCTTCAACCGAACAGCAGAAACAGTTCTTAACTTTCTCTCAGCATTCTCT  
CTGGAGATGTGGGCTTAGGTGCCAAAGGGGATATTACAGGAAAGAAAAGGAAATGGAAAACCTATAACGTCACCT  
TTATTGTGGTAATGAGTATTTTTGTGTGTTATTAGTTTTGTGTAATGTGACACTGTTTCTGAAGCTGTCAAAGA  
TAGAACATGCTGCTCAGTCTTTTTACCGTCTCCGCTCCAAGAAGAGAAATCTTTAAATTTAGCCTCTGATATGG  
TGTCAAGAGCAGAACTATTGAGAAGATAAGATCAGGCCATCGTTTAAAGGGAGTGCTCCGAGACTCCATAG  
TGATGCTTGAACAGCTGAAGAGCTCACTCATTATGCTTCAGAAAACGTTTGATCTACTAAATAAGAATAAGACTG  
GCATGGCTGTTGAAAGCTAGTGATCTGAAGGACTAAAACCGCAGAGATACTTGGAACTTAAAGAAAATACCTGG  
AGAAAACCAGACGAATGAAGGATTTTGGCATAGAACATTTCTATGTTTTTTCATTATTGAGATTTCTAATATGAA  
CATTCTCTTTCAGTAACATTTATTTGATAATTAGTTTTCTGCTGGCCTTAATAATCCATCCTTTCACTTCTTATAGA  
TATTTTTAAGCTGTGAATTTCTTCAGTGAACCATGAAATATATTATAGAACTGAATTTCTCTGATACAAAAGAA  
AATGACACACCCCTGAATTGAGTGGTATGGTCTCATTTCTACAGTGAAGTCTGATGCTTTGTTAGCACAGAATCCG  
TACATGTCCAATAGGTGCTTTTTGTAAGTGAAGATAAGACCAAGAGGATAAACAGGACAATATAAGAAGAAACCTC  
TATGTCATTACTGATTTTAAAGGTTCTGTTTTCAAGCATATAACATTTCCAGGTTTGTGTACTGTAAAGATTATA  
ATGTCCTTCATTTATTTAGCATGCAAATTTAATAGTCAAACTTTTTGAATCTGCATGTTGATGATTATCAGAA  
AGGGTCTTCTGCCATGCTGTATCTTTATGAAAGAAATAGTTGTTTTTCTTAAGGTAACATCAGAGGTGGGATT  
ATCTTGCCCTCCTCACTTAGAATACCAACAGTCAAAGGAAGAACCATCCTCTGAGTTTTAAAACCAGAAAGGTTA  
TGTTAAATCTGGGCATTTAGTGACAGATCAAATGCATACTTGAACCTAAGATTGGCTTCAGCTTAGCAGTCTTTC  
ATGGTGGAAGTGACACATCTGGTTGAAAATAATTTGTGTATTTTCAGTAACCATGTATGGCTTCCTTCTTTATGT  
ATGTGTGTGACTTGTTTAATTGGTAAGTTATAAGCCAGACATAGATTTTAGCTCTTTAATAAAAACCTCAGGGG  
CACGTATGTCCAGTACAAGTGTACTGACTATCAAGTTTTAACTCAGATGCAAGCTTTGGCTCTTTCATAAAAAG  
TTTTTATGCATATGTGTCTCCATACAAGTGGCTCATTAATAAAGAACTTTGTAACTGACTTAAATCAGATAT  
TTTTTCAAGAGTTAGGGAAAGTTGAAGTGTCTTACTGTTTTGTCTCTTGAGCCCTTTCTCTGGGGAAAAATACA  
TATCCATCTATCTATATATATAAACTGTGTATACATTCTTACTGTTTGAACAACTATTGCCTTTAATTAAATG  
TTTCATTTTTCTCCAGAGTCCCCAAAGCCACATGGCATTATTATAGTCATTTTGGAGATGCCTGTAGAGAATGAA  
AGTATTGACTCCGTTAGAGGGAAAATGGGTTTCTCTGGGTGAATTTCCAACGAAGCATACCTAGGGGTAACAGTGA  
ACCTACCTGGGTTTGTGTTTTGGTTAAGGATTTATGTAGTGTCTGGCTGTAAGCAAGAATGAGTGGATTATAA  
ACTTGAAGATTTCTCTGTTAAAGTCACAAAATGATCGACAAACAATATTTTTGTGATGTTTATTTAAACGTTGT  
ATTTTATAACATACTTCAAGGAAGAGTATCGAAGTAAGTTGCTTTATAAATTAAGACTAAATTCGTATGGATGCA  
GAATTCATTAATAAAATTTGAGCCTGTTACGTAATTTGAATATTAATAAAATTGAAAATTTCAAAA

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**FIGURE 236**

MENLSLSIEDVQPRSPGRSSLDDSGERDEKLSKSI SFTSE SISRVS ETE SFDGNSSKGGLGKE  
ESQNEKQTKKSLLP TLEKKL TRVPSKSLDLNKNE YLSLDKSSTSDSVDEENVPEKDLHGRLFI  
NRIFHISADRMFELLFTSSRFMQKFASSRNIIDV VSTPWTAE LGGDQLRTMTYTIVLNSPLTG  
KCTAATEKQ TLYKESREARFYLV DSEVLTHDVPYHDYFYTVNRYCIIRSSKQKCRLRVSTD LK  
YRKQPWGLVKSLIEKNSWSSLEDYFKQLES DLLIEESVLNQAIEDPGKLTGLRRRRRTFNRTA  
ETV PKLSSQHSSGDVGLGAKGDITGKKKEMENYNVT LIVVMSIFVLLLVLNVT LFLKLSKIE  
HAAQSFYRLRLQEEKSLN LASDMVSRAETIQKNKDQA HRLKGVLRDSIVMLEQLKSSLIMLQK  
TFDLLNKNKTGM AVES

**Transmembrane domain:**

amino acids 352-371

**N-glycosylation sites.**

amino acids 3-7, 54-58, 312-316, 349-353, 367-371, 449-453

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 81-85, 307-311

**Tyrosine kinase phosphorylation sites.**

amino acids 202-211, 246-254, 341-349

**N-myristoylation site.**

amino acids 259-265

**Amidation site.**

amino acids 339-343



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**FIGURE 237**

CAGGGGCTGGAGGGCAGGGGAGGGGATGATGTCATTCTGCTCGGCGCAATCCTGACCCTGCT  
CTGGGCGCCACGGCTCAGGCTGAGGTTCTGCTGCAGCCTGACTTCAATGCTGAAAAGTTCTC  
AGGCCTCTGGTACGTGGTCTCCATGGCATCTGACTGCAGGGTCTTCCTGGGCAAGAAGGACCA  
CCTGTCCATGTCCACCAGGGCCATCAGGCCCACAGAGGAGGGCGGCCTCCACGTCCACATGGA  
GTTCCCGGGGGCGGACGGCTGTAACCAGGTGGATGCCGAGTACCTGAAGGTGGGCTCCGAGGG  
ACACTTCAGAGTCCCGGCCTTGGGCTACCTGGACGTGCGCATCGTGGACACAGACTACAGCTC  
CTTCGCCGTCTTTACATCTACAAGGAGCTGGAGGGGGCCCTCAGCACCATGGTGCAGCTCTA  
CAGCCGGACCCAGGATGTGAGTCCCCAGGCTCTGAAGTCCTTCCAGGACTTCTACCCGACCCT  
GGGGCTCCCCAAGGACATGATGGTCATGCTGCCCCAGTCAGATGCATGCAACCCTGAGAGCAA  
GGAGGCGCCCTGACACCTCCGGAGCCCCACCCCGCCCTTCCCAGGTGGAGCCAAAGCAGCAG  
GCGCCTTTGCCCCTGGAGTCAAGACCCACAGCCCTCGGGGACCACCTGGAGTCTCTCCATCCT  
CCACCCCCCGCCTGTGGGATGCCTTGTGGGACGTCTCTTTCTATTCAATAAACAGATGCTGCA  
GCCTCA

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**FIGURE 238**

MMSFLLGAILTLLWAPTAQAEVLLQPDFNAEKFSGLWYVVSMAASDCRVFLGKKDHLSMSTRAI  
RPTEEGGLHVHMEFFPGADGCNQVDAEYLVKGSEGHFRVPALGYLDVRIVDTDYSSFAVLYIYK  
ELEGALSTMVQLYSRTQDVSPQALKSFQDFYPTLGLPKDMMVMLPQSDACNPESKEAP

**Signal peptide:**

amino acids 1-20

**Tyrosine kinase phosphorylation site.**

amino acids 110-117

**N-myristoylation sites.**

amino acids 7-13, 79-85, 130-136

**Amidation site.**

amino acids 50-54

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**FIGURE 239**

GGCGCGCTGGTCCAGGTGAGCGGGCGCGTCCCCGCGACGGCGCTGCCTGCCCCGAGGCGGTTCA  
CGTAAAGACAGCGAGATCCTGAGGGCCAGCCGGAAGGAGGCGTGGATATGGAGCTGGCTGCT  
GCCAAGTCCGGGGCCCCGCGCCGCTGCCTAGCGCGTCCTGGGGACTCTGTGGGGACGCGCCCCG  
CGCCGCGGCTCGGGGACCCGTAGAGCCCGGCGCTGCGCGC**ATG**GCCCTGCTCTCGCGCCCCG  
GCTCACCTCCTGCTCCTCCTCATGGCCGCTGTTGTCAGGTGCCAGGAGCAGGCCAGACCAC  
CGACTGGAGAGCCACCCTGAAGACCATCCGGAACGGCGTTCATAAGATAGACACGTACCTGAA  
CGCCGCTTGGACCTCCTGGGAGGCGAGGACGGTCTCTGCCAGTATAAATGCAGTGACGGATC  
TAAGCCTTTCCACGTTATGGTTATAAACCTCCCCACCGAATGGATGTGGCTCTCCACTGTT  
TGGTGTTTCATCTTAACATTGGTATCCCTTCCCTGACAAAGTGTTGCAACCAACACGACAGGTG  
CTATGAGACCTGTGGCAAAAGCAAGAATGACTGTGATGAAGAATTCCAGTATTGCCTCTCCAA  
GATCTGCCGAGATGTACAGAAAACACTAGGACTAACTCAGCATGTTTCAGGCATGTGAAACAAC  
AGTGGAGCTCTTGTTTGACAGTGTTATACATTTAGGTTGTAAACCATATCTGGACAGCCAACG  
AGCCGCATGCAGGTGTCATTATGAAGAAAAAACTGATCTTT**TAA**AGGAGATGCCGACAGCTAGT  
GACAGATGAAGATGGAAGAACATAACCTTTGACAAATAACTAATGTTTTTACAACATAAACT  
GTCTTATTTTTGTGAAAGGATTATTTTGAGACCTTAAAATAATTTATATCTTGATGTTAAAC  
CTCAAAGCAAAAAAAGTGAGGGAGATAGTGAGGGGAGGGCACGCTTGCTTCTCAGGTATCTT  
CCCCAGCATTGCTCCCTTACTTAGTATGCCAAATGTCTTGACCAATATCAAAAACAAGTGCTT  
GTTTAGCGGAGAATTTTGAAAAGAGGAATATATAACTCAATTTTCACAACCACATTTACCAA  
AAAAGAGATCAATATAAAATTCATCATAATGTCTGTTCAACATTATCTTATTTGGAAAATGG  
GGAAATTATCACTTACAAGTATTTGTTTACTATGAAATTTTAAATACACATTTATGCCTAGAA  
GGAACGGACTTTTTTTTTCTATTTTAATTACACATAATATGTAATTAAAGTACAACATAATAT  
GTTGTTTCTCTGTAGCCCGTTGAGCATATGAGTAAGTCACATTTCTATTAGGACTACTTACAA  
GGACAAGGTTTCCATTTTCCAGTTGTAAAATTGGAACCATCAGCTGATAACCTCGTAGGGAG  
CAACCCAGGATAGCTAAGTGTTATGTAATATGCCTAGAAGGTGATGTGAATGCGATTGAGAA  
GCATAGCCACTCCCATTTTATGAGCTACTCACATGACAAATGTCATCTTTTGCTATAACCTTT  
GCCAAGTTAGAGAAAAGATGGATTTAATGAGATAAATGAAAAGATATTTAACCTAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

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**FIGURE 240**

MALLSRPALTLLLLLMAAVVRCQEQAQTTDWRATLKTIRNGVHKIDTYLNAALDLLGGEDGLC  
QYKCSDGSKPFPRYGYKPSPPNGCGSPLFGVHLNIGIPSLTKCCNQHDRCYETCGKSKNDCDE  
EFQYCLSKICRDVQKTLGLTQHVQACETTVELLFDSVIHLGCKPYLDSQRAACRCHYEETDL

**Important features:****Signal peptide:**

amino acids 1-22

**N-myristoylation sites:**

amino acids 57-63, 93-99

**Phospholipase A2 histidine active site:**

amino acids 106-114

**Neuraxin and MAP1B proteins repeat proteins Block:**

amino acids 109-137

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**FIGURE 241**

GATTCCGAGCGCCTCCACTGCTGGTCCGTTGGCCAGATCAACTCGCCGCGTGGGCCGGCCGTT  
CCCTGAGAGTCTGAGCGCTCGCCGCACCCCTTCCGAGCTTCTATTGGCCGTAGCAGACGTCC  
GTCTGCCGCTATCTCCGCCCCAATACGGAAGCGGCCTAGTCCTCCGGCTCCGACAGCTGGGTG  
TCCAGGCCATGGGGCAGCCCTGGGCGGCTGGGAGCACGGACGGGGCGCCCGCGCAGCTGCCTC  
TCGTGCTCACCGCGCTGTGGGCCGCGGCCGTGGGCCTGGAGCTGGCTTACGTGCTGGTGCTCG  
GTCCCGGGCCGCGCCGCTGGGACCCCTGGCCCGGGCCTTGACAGCTGGCGCTGGCCGCTTCC  
AGCTGCTCAACCTGCTGGGCAACGTGGGGCTCTTCTGCGCTCGGATCCCAGCATCCGTGGCG  
TGATGCTGGCCGGCCGCGGTCTGGGCCAGGGCTGGGCTTACTGCTACCAATGCCAAAGCCAGG  
TGCCGCCACGCAGCGGACACTGCTCTGCCTGCCGCGTCTGCATCCTGCGTCGGGACCACCACT  
GCCGCTGCTGGGCCGCTGCGTGGGCTTCGGCAACTACCGGCCCTTCCTGTGCCTGCTGCTTC  
ATGCCGCCGGCGTCTGCTCCACGTCTCTGTGCTGCTGGGCCCTGCACTGTCGGCCCTGCTGC  
GAGCCCACACGCCCTCCACATGGCTGCCCTCCTCCTGCTTCCCTGGCTCATGTTGCTCACAG  
GCAGAGTGTCTCTGGCACAGTTTGCCTTGGCCTTCGTGACGGACACGTGCGTGGCGGGTGCGC  
TGCTGTGCGGGGCTGGGCTGCTCTTCCATGGGATGCTGCTGCTGCGGGGCCAGACCACATGGG  
AGTGGGCTCGGGGCCAGCACTCCTATGACCTGGGTCCCTGCCACAACCTGCAGGCAGCCCTGG  
GGCCCCGCTGGGCCCTCGTCTGGCTCTGGCCCTTCCTGGCCTCCCCATTGCCTGGGGATGGGA  
TCACCTTCCAGACCACAGCAGATGTGGGACACACAGCCTCCTTGACTCCAGGAAGAGCCAGAGC  
TGTGCAGGGAGGAAGGGGTGAGAGGGGGGCCCCACACCTAGACTCAGTAAGGAAGTCGGGTT  
GGACCTTAACATCTGCATTGGACAACTCCACCCCTTCCTTGGCCTTGCCCCTGCCCCGCTACA  
CTCCTACGTGTCCAGGGCTTGGGCCGTGACTTAGGCAGAGGAGTGCAGAGGAGGGTCTGGCAG  
GGGCTGCTCAGGCCGCCTAGCTGCCCCTTTGCCAGGTTAATAAAGCACTGACTTGTTAA

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**FIGURE 242**

MGQPWAAGSTDGAPAQLPLVLTALWAAVGLLAYVLVLGPGPPPLGPLARALQLALAAFQLL  
NLLGNVGLFLRSDPSIRGVMLAGRGLGQGWAYCYQCQSQVPPRSGHCSACRVCILRRDHHCRLL  
LGRCVGFGNYRPFCLLLLHAAGVLLHVSVLLGPALSALLRAHTPLHMAALLLLPWLMLLTGRV  
SLAQFALAFVTDTCVAGALLCGAGLLFHGMILLRGQTTWEWARGQHSYDLGPCHNLQAALGPR  
WALVWLWPFLASPLPGDGITFQTTADVGHSTAS

**Important features:****Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 51-66, 143-160, 174-191, 198-214

**N-myristoylation sites:**

amino acids 2-8, 8-14, 30-36, 81-87, 88-94, 90-96, 206-212

**Leucine zipper pattern:**

amino acids 143-165, 150-172, 157-179, 164-186

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**FIGURE 243**

CTTGTCTTTGTGTCGGTTGTGATTTTCCTAATCTCTGATTTTCCTTTTCTCTCGGACGCTCTC  
CCTCTTCGGACCCATTTTCTCCCGTGCTTCATGCCCTGATAGCCTGGCCCCCTTCCCGGCTTCC  
TTCGCTACCGGGGACGCCTCTAGTTTTTCTGAATTTCTGGCTGGCTCCACCCTCCGCGTTTCAT  
CTTCTCAAGAGTTCGCCCCCTCTGGGGGCTCCTCTGTGTAATCGTCGCCTTCTCTGGGTATTT  
CTGTGAACTCCGTCTCACACCATCCCGCCATCTTCTCTGCCTTGGCCCCCTTTTCTCTGTACAG  
CCAGCTCTGTGTCCTTTTCTTCTCCCCCTCTAAAATCGACTCCTCTTCTCCCTGAGAGCCCCA  
CCTTTGTGCCCCACTCCTCATTTTCTACGCCTCCCTCTCTCTGCTGGTCTCTCTCTCCCTG  
CAAGGTTCCATTCCATCAATTTGTTTGTCTTTTGTAGGGGTGGCATCCCCCTCTGACTACTGCT  
CCATCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTCTGAGGATTTCACTTCAATCTTTTCTGGT  
TGCGTCTCCACTTGTACTCAGCTTGTTAGGTCCAGGTCCAGTTGTTCTGCATCTGAGGCTGGC  
GTGTGCTGTCTTCTCTGATTGGCCTAATCTCCCTCACCCCGTGAGATCTGTTGTACGCCTTC  
GTTTCTCTTTCTGTGTCCCAGCTTTTCTGCGGGTCTTGGCACCTTTCTTGGCCACAGATTTCT  
TGGGTTACAGAGCATGTGTGTCTGAGGCATTGCAGGCAGAAAAGGGTGGCCGACGTGACCTCT  
AGCTGGACTGCTGGGCAGGGGAGCTGTCCTAGATAAAATTGGAAAGAAACAGTGACCCAGAGA  
CAGGTGGACAAAGAATTCGGGGACTGATGGGAAGTGAAGTGGGATCCAGACTGAAACTGATT  
CCAGACTGACCTCTAGCACCCAGGACCCAGACACAGGGGCCATGGGACCCCAGCATTTGAGACT  
TGTGCAGCTGTTCTGCCTTCTAGGGGCCATCCCCACTCTGCCTCGGGCTGGAGCTCTTTTGTG  
CTATGAAGCAACAGCCTCAAGATTCAGAGCTGTTGCTTTCCATAACTGGAAGTGGCTTCTGAT  
GAGGAACATGGTGTGTAAGCTGCAAGAGGGCTGCGAGGAGACGCTAGTGTTCAATTGAGACAGG  
GACTGCAAGGGGAGTTGTGGGCTTTAAAGGCTGCAGCTCGTCTTCGTCTTACCCTGCGCAAAT  
CTCCTACCTTGTTTCCCCACCCGGAGTGTCCATTGCCTCCTACAGTCGCGTCTGCCGGTCTTA  
TCTCTGCAACAACCTCACCAATTTGGAGCCTTTTGTGAAACTCAAGGCCAGCACTCCTAAGTC  
TAATTTTGTACCACTAATTCTTGCCCCCTGGCTGCTTCTACGTGTTACAGTTCCACCTTAAA  
ATTTTCAGGCAGGGTTTCTCAATACCACCTTCCTCCTCATGGGGTGTGCTCGTGAACATAACCA  
GCTTTTAGCAGATTTTCATCATATTGGGAGCATCAAAGTGAAGTGGTCTCAACATCTTAGA  
GAAGTCTCAGATTGTTGGTGCAGCATCCTCCAGGCAAGATCCTGCTTGGGGTGTGCTCTTAGG  
CCTCCTGTTTGCCTTCAGGGACTGACCATCTAGCTGCACCCGACAAGCACCCAGACTCTTTCA  
CATAACAAATAAAATAGCAGAGTTCCCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAA

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**FIGURE 244**

MGPQHLRLVQLFCLLGAIPTLPRAGALLCYEATASRFRAVAFHNWKWLLMRNMVCKLQEGCEE  
TLVFIETGTARGVVGFKGCSSSSSYPAQISYLVSPPGVSIASYSRVCRSYLCNNLTNLEPFVK  
LKASTPKSITSASCSCPTCVGEHMKDCLPNFVTTNSCPLAASTCYSSTLKFQAGFLNTTFLLM  
GCAREHNQLLADFHHIGSIKVTEVLNILEKSQIVGAASSRQDPAWGVVLGLLFAFRD

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation sites:**

amino acids 117-121,183-187

**N-myristoylation sites:**amino acids 16-22,25-31,60-66,71-77,81-87,100-106,224-230,  
235-241,239-245**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 181-192



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**FIGURE 245**

GTGGAGTTGGGTGGTGTCTGGGAGCCTCTCCCTGAGGGGCACCGCTCTTCAGGAGCTGGGCCTCCAGTGCGGGCGC  
GATGTCAGGCGCGGTGACAGCTCTGTGAGTCCGAGGCCGCGGCCGTGGCGCTGGGCGGCTGCGGGGCTGACCGG  
TCCGCTCCATGGTGCCGCCACGACGCCATCGCGGGCAGGAAGGCCAGGGGTGCTGAGTTCTTCACCTCCTTTTAG  
ACTGAGATCTGCCAAGTTTTCCGGCATTGCTCTTGAGGATCTCAGAAGGGCTCTTAAGACAAGACTGCAAATGGT  
GTGTGATTTGTGTCATGAACCGAATGAATCCCAGAACAGTGGTTTCACTCAGCGCAGGCGAATGGCTCTTGGGAT  
TGTTATTCTTCTGCTTGTTGATGTGATATGGGTTGCTTCTCTGAACCTACTTCGTATGTTTTTACCCAGTACAA  
CAAACCATTCTTCAGCACCTTTGCAAAAACATCTATGTTTGTTTTGTACCTTTTGGGCTTTATTATTGGAAGCC  
ATGGAGACAACAGTGTACAAGAGGACTTCGCGGAAAGCATGCTGCTTTTTTGCAGATGCTGAAGGTTACTTTGC  
TGCTTGACACAACAGATACAACCTATGAATAGTTCTTTGAGTGAACCTCTGTATGTGCCTGTGAAATCCATGATCT  
TCCAAGTGAAAAACCTGAGAGCACAACATTGATACTGAAAAACCCCCAAAAAGTCTCGTGTGAGGTTTCTAGTAA  
TATCATGGAGATTTCGACAGCTTCCGTCAAGTCATGCATTGGAAGCAAAGTTGTCTCGCATGTCATATCCTGTGAA  
AGAACAAGAATCCATACTGAAAACTGTGGGGAACTTACTGCAACTCAAGTAGCGAAAATTAGCTTTTTTTTTTTG  
CTTTGTGTGGTTTTTTGGCAAATTTGTCATATCAAGAAGCACTTTCAGACACACAAGTTGCTATAGTTAATATTTT  
ATCTTCAACTTCCGGACTTTTTACCTTAATCCTTGCTGCAGTATTTCCAAGTAACAGTGGAGATAGATTTACCTT  
TTCTAAACTATTAGCTGTAATTTTAAGCATTGGAGGCGTTGTACTGGTAAACCTGGCAGGGTCTGAAAAACCTGC  
TGGAAGAGACACAGTAGGTTCCATTTGGTCTCTTGCTGGAGCCATGCTCTATGCTGTCTATATTGTTATGATTAA  
GAGAAAAGTAGATAGAGAAGACAAGTTGGATATTCCAATGTTCTTTGGTTTTGTAGGTTTGTTAATCTGCTGCT  
CTTATGGCCAGGTTTTCTTTTTACTTCATTATACTGGATTTGAGGACTTCGAGTTTCCCAATAAAGTAGTATTAAT  
GTGCATTATCATTAAATGGCCTTATTGGAACAGTACTCTCAGAGTTCCTGTGGTTGTGGGGCTGCTTTCTTACCTC  
ATCATTGATAGGCACACTTGCACTAAGCCTTACAATACCTCTGTCCATAATAGCTGACATGTGTATGCAAAAGGT  
GCAGTTTTCTTGGTTATTTTTTGCAGGAGCTATCCCTGTATTTTTTTCATTTTTTATTGTAACCTCTCCTATGCCA  
TTATAATAATTGGGATCCTGTGATGGTGGGAATCAGAAGAATATTTGCTTTTATATGCAGAAAAACATCGAATTCA  
GAGAGTTCAGAAGACAGCGAACAGTGTGAGAGTCTCATTTCTATGCACAGTGTCTCAGGAGGATGGAGCTAG  
TTAGCTGTCTGTTGTCTGTAGCCCAGCTTGATAATGGAACATACAGCGAAGAGACAATCTCTGGCAAGTTTTTG  
TAGAAAAATGTTTCAGTGCCTAGTCTGAAAAATAACAGTTTGAGTTCTTTGAACTCTAAAAATATTTTTTCTC  
ATACCTGTTTTCTTCATTTTCATAATGAAGCACTTTGCTATGTAGCTGTGTACATATCACTACAGTTATAGGAAG  
TTTCAGTCTACAGTCCATCCAAAGGACCAACCTGCCTTACACATCTCAAGGAATTCAGCTGTTGAAATCATTTGA  
ACTAATCAAGGAATAAATCCTAATGTTCTGGGACTTTATTTTCACATGTTAAATGCTGGAATATATTATGAAAAT  
GTTTTCAAGAAATCACTTAAGTGTTCATAGACCAGTATTTCTGACAGGTAAAATGCTAAAATAAGCTACCTGTAA  
TAAGTGTGGATTATATTTTTGGGTTTTGTAGAATATTGCAAATTAACCACACAAAAATGTTTAATTTATGCAAC  
AAGCATGTTTGTGCAAATTTTCATGGGACTTTAAAAAGAATAAGTATTTGAGAAAATATCTGGTTCACTTACACTA  
CATTTACTGTATTATTCTTTTATAGCATTAGGTGCCTTGATTTTAAATCTGTGACAAACCATGGCAAATTTTTTA  
AAGGGGAAGTATTATTATAAAATGAAGAAATATGTATTTCTAAAGGCTATATTGCTGTAACTTAATTGATAAAG  
CTCTGTTTAATTTAGAGTTTTGAAGAAATAGTCTCCCTCAATTAAGAAATTTTCATAATGGAATGATTTAAATT  
GAAGTGACAAAGAGTATTATTAAAAATACAATGTTTATAAAAAAA

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**FIGURE 246**

MVPPRRHRGAGRPGVLSSSPFFRLRSKFSGIALEDLRRALKTRLQMVCVFVMNRMNSQNSGF  
TQRRRMALGIVILLLLVDVIWVASSELTSYVFTQYNKPFSTFAKTSMFVLYLLGFIIWKPWRQ  
QCTRGLRGKHAAFFADAEGYFAACTDDTTMNSLSEPLYVPVKFHDLPSEKPESTNIDTEKTP  
KKSRRVRFNIMEIRQLPSSHALEAKLSRMSYPVKEQESILKTVGKLTATQVAKISFFFCFVWF  
LANLSYQEALSDTQVAIVNILSSTSGLFLLILAAVFPSNSGDRFTLSKLLAVILSIGGVVLVN  
LAGSEKPAGRDTVGSIWLAGAMLYAVYIVMIKRKVDREDKLDIPMFFGFVGLFNLLLLWPGE  
FLLHYTGFEDEFEPNKVVLNCIIINGLIGTVLSEFLWLWGCFLTSSLIGTLALSLTIPLSIIA  
DMCMQKVQFSWLFFAGAIPVFFSFFIVTLLCHYNNWDPVMVGIRRIFAFICRKHRIQRPEDS  
EQCESLISMHSVSQEDGAS

**Important features:****Transmembrane domain:**

amino acids 69-87, 105-118, 237-256, 266-285, 300-316, 332-346,  
364-379, 399-419, 453-472

**N-glycosylation sites:**

amino acids 157-161, 255-259

**N-myristoylation sites:**

amino acids 14-20, 329-335, 404-410, 407-413, 418-424

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**FIGURE 247**

CGTCTGTAGAGATATCATGAACTTCAACTTAGCTTTGGTACTTTCTTCCCTGAAGACAGAGGG  
CAGAACTCTGAGTTCCAGAACCATTTTCAACTGTATTGGGGACCAATCACTTGACTCTATTCT  
TGTCTCTCTGACAGATGACGCTACACTCTCCTCTGAATAATGGACACCATTTCTAAACTGAA  
TCCTGCTACTAAAATAATTCAGATGATATATTTTTCCAATTCTACAATCTTGCTTTGTTTTAT  
TTAGTTGTTTTCTCTCTCTCTTCCCAGTTTTCCAGAGACTGGAGCTAAACTGGGCTTTCAACA  
TCATCATGAAGTTTATCCTCCTCTGGGCCCTCTTGAATCTGACTGTTGCTTTGGCCTTTAATC  
CAGATTACACAGTCAGCTCCACTCCCCCTTACTTGGTCTATTTGAAATCTGACTACTTGCCCT  
GCGCTGGAGTCCTGATCCACCCGCTTTGGGTGATCACAGCTGCACACTGCAATTTACCAAAGC  
TTCGGGTGATATTGGGGGTTACAATCCCAGCAGACTCTAATGAAAAGCATCTGCAAGTGATTG  
GCTATGAGAAGATGATTCATCATCCACACTTCTCAGTCACCTTCTATTGATCATGACATCATGC  
TAATCAAGCTGAAAACAGAGGCTGAACTCAATGACTATGTGAAATTAGCCAACCTGCCCTACC  
AAACTATCTCTGAAAATACCATGTGCTCTGTCTCTACCTGGAGCTACAATGTGTGTGATATCT  
ACAAAGAGCCCGATTCACTGCAAACCTGTGAACATCTCTGTAATCTCCAAGCCTCAGTGTGCGG  
ATGCCTATAAAACCTACAACATCACGGAAAATATGCTGTGTGTGGGCATTGTGCCAGGAAGGA  
GGCAGCCCTGCAAGGAAGTTTCTGCTGCCCCGGCAATCTGCAATGGGATGCTTCAAGGAATCC  
TGTCTTTTGC GGATGGATGTGTTTTGAGAGCCGATGTTGGCATCTATGCCAAAATTTTTTACT  
ATATACCCTGGATTGAAAATGTAATCCAAAATAACTGAGCTGTGGCAGTTGTGGACCATATGA  
CACAGCTTGTCCCCATCGTTCACCTTTAGAATTAAATATAAATTAACCTCCTC

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**FIGURE 248**

MKFILLWALLNLTVALAFNPDYTVSSTPPYLVYLKSDYLPAGVLIHPLWVITAHCNLPKLR  
VILGVTIPADSNEKHLQVIGYEKMIHHPHFSVTSIDHDIMLIKTEAELNDYVKLANLPYQT  
ISENTMCSVSTWSYNVCDIYKEPDSLQTVNISVISKPQCRDAYKTYNITENMLCVGIVPGRRQ  
PCKEVSAAPAICNGMLQGILSFADGCVLRADVGIIYAKIFYIIPWIENVIQNN

**Important features:****Signal peptide:**

amino acids 1-17

**N-glycosylation sites:**

amino acids 11-15, 156-160, 173-177

**Tyrosine kinase phosphorylation site:**

amino acids 108-117

**N-myristoylation sites:**

amino acids 182-188, 203-209

**Amidation site:**

amino acids 185-189

**Serine proteases, trypsin family, histidine active site:**

amino acids 52-58

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**FIGURE 249**

GCGAGGCGGCCGCTGTCTTCTGCTGCGGCTTCCGCGACCACAAGTACTGCTGCGACGACCCGC  
ACAGCTTCTTCCCCTACGAGCACAGCTACATGTGGTGGCTCAGCATTGGCGCTCTCATAGGCC  
TGTCCGTAGCAGCAGTGGTTCTTCTCGCCTTCATTGTTACCGCCTGTGTGCTCTGCTACCTGT  
TCATCAGCTCTAAGCCCCACACAAAGTTGGACCTGGGCTTGAGCTTACAGACAGCAGGCCCTG  
AGGAGGTTTCTCCTGACTGCCAAGGTGTGAACACAGGCATGGCGGCAGAAGTGCCAAAAGTGA  
GCCCTCTCCAGCAGAGTTACTCCTGCTTGAACCCGCAGCTGGAGAGCAATGAGGGGCAGGCTG  
TGAACTCCAAACGCCTCCTCCATCATTGCTTCATGGCCACAGTGACCACCAGTGACATTCCAG  
GCAGCCCTGAGGAAGCCTCTGTACCCAACCCTGACCTATGTGGACCAGTCCCATAAACATTCA  
ATAAATGTCTCCATACCATCAA

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**FIGURE 250**

MWWLSIGALIGLSVAADVLLAFIVTACVLCYLFISSKPHTKLDLGLSLQTAGPEEVSPDCQGV  
NTGMAAEVVPKVSPLQQSYSCLNPOLESNEGQAVNSKRLHHCFMATVTTSDIPGSPEEASVPN  
PDL CGPVP

**Important features:**

**Signal peptide:**

Amino acids 1-26

**N-myristoylation sites:**

Amino acids 7-13, 11-17, 62-68, 93-99

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**FIGURE 251**

GTGGTTTGGATTGAGCCGGGCCCCGGCCGGGGCGCCGAGTCGGAGGGGGTGGCAGTGAGCGGCG  
GCAGAGGCTACGGGGCTCGGTTTGGCTGACTGGGGAGTCGGCAGGCGGCAGGAACCATGCGAG  
GCCAGCGGAGCCTGCTGCTGGGCCCCGGCCCGCCTCTGCCTCCGCCTCCTTCTGCTGCTGGGT  
ACAGGCGCCGCTGTCCACCTCTACTCCGGGGTCTAGTACAGCGCTGGCGCTACGGCAAGGTCT  
GCCTGCGCTCCCTGCTCTACAACCTCCTTTGGGGGAGTGACACCGCTGTTGATGCTGCCTTTG  
AGCCTGTCTACTGGCTGGTAGACAACGTGATCCGCTGGTTTGGAGTGGTGTTCGTGGTCCTGG  
TGATCGTGCTGACAGGCTCCATTGTAGCTATCGCCTACCTGTGTGTCTGCCTCTCATCCTCC  
GAACCTACTCAGTGCCACGACTCTGCTGGCATTCTTCTATAGCCACTGGAATCTGATCCTGA  
TTGTCTTCCACTACTACCAGGCCATCACCCTCCGCCTGGGTACCCACCCAGGGCAGGAATG  
ATATCGCCACCGTCTCCATCTGTAAGAAGTGCATTTACCCCAAGCCAGCCCGAACACACCCT  
GCAGCATCTGCAACAGGTGTGTGCTGAAGATGGATCACCCTGCCCTGGCTAAACAATTGTG  
TGGGCCACTATAACCATCGGTACTTCTTCTCTTCTGCTTTTTTCATGACTCTGGGCTGTGTCT  
ACTGCAGCTATGGAAGTTGGGACCTTTTCCGGGAGGCTTATGCTGCCATTGAGACTTATCACC  
AGACCCACCCACCCACCTTCTCCTTTTCGAGAAAGGATGACTCACAAGAGTCTTGTCTACCTCT  
GGTTCCTGTGCAGTTCTGTGGCACTTGCCCTGGGTGCCCTAACTGTATGGCATGCTGTTCTCA  
TCAGTCGAGGTGAGACTAGCATCGAAAGGCACATCAACAAGAAGGAGAGACGTCGGCTACAGG  
CCAAGGGCAGAGTATTTAGGAATCCTTACAACCTACGGCTGCTTGGACAACCTGGAAGGTATTCC  
TGGGTGTGGATACAGGAAGGCACTGGCTTACTCGGGTGCTCTTACCTTCTAGTCACTTGCCCC  
ATGGGAATGGAATGAGCTGGGAGCCCCCTCCCTGGGTGACTGCTCACTCAGCCTCTGTGATGG  
CAGTGTGAGCTGGACTGTGTGAGCCACGACTCGAGCACTCATTCTGCTCCCTATGTTATTTCA  
AGGGCCTCCAAGGGCAGCTTTTCTCAGAATCCTTGATCAAAAAGAGCCAGTGGGCCTGCCTTA  
GGGTACCATGCAGGACAATTCAAGGACCAGCCTTTTTTACCACTGCAGAAGAAAGACACAATGT  
GGAGAAATCTTAGGACTGACATCCCTTTACTCAGGCAAACAGAAGTTCCAACCCAGACTAGG  
GGTCAGGCAGCTAGCTACCTACCTTGCCCAGTGCTGACCCGGACCTCCTCCAGGATACAGCAC  
TGGAGTTGGCCACCACCTCTTCTACTTGCTGTCTGAAAAACACCTGACTAGTACAGCTGAGA  
TCTTGGCTTCTCAACAGGGCAAAGATACCAGGCCTGCTGCTGAGGTCACTGCCACTTCTCACA  
TGCTGCTTAAGGGAGCACAATAAAGGTATTCGATTTTTTAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

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**FIGURE 252**

MRGQRSLLLGPARLCLRLLLLLGYRRRCPLLRLVQRWRYGKVCLRSLLYNSFGGSDTAVDA  
AFEPVYWLVDNVIRWFGVVFVVLVIVLTGSIVAIAYLCVLPLILRTYSVPRLCWHFFYSHWNL  
ILIVFHYYQAITTPPGYPPQGRNDIATVSICKKCIYPKPARTHHCSICNRCVLKMDHHCPWLN  
NCVGHYNHRYFFSFCFFMTLGCVCYSYGSWDLFREAYAAIETYHQTPPPTFSFRERMTHKSLV  
YLWFLCSSVALALGALTVWHAVLISRGETSIERHINKKERRRLQAKGRVFRNPYNYGCLDNWK  
VFLGVDTGRLHLTRVLLPSSHLPNGMSWEPPPWVTAHSASVMAV

**Important features:****Transmembrane domain:**

amino acids 88-100,202-216,254-274

**N-myristoylation sites:**

amino acids 55-61,56-62,92-98,210-216,309-315,319-325,340-346

**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 201-212



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**FIGURE 253**

GATCAAGCGCCTTCCTTTCCCTTCCTCTCCCTACTTGGCCTTTGCCCTAAGCCAAGACCTGGCCATCAGCCTGGC  
TGCAGGGGCGCTGCAGAGCCAGCTGCACTTTTTCAGGTATGGGGGAGGGCCAGGCACCATGAAGCCAGTGTGGGTG  
GCCACCCTTCTGTGGATGCTACTGCTGGTGGCCAGGCTGGGGGCGCCCGGAAGGGGTCCCCAGAAGAGGCCTCC  
TTCTACTATGGAACCTTCCCTCTTGGCTTCTCCTGGGGCGTGGGCAGTTCTGCCTACCAGACGGAGGGCGCCTGG  
GACCAGGACGGGAAAGGGCCTAGCATCTGGGACGTCTTCACACACAGTGGGAAGGGGAAAGTGCTTGGGAATGAG  
ACGGCAGATGTAGCCTGTGACGGCTACTACAAGGTCCAGGAGGACATCATTCTGCTGAGGGAAGTGCACGTCAAC  
CACTACCGATTCTCCCTGTCTTGGCCCCGGCTCCTGCCCACAGGCATCCGAGCCGAGCAGGTGAACAAGAAGGGA  
ATCGAATTCTACAGTGATCTTATCGATGCCCTTCTGAGCAGCAACATCACTCCCATCGTGACCTTGCACTACTGG  
GATCTGCCACAGCTGCTCCAGGTCAAATACGGTGGGTGGCAGAATGTGAGCATGGCCAACTACTTCAGAGACTAC  
GCCAACCTGTGCTTTGAGGCCTTTGGGGACCGTGTGAAGCACTGGATCACGTTCACTGATCCTCGGGCAATGGCA  
GAAAAAGGCTATGAGACGGGGCCACCATGCGCCGGGCGCTGAAGCTCCGCGGCACCGGCCTGTACAAGGCAGCACAC  
CACATCATTAAAGGCCCACGCCAAAACCTGGCATTCTTATAACACCACGTGGCGCAGCAAGCAGCAAGGTCTGGTG  
GGAATTTCACTGAACTGTGACTGGGGGGAACCTGTGGACATTAGTAACCCCAAGGACCTAGAGGCTGCCGAGAGA  
TACCTACAGTTCTGTCTGGGCTGGTTTGGCAACCCCATTTATGCCGGTGACTACCCCAAGTCATGAAGGACTAC  
ATTGGAAGAAAGAGTGCAGAGCAAGGCCTGGAGATGTGAGGTTACCGGTGTTCTCACTCCAGGAGAAGAGCTAC  
ATTAAAGGCACATCCGATTTCTTGGGATTAGGTCATTTTACTACTCGGTACATCACGGAAAGGAAGTACCCCTCC  
CGCCAGGGGCCCAGCTACCAGAACGATCGTGACTTGATAGAGCTGGTTGACCCAACTGGCCAGATCTGGGGTCT  
AAATGGCTATATTCTGTGCCATGGGGATTTAGGAGGCTCCTTAACCTTTGCTCAGACTCAATACGGTGATCCTCCC  
ATATATGTGATGAAAAATGGAGCATCTCAAAAATTCCACTGTACTCAATTATGTGATGAGTGGAGAATTCAATAC  
CTTAAAGGATACATAAATGAAATGCTAAAAGCTATAAAAGATGGTGCTAATATAAAGGGGTATACTTCCTGGTCT  
CTGTTGGATAAGTTTGAATGGGAGAAAGGATACTCAGATAGATATGGATTCTACTATGTTGAATTTAACGACAGA  
AATAAGCCTCGCTATCCAAAGGCTTCAGTTCAATATTACAAGAAGATTATCATTGCCAATGGGTTTCCCAATCCA  
AGAGAGGTGGAAAGTTGGTACCTCAAAGCTTTGGAAACTTGCTCTATCAACAATCAGATGCTTGCTGCAGAGCCT  
TTGCTAAGTCACATGCAAATGGTTACGGAGATCGTGGTACCCACTGTCTGCTCCCTCTGTGCTCCTCATCACTGCT  
GTTCTACTAATGCTCCTCCTGAGGAGGCAGAGCTAGAGACAGGATTATCAATTTTGGAGCTTCATAAGAGAATCTT  
CAGGATCTTCCTCCCTTTTCTGCTTTGAGGGTTCCATACATTGCTGTTTTTCAGGTTCTACAATAATTACCTTTT  
TTTCTCTTTCTCTTTTGGCTTGTGCTGGGATTTAAGAATTAGAAAATAAAAAATAAGCAGAAATTA

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**FIGURE 254**

MKPVWVATLLWMLLLVPRLLGAARKGSPEEASFYYGTFPLGFSWGVGSSAYQTEGAWDQDGKGPSIWDVFTHSGKG  
KVLGNETADVACDGYKQVEDIILLRELHVNHYRFSLSWPRLPTGIRAEQVNKKGIEFYSDLIDALLSSNITPI  
VTLHHWDLPLQLQVKYGGWQNVSMANYFRDYANLCFEAFGDRVKHWITFSDPRAMAEKGYETGHHAPGLKLRGTG  
LYKAAHHIIKAHAKTWHSYNTTWRSKQQGLVGISLNCDWGEPVDISNPKDLEAAERYLQFCLGWFANPIYAGDYP  
QVMKDYIGRKSAEQGLEMSRLPVFSLQEKSYIKGTSDFLGLGHFTTRYITERNYPSRQGPSYQNDRLIELVDPN  
WPDLGSKWLYSVPWGFRRLLNFAQTQYGDPIIYVMENGASQKFHCTQLCDEWRIQYLKGYINEMLKAIKDGANIK  
GYTSWSLLDKFEWEKGYSDRYGFYYVEFNDRNKPRYPKASVQYYKKIIANGFPNPREVESWYLKALETCSINNQ  
MLAAEPLLSHMQMVTETIVVPTVCSLCVLITAVLLMLLLRRQS

**Important features:****Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 541-558

**N-glycosylation sites:**

amino acids 80-84, 171-175, 245-249

**Glycosaminoglycan attachment site:**

amino acids 72-76

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

amino acids 23-27, 564-568

**Tyrosine kinase phosphorylation sites:**

amino acids 203-211, 347-355, 460-468, 507-514

**N-myristoylation sites:**

amino acids 44-50, 79-85, 167-173, 225-231, 257-263, 315-321

**Amidation site:**

amino acids 307-311

**Glycosyl hydrolases family 1 active site:**

amino acids 407-416

**Glycosyl hydrolases family 1 N-terminal signature:**

amino acids 41-56

**Motif name Glycosyl hydrolases family:**

amino acids 37- 67

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**FIGURE 255**

CGCGAAGATGCGAAAGGTGGTTTTTGATCACCGGGGCTAGCAGTGGCATTGGCCTGGCCCTCTG  
CAAGCGGCTGCTGGCGGAAGATGATGAGCTTCATCTGTGTTTGGCGTGCAGGAACATGAGCAA  
GGCAGAAGCTGTCTGTGCTGCTCTGCTGGCCTCTCACCCCACTGCTGAGGTCACCATTGTCCA  
GGTGGATGTCAGCAACCTGCAGTCGGTCTTCCGGGGCCTCCAAGGAACTTAAGCAAAGGTTTCA  
GAGATTAGACTGTATATATCTAAATGCTGGGATCATGCCTAATCCACAATAAATATCAAAGC  
ACTTTTCTTTGGCCTCTTTTCAAGAAAAGTGATTTCATATGTTCTCCACAGCTGAAGGCCTGCT  
GACCCAGGGTGATAAGATCACTGCTGATGGACTTCAGGAGGTGTTTGAGACCAATGTCTTTGG  
CCATTTTATCCTGATTTCGGGAACTGGAGCCTCTCCTCTGTACAGTGACAATCCATCTCAGCT  
CATCTGGACATCATCTCGCAGTGCAAGGAAATCTAATTTTCAGCCTCGAGGACTTCCAGCACAG  
CAAAGGCAAGGAACCCTACAGCTCTTCCAAATATGCCACTGACCTTTTGAGTGTGGCTTTGAA  
CAGGAACTTCAACCAGCAGGGTCTCTATTCCAATGTGGCCTGTCCAGGTACAGCATTGACCAA  
TTTGACATATGGAATTCTGCCTCCGTTTATATGGACGCTGTTGATGCCGGCAATATTGCTACT  
TCGCTTTTTTGGAAATGCATTCACTTTGACACCATATAATGGAACAGAAGCTCTGGTATGGCT  
TTTCCACCAAAGCCTGAATCTCTCAATCCTCTGATCAAATATCTGAGTGCCACCACTGGCTT  
TGGAAGAAATTATATTATGACCCAGAAGATGGACCTAGATGAAGACACTGCTGAAAAATTTTA  
TCAAAAGTTACTGGAAGTGGAAAAGCACATTAGGGTCACTATTCAAAAAACAGATAATCAGGC  
CAGGCTCAGTGGCTCATGCCTATTAAATTCCAGCACTTTGGGAGGCCAAGGCAGAAGGATCACTT  
GAGACCAGGAGTTCAAGACCAGCCTGAGAAACATAGTGAGCCCTTGTCTCTACAAAAGAAAT  
AAAAATAATAGCTGGGTGTGGTGGCATGCGCATGTAGTCCCAGCTACTCAGAAGGATGAGGTG  
GGAGGATCTCTTGAGGCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACTCC  
AGCCTGGGTGACAGCGAGACCCTGTCTCAAAATATGTATATATTTAATATATATATAAAACCA  
GAGCTGACAATGACACTCTGGAACATTGCATACCTTCTGTACATTCTGGGGTACATGGATTTC  
TACTGAGTTGGATAATATGCATTTGTAATAAACTATGAACTATGAA

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**FIGURE 256**

MRKVVLITGASSGIGLALCKRLLAEDDELHLCLACRNMSKAEAVCAALLASHPTAEVTIVQVD  
VSNLQSVFRASKELKQRFQRLDCIYLNAGIMPNPQLNIKALFFGLFSRKVIHMFSTAEGLLTQ  
GDKITADGLQEVFETNVFGHFILIRELEPLLCHSDNPSQLIWTSSRSARKSNFSLEDFQHSKG  
KEPYSSSKYATDLLSVALNRNFNQQGLYSNVACPGTALTNLTYGILPPFIWTLLMPAILLLRF  
FANAFTLTPYNGTEALVWLFHQKPESLNPLIKYLSATTGFGGRNYIMTQKMDLDEDTAEKFYQK  
LLELEKHIRVTIQKTDNQARLSGSL

**Important features:****Transmembrane domain:**

amino acids 234-254

**N-glycosylation sites:**

amino acids 37-41,178-182,229-233,263-267

**Glycosaminoglycan attachment site:**

amino acids 12-16

**N-myristoylation sites:**

amino acids 9-15,13-19,15-21,215-221,224-230

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**FIGURE 257**

CGGACGCGTGGGGCCGT**ATG**CGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCCC  
CCAGCCCCCTGCTCCTTTGGACTCTACTTCTGTTTGCAGCCCCATTTGGCCTGCTGGGGGAGA  
AGACCCGCCAGGTGTCTCTGGAGGTCATCCCTAACTGGCTGGGCCCCCTGCAGAACCTGCTTC  
ATATACGGGCAGTGGGCACCAATTCCACACTGCACTATGTGTGGAGCAGCCTGGGGCCTCTGG  
CAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCTGAGCATCAACTGGAGCCTCCTGC  
TATCCCCTGAGCCCGATGGGGGCTGATGGTGTCTCCCTAAGGACAGCATTTCAGTTTTCTTCTG  
CCCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGC  
CTTTGGGAAGACCATATCCTCCATACTCCTTGCCGATTTCTCTTGGAACAACATCACTGATT  
CATTGGATCCTGCCACCCTGAGTGCCACATTTCAAGGCCACCCCATGAACGACCCTACCAGGA  
CTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCTTTTCCAGGTCCAGCCGACCAGCCC  
AACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCTGATTGGAGCCT  
CTCCCCGGGGAAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGACT  
GCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGG  
ACCAGCTACTGTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCC  
AGAAGCCGGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTTCCCCTCTTCATCCTGCCTTAG  
CATACTCTCTTCCCCAGTCACCCATTGTCCGAGCCTTCTTTGGGTCCCAGAATAACTTCTGTG  
CCTTCAATCTGACGTTTCGGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT  
GGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCCCACTAGTCCTGGGCA  
TCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGGTTCTGCTGĈ  
TGCACCACAAGAAGTACTCAGAGTACCAGTCCATAAAT**TAA**GGCCCGCTCTCTGGAGGGAAGG  
ACATTACTGAACCTGTCTTGCTGTGCCTCGAACTCTGGAGGTTGGAGCATCAAGTTCCAGCC  
GGCCCTTCACTCCCCCATCTTGCTTTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCCTGG  
AGACCCCCAGGTGGGGCTTCCTTCATACTTTGTTGGGGGACTTTGGAGGCGGGCAGGGGACAG  
GGCTATTGATAAGGTCCCCTTGGTGTTCCTTCTTGCACTCTCCACACATTTCCCTTGGATGGG  
ACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGA  
TTTATTTTTTTTTCACAGGGAAAAAAAAAAAA

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**FIGURE 258**

MRGSVECTWGWGHCAPSPLLLWTLTLLFAAPFGLLGEKTRQVSLEVIPNWLGPLQNLLHIRAVG  
TNSTLHYVWSSLGPLAVVMVATNTPHSTLSINWSLLLSPEPDGGLMVLPKDSIQFSSALVFTR  
LLEFDSTNVSDTAAKPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHMNDPTRTFANGS  
LAFRVQAFSRSSRPAQPPRLLHTADTCQLEVALIGASPRGNRSLEFGLLEVATLGQGPDCPSMQE  
QHSIDDEYAPAVFQLDQLLWGS LPSGFAQWRPVAYSQKPGGRESALPCQASPLHPALAYSLPQ  
SPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGFPVVDGLSPLVLGIMAVAL  
GAPGLMLLGGGLVLLLHHKKYSEYQSIN

**Important features:****Signal peptide:**

amino acids 1-35

**Transmembrane domain:**

amino acids 365-386

**N-glycosylation sites:**

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234, 333-337

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 397-401

**N-myristoylation sites:**

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

**Leucine zipper pattern:**

amino acids 371-393

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**FIGURE 259**

CAGGCGGGCCCCGCGCGGCAGGGCCCTGGACCCGCGCGGCTCCCGGGGATGCTGAGCAAGGCGCTGCTGCGCCT  
CGTGTCTGCCGTCAACCGCAGGAGGATGAAGCTGCTGCTGGGCATCGCCTTGCTGGCCTACGTGCGCTCTGTTTG  
GGGCAACTTCGTTAATATGAGGTCTATCCAGGAAAATGGTGAATAAAATTGAAAGCAAGATTGAAGAGATGGT  
TGAACCACTAAGAGAGAAAATCAGAGATTTAGAAAAAGCTTTACCCAGAAAATACCCACCAGTAAAGTTTTTATC  
AGAAAAGGATCGGAAAAGAATTTTGATAACAGGAGGCGCAGGGTTCGTGGGCTCCCATCTAACTGACAACTCAT  
GATGGACGGCCACGAGGTGACCGTGGTGGACAAATTTCTTCACGGGCAGGAAGAGAAAACGTGGAGCACTGGATCGG  
ACATGAGAACTTCGAGTTGATTAACCACGACGTGGTGGAGCCCCTCTACATCGAGGTTGACCAGATATACCATCT  
GGCATCTCCAGCCTCCCCTCCAACTACATGTATAATCCTATCAAGACATTAAGACCAATACGATTGGGACATT  
AAACATGTTGGGGCTGGCAAAACGAGTCGGTGGCCGTCTGCTCCTGGCCTCCACATCGGAGGTGTATGGAGATCC  
TGAAGTCCACCCTCAAAGTGAGGATTACTGGGGCCACGTGAATCCAATAGGACCTCGGGCCTGCTACGATGAAGG  
CAAACGTGTTGCAGAGACCATGTGCTATGCCTACATGAAGCAGGAAGGCGTGGAAAGTGCAGTGGCCAGAATCTT  
CAACACCTTTGGGCCACGCATGCACATGAACGATGGGCGAGTAGTCAGCAACTTCATCCTGCAGGCGCTCCAGGG  
GGAGCCACTCACGGTATACGGATCCGGGTCTCAGACAAGGGCGTTCCAGTACGTACGTCAGCGATCTAGTGAATGGCCT  
CGTGGCTCTCATGAACAGCAACGTGAGCAGCCCGTCAACCTGGGGAACCCAGAAGAACACACAATCCTAGAATT  
TGCTCAGTTAATTAAAAACCTTGTTGGTAGCGGAAGTGAAATTCAGTTTCTCTCCGAAGCCCAGGATGACCCACA  
GAAAAGAAAACCAGACATCAAAAAGCAAAGCTGATGCTGGGGTGGGAGCCCGTGGTCCCGCTGGAGGAAGGTTT  
AAACAAAGCAATTCATACTTCCGTAAAGAACTCGAGTACCAGGCAAATAATCAGTACATCCCCAAACCAAAGCC  
TGCCAGAATAAAGAAAGGACGGACTCGCCACAGCTGAACCTCCTCACTTTTAGGACACAAGACTACCATTGTACAC  
TTGATGGGATGTATTTTGGCTTTTTTTTGTGTCGTTTAAAGAAAGACTTTAACAGGTGTCATGAAGAACAAC  
TGGAATTTCACTCTGAAGCTTGCTTTAATGAAATGGATGTGCCTAAAAGCTCCCTCAAAAACTGCAGATTTTG  
CCTTGCACTTTTGAATCTCTCTTTTATGTAAATAGCGTAGATGCATCTCTGCGTATTTTCAAGTTTTTTTAT  
CTTGCTGTGAGAGCATATGTTGTGACTGTGCTTGACAGTTTTATTTACTGGTTTCTTTGTGAAGCTGAAAAGGAA  
CATTAAAGCGGGACAAAAATGCCGATTTTATTTATAAAAGTGGGTACTTAATAAATGAGTCGTTATACTATGCAT  
AAAGAAAATCCTAGCAGTATTGTGAGGTGGTGGTGCCTGGCATTGATTTTAGGGCAGATAAAAGAATTCGTG  
TGAGAGCTTTATGTTTCTCTTTAATTCAGAGTTTTTCCAAGGTCTACTTTTGAGTTGCAAACCTGACTTTGAAA  
TATTCCTGTTGGTCATGATCAAGGATATTTGAAATCACTACTGTGTTTGGCTGCGTATCTGGGGCGGGGCAGGT  
TGGGGGGCACAAAGTTAACATATTCTTGGTTAACCATGGTTAAATATGCTATTTTAATAAAATATTGAAACTCA

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**FIGURE 260**

MVSKALLRLVSAVNRMRMKLLLGIALLAYVASVWGNFVNMRSIQENGELKIESKIEEMVEPLR  
EKIRDLEKSFTQKYPPVKFLSEKDRKRILITGGAGFVGSHLTDKLMMDGHEVTVVDNFFTGRK  
RNVEHWIGHENFELINHDVVEPLYIEVDQIYHLASPPNMYNPIKTLKTNTIGTLNMLGL  
AKRVGARLLLASTSEVYGDPEVHPQSEDYWGHNPIGPRACYDEGKRVAETMCYAYMKQEGVE  
VRVARIFNTFGPRMHMNDGRVVSFILQALQGEPLTVYSGSQTRAFQYVSDLVNLVALMNS  
NVSSPVNLGNPEEHTILEFAQLIKNLVGSGSEIQFLSEAQDDPQKRKPDIKKAKMLGWEPVV  
PLEEGLNKAIHYFRKELEYQANNQYIPKPKPARIKKGRTRHS

**Important features:****Signal peptide:**

amino acids 1-32

**N-glycosylation site:**

amino acids 316-320

**Tyrosine kinase phosphorylation site:**

amino acids 235-244

**N-myristoylation sites:**

amino acids 35-41,101-107,383-389

**Amidation sites:**

amino acids 123-127,233-237



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**FIGURE 261**

GCGTGGTGCGGGGGCGTGGGGAAATCGGGTTGCCCCAGCCGTTACTGGTCCGCGCAGTCAGGG  
CATCCTCCGCATCCTCCACATCCTTCC**ATG**GCTCTGAAGAATAAATTCAGTTGTTTATGGATC  
TTGGGTCTGTGTTTGGTAGCCACTACATCTTCCAAAATCCCATCCATCACTGACCCACACTTT  
ATAGACAACATGCATAGAAGCCCACAACGAATGGCGTGGCAAAGTCAACCCTCCCGCGGCCGAC  
ATGAAATACATGATTTGGGATAAAGGTTTAGCAAAGATGGCTAAAGCATGGGCAAACCAAGTGC  
AAATTTGAACATAATGACTGTTTGGATAAATCATATAAATGCTATGCAGCTTTTGAATATGTT  
GGAGAAAATATCTGGTTAGGTGGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGG  
TATAATGAAACCCAATTTTATGATTTTGATAGTCTATCATGCTCCAGAGTCTGTGGCCATTAT  
ACACAGTTAGTTTGGGCCAATTCATTTTATGTGCGTTGTGCAGTTGCAATGTGTCCTAACCTT  
GGGGGAGCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAATATG  
CCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAGAAGAGAAATGTGTAAAGAAC  
CTCTGCAGGACTCCACAACCTTATTATACCTAACCAAATCCATTTCTGAAGCCAACGGGGAGA  
GCACCTCAGCAGACAGCCTTTAATCCATTCAGCTTAGGTTTTCTTCTTCTGAGAATCTTT**TAA**  
TGTCATTTATATACAAAAGAAATTCTCAAATGTAAATAAAGGAATAGTTTATTGCTTAATA

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**FIGURE 262**

MALKNKFSLWILGLCLVATTSSKIPSIDPHFIDNCIEAHNEWRGKVNPPAADMKYMIWDKG  
LAKMAKAWANQCKFEHNDCLDKSYKCYAAFEYVGENIWLGGIKSFTPRHAITAWYNETQFYDF  
DSLSCSRVCGHYTQLVWANSFYVGCAMCPNLGGASTAIFVCNYGPAGNFANMPYPYARGESC  
SLCSKEEKCVKNLCRTPQLIIPNQNPFLKPTGRAPQQTAFNPFSLGFLLLRIF

**Important features:****Signal peptide:**

amino acids 1-23

**N-glycosylation site:**

amino acids 119-123

**N-myristoylation sites:**

amino acids 103-109,150-156,160-166,161-167,175-181

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1:**

amino acids 136-156

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:**

amino acids 166-178

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**FIGURE 263**

CGCCCTCCGACCCGCCCCGCGGCGCATTGTGGGATCTGTGCGCTTGTCAGGTGGTGGAGGAAA  
AGGCGCTCCGTCA**ATG**GGGATCCAGACGAGCCCCGTCCTGCTGGCCTCCCTGGGGGTGGGGCTG  
GTCACCTCTGCTCGGCCTGGCTGTGGGCTCCTACTTGGTTCGGAGGTCCCGCCGGCCTCAGGTG  
ACTCTCCTGGACCCCAATGAAAAGTACCTGCTACGACTGCTAGACAAGACGACTGTGAGCCAC  
AACACCAAGAGGTTCCGCTTTGCCCTGCCCACCGCCCACCACACTCTGGGGCTGCCTGTGGGC  
AAACATATCTACCTCTCCACCCGAATTGATGGCAGCCTGGTCATCAGGCCATACACTCCTGTC  
ACCAGTGATGAGGATCAAGGCTATGTGGATCTTGTCATCAAGGTCTACCTGAAGGGTGTGCAC  
CCCAAATTTCTGAGGGAGGGAAGATGTCTCAGTACCTGGATAGCCTGAAGGTTGGGGATGTG  
GTGGAGTTTCGGGGGCCAAGCGGGTTGCTCACTTACACTGGAAAAGGGCATTTTAAACATTGAG  
CCCAACAAGAAATCTCCACCAGAACCCCGAGTGGCGAAGAACTGGGAATGATTGCCGGCGGG  
ACAGGAATCACCCCAATGCTACAGCTGATCCGGGCCATCCTGAAAGTCCCTGAAGATCCAACC  
CAGTGCTTTCTGCTTTTTGCCAACCAGACAGAAAAGGATATCATCTTGCGGGAGGACTTAGAG  
GAACTGCAGGCCCCGCTATCCCAATCGCTTTAAGCTCTGGTTCACCTCTGGATCATCCCCAAAA  
GATTGGGCCTACAGCAAGGGCTTTGTGACTGCCGACATGATCCGGGAACACCTGCCCGCTCCA  
GGGGATGATGTGCTGGTACTGCTTTGTGGGCCACCCCCAATGGTGCAGCTGGCCTGCCATCCC  
AACTTGACAACTGGGCTACTCACAAAAGATGCGATTACCTACT**TGAG**CATCCTCCAGCTTC  
CCTGGTGCTGTTGCTGTCAGTTGTTCCCCATCAGTACTCAAGCACTATAAGCCTTAGATTCCCT  
TTCCTCAGAGTTTCAGGTTTTTTCAGTTACATCTAGAGCTGAAATCTGGATAGTACCTGCAGG  
AACAATATTCCTGTAGCCATGGAAGAGGGCAAGGCTCAGTCACTCCTTGGATGGCCTCCTAAA  
TCTCCCCGTGGCAACAGGTCCAGGAGAGGCCCATGGAGCAGTCTCTTCCATGGAGTAAGAAGG  
AAGGGAGCATGTACGCTTGGTCCAAGATTGGCTAGTTCCTTGATAGCATCTTACTCTCACCTT  
CTTTGTGTCTGTGATGAAAGGAACAGTCTGTGCAATGGGTTTTACTTAAACTTCACTGTTCAA  
CCTATGAGCAAATCTGTATGTGTGAGTATAAGTTGAGCATAGCATACTTCCAGAGGTGGTNTT  
ATGGAGATGGCAAGAAAGGAGGAAATGATTTCTTCAGATNTCAAAGGAGTCTGAAATATCATA  
TTTCTGTGTGTGTCTCTCTCAGCCCCTGCCCAGGCTAGAGGGAAACAGCTACTGATAATCGAA  
AACTGCTGTTTGTGGCANGAACCCCTGGCTGTGCAAATAAATGGGGCTGAGGCCCTGTGTGA  
TATTGAAGA

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**FIGURE 264**

MGIQTSPVLLASLGVGLVTLLGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTR  
FRFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQGYVDLVIKVYLKGVHPKFP  
EGGKMSQYLDLKVGDVVEFRGPSGLLTYTGKGHFNIQPNKSPPEPRVAKKLGMIAGGTGIT  
PMLQLIRAILKVPEDPTQCFLLFANQTEKDIIILREDLEELQARYPNRFLWFTLDHPPKDWAY  
SKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQKMRFTY

**Important features:****Signal peptide:**

amino acids 1-26

**N-glycosylation site:**

amino acids 214-218

**N-myristoylation sites:**

amino acids 22-28, 76-82, 128-134, 180-186

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**FIGURE 265**

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAGA  
ACGCGGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTATAG  
AATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAAGTGCACCTCGGT  
TCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACG**ATG**TTGGGGGCCCCGCTCAGG  
CTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCC  
TCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC  
AGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTAC  
AGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTGTGGTGATTACAGGTGTGATGAGCAGA  
AGATACCTCTGCATGGATTTTCAGAGGCAACATTTTTGGATCACACTATTTTCGACCCGGAGAAC  
TGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCAC  
TTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTAC  
TCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTCAACACCCCCATACCACGG  
CGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGG  
GCCCCGATGACCCCGGCCCCGGCCTCCTGTTACAGGAGCTCCCGAGCGCCGAGGACAACAGC  
CCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTTCGAGTGAACACGCACGCTGGGGGA  
ACGGGCCCCGAAGGCTGCCGCCCCCTTCGCCAAGTTCATC**TAG**GGTCGCTGG

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**FIGURE 266**

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARN SYHLQIHKN GHVDG  
APHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDV  
YHSPQYHFLVSLGRAKRAFLPGMNPPYPYSQFLSRRNEIPLIHFNTPIPRRHTRSAEDDSERDP  
LNVLKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFAKFI

**Important features:****Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 175-179

**N-myristoylation site.**

amino acids 33-39, 100-106, 225-231, 229-235

**HBGF/FGF family proteins**

amino acids 73-124

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**FIGURE 267**

GGCTGAGGGGAGGCCCGGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGAGAGAAGCGCCTGC  
AGCCAACCAAGGGTCAGGCTGTGCTCACAGTTTCCTCTGGCGGCATGTAAAGGCTCCACAAAGGAGTTGGGAGTTC  
AAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCCCAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGG  
CTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTG  
CCGGAGCCCTCTGTGGAGGCAGAGCCAGTGGAGCCAGTGGAGCAGGGCTGCTTGGCAGCCACCGGCCCTGCAACT  
CAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATGTGAGGAGCCGCCCCGG  
AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGAATAACCACCATTTTGCAAGGACCATGAGG  
CCACTGTGCGTGACATGCTGGTGGCTCGGACTGCTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTT  
GAGGGCACTGAGGAGGGCTCGCCAAGAGAGTTTACCTAAACAGGTACAAGCGGGCGGGCAGTCCCAGGAC  
AAGTGCACCTACACCTTATTGTGCCCCAGCAGCGGGTACGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG  
GTGCTTCTGGAGAACCAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCAGAAGCGGCAG  
ATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTGTGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGC  
CGCAACATGAACTCGCGGGTCACGCAGCTCTACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACCGG  
TTGGAGCTCTCCAGCTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG  
GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCAACAACCAATCAGAGATCATCGCGCAGCTTGAGGAG  
CACTGCCAGAGGGTGCCCTCGGCCAGGCCCTCCCCAGCCACCCCCGCTGCCCCGCCCCGGGTCTACCAACCA  
CCCACCTACAACCGCATCATCAACCAGATCTCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCA  
CCCCCTCTGCCCCACTATGCCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGCCCCATGGAGAGAC  
TGCCTGCAGGCCCTGGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACCAACCGCCTC  
ATGCAGGTGTGGTGGCAGCAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTGGATGGCTCTGTT  
AACTTCTTCAGGAAGTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGACGGCGAATACTGGCTGGGCCTGGAG  
AACATTTACTGGCTGACGAACCAAGGCAACTACAACTCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAGTC  
TTTGCAGAATACGCCAGTTTCCGCCTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGC  
AATGCGGGTGACTCCTTTACATGGCACAACGGCAAGCAGTTCACCACCCTGGACAGAGATCATGATGTCTACACA  
GGAAACTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAACCTCAACGGGGTCTGG  
TACCGCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA  
CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCAACACCTTCCACTAAGCCAGCTCCCCCTCTGACCTCTC  
GTGGCCATTGCCAGGAGCCACCCCTGGTCACGCTGGCCACAGCACAAGAACAACCTCCTCACCAGTTCATCCTGA  
GGCTGGGAGGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAAGTGAATCGATACGGT  
GTTTTCTGTCCCTCTACTTTCCTTACACCAGACAGCCCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA  
CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA

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**FIGURE 268**

MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQQ  
RVTGAICVNSKEPEVLLLENRVHKQELELLNNELLKQKRQIETLQQLEVDGGIVSEVKLLRKE  
SRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLEHKYQHLATL  
AHNQSEIIAQLEEHQCRVPSARVPVQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNLKVLP  
PPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSIIYLVKPENTNRLMQVWCDQRHDPGG  
WTVIQRRLDGSVNFFRNWETKQGFQGNIDGEYWLGLENIYWLTNQGNKLLVTMEDWSGRKVF  
AEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAPHYQKGGWWYN  
ACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVVMIRPNPNTFH

**Important features:****Signal peptide:**

amino acids 1-22

**N-glycosylation sites:**

amino acids 164-168, 192-196

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 124-128

**Tyrosine kinase phosphorylation sites:**

amino acids 177-184, 385-393, 385-394, 461-468

**N-myristoylation sites:**amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347, 465-471,  
473-479**Amidation site:**

amino acids 373-377

**Fibrinogen beta and gamma chains C-terminal domain signature:**

amino acids 438-451

**Fibrinogen beta and gamma chains C-terminal domain proteins:**

amino acids 305-343, 365-402, 411-424, 428-458

**Trehalase proteins:**

amino acids 275-292



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**FIGURE 269**

GCCGAGCTGAGCGGATCCTCAC**ATG**ACTGTGATCCGATTCTTTCCAGCGGCTTCTGCAACCAA  
GCGGGTCTTACCCCCGGTCCCTCCGCGTCTCCAGTCCTCGCACCTGGAACCCCAACGTCCCCGA  
GAGTCCCCGAATCCCCGCTCCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGC  
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAGGGCGGACCCGTGCAGTC  
CAAGTCGCCGCGCTTTGCGTCCTGGGACGAGATGAATGTCTGGCGCACGGACTCCTGCAGCT  
CGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCTGGAGCGGCG  
CCTGAGCGCGTGCGGGTCCGCGCTGTCAGGGAACCGAGGGGTCCACCGACCTCCCGTTAGCCCC  
TGAGAGCCGGGTGGACCCCTGAGGTCTTACAGCCTGCAGACACAACCTCAAGGCTCAGAACAG  
CAGGATCCAGCAACTCTTCCACAAGGTGGCCAGCAGCAGCGGCACCTGGAGAAGCAGCACCT  
GCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCACAAGCACCTAGACCATGAGGT  
GGCCAAGCCTGCCCCGAAGAAAGAGGCTGCCCCGAGATGGCCAGCCAGTTGACCCGGCTCACAA  
TGTCAGCCGCGCTGCACCGGCTGCCCAGGGATTGCCAGGAGCTGTTCCAGGTTGGGGAGAGGCA  
GAGTGGACTATTTGAAATCCAGCCTCAGGGGTCTCCGCCATTTTTGGTGAAGTCAAGATGAC  
CTCAGATGGAGGCTGGACAGTAATTCAGAGGCGCCACGATGGCTCAGTGGACTTCAACCGGCC  
CTGGGAAGCCTACAAGGCGGGGTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAA  
GGTGCATAGCATCACGGGGGACCGCAACAGCCGCCTGGCCGTGCAGCTGCGGGACTGGGATGG  
CAACGCCGAGTTGCTGCAGTTCTCCGTGCACCTGGGTGGCGAGGACACGGCCTATAGCCTGCA  
GCTCACTGCACCCGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGT  
ACCCTTCTCCACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAACTGCGCCAAGAGCCT  
CTCTGGAGGCTGGTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTC  
CATCCACAGCAGCGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTA  
CTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCCT**AGCG**  
TCCTGGCTGGGCCTGGTCCCAGGCCCCAGAAAGACGGTGAAGTCTTGGCTCTGCCCGAGGATGT  
GGCCGTTCCTGCCTGGGCAGGGGCTCCAAGGAGGGGCCATCTGGAAACTTGTGGACAGAGAA  
GAAGACCACGACTGGAGAAGCCCCCTTTCTGAGTGCAGGGGGGCTGCATGCGTTGCCTCCTGA  
GATCGAGGCTGCAGGATATGCTCAGACTCTAGAGGCGTGGACCAAGGGGCATGGAGCTTCACT  
CCTTGCTGGCCAGGGAGTTGGGGACTCAGAGGGACCACTTGGGGCCAGCCAGACTGGCCTCAA  
TGGCGGACTCAGTCACATTGACTGACGGGGACCAAGGCTTGTGTGGTTCGAGAGCGCCCTCAT  
GGTGCTGGTGCTGTTGTGTGTAGGTCCCCTGGGGACACAAGCAGGCGCCAATGGTATCTGGGC  
GGAGCTCACAGAGTTCTTGAATAAAAGCAACCTCAGAACAC

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**FIGURE 270**

MTVIRFFPAASATKRVLPVLRVSSPRTWNPVPESPRIPAPRLPKRMSGAPTAGAALMLCAA  
TAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAERTRSQLSALERRLSACGSA  
CQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFHKVAQQQRHLEKQHLRIQHLQS  
QFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSRLHRLPRDCQELFQVGERQSGLFQI  
PQGSPPFLVNCKMTSDGGWTVIQRRHDGSVDENRPWEAYKAGFGDPHGEFWLGLEKVHSITGD  
RNSRLAVQLRDWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPSPGLSVPFSTWDQ  
DHDLRDKNCAKSLSGGWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATT  
MLIQPMAAEAAS

**Important features:****Signal peptide:**

Amino acids 1-13

**Transmembrane domain:**

Amino acids 53-70

**N-glycosylation site:**

Amino acids 224-228

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 46-50;118-122

**N-myristoylation sites:**

Amino acids 50-56;129-135;341-347;357-363

**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 396-409

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**FIGURE 271**

CGGACGCGTGGGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGGG  
AACAAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGCTG  
CTGCTGCTGACCATGGCCTTGGCCGGAGGTTCTGGGGACCGCTTCGGCTGAAGCATTTGACTCG  
GTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACACCTAC  
CCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTT  
GTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATTCCTAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTCGCT  
GAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAACT  
CTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACCTCTTCATGG  
ACTTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCCAGAAATCCAG  
TACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAAGCAAAATGTCC  
TATCTGCAAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGAGAAAGTGATGGC  
TTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCTGTCTCTCGGTG  
ATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGCAGTATGTTCCCTCT  
GAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAGCTAAACAGATATCCA  
GCTTCTTCTCTTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGAAGCAGGGCCTCTACCT  
ACAAAAGTGAATCTTGCTCATTCTGAAATTTTAAGCATTTTCTTTTAAAAGACAAGTGTAATA  
GACATCTAAAATTCCACTCCTCATAGAGCTTTTAAAATGGTTTCATTGGATATAGGCCTTAAG  
AAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

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**FIGURE 272**

MAAPKGS LWVRTQLGLPPLLLLT MALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYPK  
EEELYACQ RGCRLFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCQNQLPFAEL  
RQEQLMSLMPKMHLLFPLTLVRSFWS DMMSAQSFITSSWTFY LQADDGKIVIFQSKPEIQYA  
PHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVLSVMV  
LLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAGPLPTK  
VNLAHSEI

**Important features:****Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation site:**

amino acids 90-94

**N-myristoylation sites:**

amino acids 28-34, 29-35, 31-37, 86-92

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**FIGURE 273**

CCCACGCGTCCGAACCTCTCCAGCG**ATG**GGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGTG  
CTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACCGA  
CCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCACGT  
GCAGGTCACCGGGCGTTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGCTCAT  
AGTGGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAGTACAT  
CTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTGCGTGTT  
CACGGAGATCGTGCTGGAGAACAACCTATACGGCCTTCCAGAACGCCCGGCACGAGGGCTGGTT  
CATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAACCAGCGCGA  
GGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCAGCCGAGAAGCA  
GAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACCCGCCGACCAAGCGCACACGGCGGCCCCA  
GCCCCTCACG**TAG**TCTGGGAGGCAGGGGGCAGCAGCCCCTGGGCCGCCTCCCCACCCCTTTCC  
CTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCCGAGGGAGGACCC  
TGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTGCCCCAGGGGCGGC  
TGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACTGAGTGTACCCCTGA  
TCTCAGGCCACCAGCCTCTGCCGGCCTCCCAGCCGGGCTCCTGAAGCCCGCTGAAAGGTCAGC  
GACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCCTCAAATCTGCTTCTCGGATCT  
CCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTAGGAAGGGACTTTTGTTT  
GTTTGTTTGTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAAATAGAGGGTTGTCCACTCCTCA  
CATTCCACGACCCAGGCCTGCACCCCACCCCCAACTCCCAGCCCCGGAATAAAACCATTTTCC  
TGC

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**FIGURE 274**

MGAARLLPNLTLCQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHHVQVTGRRIS  
ATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLIGKPSGKSKDCVFTEIVLENN  
YTAFQONARHEGWFMATFRQGRPRQASRSRQNRQEAHFIRLYQGQLPFPNHAEEKQKQFEFVGS  
APTRRTKRTRRPQPLT

**Important features:****Signal peptide:**

Amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

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**FIGURE 275**

TATTTACCATATCAGATTCACATTCAGTCCTCAGCAAAATGAAGGGCTCCATTTTCACTCTGT  
TTTTATTCTCTGTCTTATTGCCATCTCAGAAGTGCGGAGCAAGGAGTCTGTGAGACTCTGTG  
GGCTAGAATACATACGGACAGTCATCTATATCTGTGCTAGCTCCAGGTGGAGAAGGCATCTGG  
AGGGGATCCCTCAAGCTCAGCAAGCTGAGACAGGAACTCCTTCCAGCTCCCACATAAACGTG  
AGTTTTCTGAGGAAAATCCAGCGCAAAACCTTCCGAAGGTGGATGCCTCAGGGGAAGACCGTC  
TTTGGGGTGGACAGATGCCCACTGAAGAGCTTTGGAAGTCAAAGAAGCATTTCAGTGATGTCAA  
GACAAGATTTACAACTTTGTGTTGCACTGATGGCTGTTCCATGACTGATTTGAGTGCTCTTT  
GCTAAGACAAGAGCAAATACCCAATGGGTGGCAGAGCTTTATCACATGTTTAATTACAGTGTT  
TTACTGCCTGGTAGAACACTAATATTGTGTTATTAAATGATGGCTTTTGGGTAGGCAAAACCT  
TCTTTTCTAAAAGGTATAGCTGAGCGGTTGAAACCACAGTGATCTCTATTTTCTCCCTTTGCC  
AAGGTTAATGAAGTGTCTTTTCAAATTCTACTAATGCTTTGAAATTCAAATGCTGCGCAAA  
ATTGCAATAAAAATGCTATAAA

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**FIGURE 276**

MKGSIFTLFLFSVLFAISEVRSKESVRLCGLEYIRTVIYICASSRWRRLHLEGIPQAQQAETGN  
SFQLPHKREFSEENPAQNLPKVDASGEDRLWGGQMPTEELWKSCKHVSMSRQDLQTLCCCTDGC  
SMTDLSALC

**Important features:**

**Signal sequence:**

amino acids 1-18

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 107-111

**N-myristoylation sites:**

amino acids 3-9, 52-58, 96-102, 125-131

**Insulin family signature:**

amino acids 121-136

**Insulin family proteins:**

amino acids 28-46



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**FIGURE 277**

GCAGCTGGTTACTGCATTTCTCCATGTGGCAGACAGAGCAAAGCCACAACGCTTTCTCTGCTGGATTAAAGACGG  
CCCACAGACCAGAACTTCCACTATACTACTTAAATACATAGGTGGCTTGTCAAATTCATTTGATTAGTATTGT  
AAAAGGAAAAAGAAGTTCCTTCTTACAGCTTGGATTCAACGGTCCAAAACAAAATGCAGCTGCCATTAAGTCT  
CAGATGAACAACTTCTACACTGATTTTAAATCAAGAATAAGGGCAGCAAGTTTCTGGATTCACTGAATCAAC  
AGACACAAAAGCTGGCAATATAGCAACTATGAAGAGAAAAGCTACTAATAAAATTAACCCAACGCATAGAAGAC  
TTTTTTTTCTCTTCTAAAAACAATAAGTAAAGACTTAAATTTAAACACATCATTTTACAACCTCATTTCAAAAT  
GAAGACTTTTACCTGGACCCTAGGTGTGCTATTCTTCTACTAGTGGACACTGGACATTGCAGAGGTGGACAATT  
CAAAATTAATAAAATAAACCAGAGAAGATACCCCTCGTGCCACAGATGGTAAAGAGGAAGCAAAGAAATGTGCATA  
CACATTCCTGGTACCTGAACAAAGAATAACAGGGCCAATCTGTGTCAACACCAAGGGGCAAGATGCAAGTACCAT  
TAAAGACATGATCACCAGGATGGACCTGAAAACCTGAAGGATGTGCTCTCCAGGCAGAAGCGGGAGATAGATGT  
TCTGCAACTGGTGGTGGATGTAGATGGAAACATTGTGAATGAGGTAAAGCTGCTGAGAAAGGAAAGCCGTAACAT  
GAACTCTCGTGTACTCAACTCTATATGCAATTATTACATGAGATTATCCGTAAGAGGGATAATTCACTTGAAC  
TTCCCAACTGGAAAACAAAATCCTCAATGTCAACACAGAAATGTTGAAGATGGCAACAAGATACAGGGAACCTAGA  
GGTGAATACGCTTCCTTGACTGATCTTGTCAATAACCAATCTGTGATGATCACTTTGTTGGAAGAACAGTGCTT  
GAGGATATTTTCCCGACAAGACACCCATGTGTCTCCCCACTTGTCCAGGTGGTGCCACAACATATTCCTAACAG  
CCAACAGTATACTCCTGGTCTGCTGGGAGGTAAAGAGATTCAAGAGGGATCCAGGTATCCAGAGATTTAATGCC  
ACCACCTGATCTGGCAACTTCTCCACCAAAAGCCCTTTCAAGATACCACCGGTAACCTTTCATCAATGAAGGACC  
ATTCAAAGACTGTCAGCAAGCAAAGAAGCTGGGCATTCCGTCAAGAGGGATTATATGATTAAACCTGAAAACAG  
CAATGGACCAATGCAGTTATGGTGTGAAAACAGTTTGGACCCTGGGGGTTGGACTGTTATTAGAAAAGAACAGA  
CGGCTCTGTCAACTTCTTCAGAAATTGGGAAAATTATAAGAAAGGGTTTGGAAACATTGACGGAGAATACTGGCT  
TGGACTGGAAAATATCTATATGCTTAGCAATCAAGATAATTACAAGTTATTGATTGAATTAGAAGACTGGAGTGA  
TAAAAAGTCTATGCAGAATACAGCAGCTTTCGTCTGGAACCTGAAAGTGAATTCTATAGACTGCGCCTGGGAAC  
TTACCAGGGAAATGCAGGGGATTCTATGATGTGGCATAATGGTAAACAATTCACCACACTGGACAGAGATAAAGA  
TATGTATGCAGGAACTGCGCCCACTTTCATAAAGGAGGCTGGTGGTACAATGCCTGTGCACATTCTAACCTAAA  
TGGAGTATGGTACAGAGGAGGCCATTACAGAAGCAAGCAAGATGGAATTTTCTGGGCCGAATACAGAGGCGG  
GTCAATACTCCTTAAGAGCAGTTCAAGATGATGATCAAGCCTATTGACTGAAGAGAGACACTCGCCAATTTAAATGA  
CACAGAACTTTGTACTTTTCAGCTCTTAAAAATGTAAATGTTACATGTATATTACTTGGCACAATTTATTTCTAC  
ACAGAAAGTTTTTAAATGAATTTTACCCTAATAAAGGGAACCTATAAATGTAGTTTCATCTGTCTGCTCAAT  
TACTGCAGAAATTTATGTATCCACAACCTAGTTATTTTAAAAATTATGTTGACTAAATACAAAGTTTGTTTTC  
TAAAAATGTAAATATTTGCCACAATGTAAAGCAAATCTTAGCTATATTTTAAATCATAAATAACATGTTCAAGATA  
CTTAACAATTTATTTTAAATCTAAGATTGCTCTAACGCTCTAGTGAAAAAATATTTTTTAAATTTTCAAGCAATA  
ATGCATTTTATTTTATAAATAACAGACAGAAATTAGGGAGAACTTCTAGTTTTGCCAATAGAAAATGTTCTT  
CCATTGAATAAAAGTTATTTCAAATTTGAATTTGTGCCTTTCACACGTAATGATTAAATCTGAATTTCTAATAATA  
TATCCTATGCTGATTTTCCCAAAACATGACCCATAGTATTAAATACATATCATTTTAAAAATAAAAAAAACCC  
AAAAATAATGCATGCATAATTTAAATGGTCAATTTATAAAGACAAATCTATGAATGAATTTTTCAGTGTTATCTT  
CATATGATATGCTGAACACCAAAATCTCCAGAAATGCATTTTATGTAGTTCTAAATCAGCAAAATATTGGTATT  
ACAAAAATGCAGAATATTTAGTGTGCTACAGATCTGAATTATAGTTCTAATTTATTATTACTTTTTTCTAATTT  
ACTGATCTTACTACTACAAAGAAAAAAACCCCAACCCATCTGCAATTCAAATCAGAAAGTTTGGACAGCTTTAC  
AAGTATTAGTGCATGCTCAGAACAGGTGGGACTAAAACAACTCAAGGAAGTTGGCTGTTTTCCCGATACTGA  
GAATTCACAGCTCCAGAGCAGAAGCCACAGGGGCATAGCTTAGTCCAACTGCTAATTTTCAATTTTACAGTGTAT  
GTAAAGCTTAGTCTCACAGTGTCTTAACTCATCTTTGCAATCAACAACCTTTACTAGTGACTTTCTGGAACAATT  
TCCTTTCAGGAATACATATTTCACTGCTTAGAGGTGACCTTGCCTTAATATATTTGTGAAGTTAAATTTTAAAGA  
TAGCTCATGAAACTTTTGTGTTAAGCAAAAAGAAACCTCGAATTGAAATGTGTGAGGCAAACTATGCATGGGAAT  
AGCTTAATGTGAAGATAATCATTTGGACAACCTCAATCCATCAACATGACCAATGTTTTTTCATCTGCCACATCTC  
AAAATAAACTTCTGGTGAACAAATTAACAAAATATCCAAACCTCAAAAAAA

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**FIGURE 278**

MKTFTWTLGVLFFLLVDTGHCRGGQFKIKKINQRRYPRATDGKEEAKKCAYTFLVPEQRITGP  
ICVNTKGQDASTIKDMITRMDLENLKDVLRSQKREIDVLQLVVDVDGNIVNEVKLLRKESRNM  
NSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNNQ  
SVMITLLEEQCLRIFSRQDTHVSPPLVQVVPQHIPNSQQYTPGLLGGNEIQRDPGYPRDLMPP  
PDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMQLWCENSLDP  
GGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLENIYMLSNQDNKLLIELEDWSDKK  
VYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMMWHNGKQFTTLDRDKDMYAGNCAHFHKGWW  
YNACAHSNLNGVWYRGGHYRSKHQDGIFWAEYRGGSYSLRAVQMMIKPID

**Important features:****Signal sequence:**

Amino acids 1-23

**N-glycosylation sites:**

Amino acids 160-164;188-192

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 120-124

**Tyrosine kinase phosphorylation sites:**

Amino acids 173-180;387-396

**N-myristoylation sites:**Amino acids 70-76;110-116;232-238,343-349;400-406;467-473;  
475-487**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 440-453

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**FIGURE 279**

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCCGCGATCCCGGC  
CCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGCCG  
CCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAAGCC  
CGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAGCGGA  
GGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGGCGTCG  
TGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCGAGCGCG  
AGAAATCCAACGCCTGCAAGTGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGCGACAAAA  
ACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAGAAGAAGAC  
CAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACCACTTGCAGC  
TGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACTCTGTTTAACC  
TCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCTGTACTTGGCAA  
TGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCAAATTCAAAGAAT  
CAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAGCAGCAGTCAGGCC  
GAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAACCATGTGAAGAAGA  
ACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGTACAAGGAGCCATCAC  
TGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACCAAGAGCAGAAGTGTCT  
CTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAACGTAGCCAGTGAGGGCAA  
AAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAATTCTTCTAGCAGTCCTTCA  
CCCAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGGCAGAGTTCACTATTCTATC  
TGCCATTAGACCTTCTTATCATCCATACTAAAGC

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**FIGURE 280**

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTKSCDKNKLVFSRVKLFSGSKRRRRRPE  
PQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDSTYTLFNLI PVGLRVVAIQGVQTKLYLAMN  
SEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVKKNK  
PAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSVSGVLNGGKSMSHNEST

**Important Features:****N-glycosylation site:**

Amino acids 242-246

**Glycosaminoglycan attachment sites:**

Amino acids 165-169, 218-222

**Tyrosine kinase phosphorylation site:**

Amino acids 93-100

**N-myristoylation sites:**

Amino acids 87-93, 231-237

**ATP/GTP-binding site motif A (P-loop):**

Amino acids 231-239

**HBGF/FGF family proteins:**

Amino acids 78-94, 102-153

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**FIGURE 281**

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGGA  
CTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGGCA  
ACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCTCCA  
TTTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTTCCCTTCCTGACATTGGCAGTGCCCC  
AGTAGGGGTGGGATGAGCGAATATTCCTCAAAGCTAAAGTCCCACACCCTGTAGATTACAAGAG  
TGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAAACCACG  
TCTTGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTGGAGAGGA  
GGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGGAGTACATA  
GGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACTGGCTGCTGTGGAGGGG  
GGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAGCGAGTCGGGG  
CCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAGCGCGCTCCGGG  
CGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGGCGGCGCTGGCCAGTAGCCTGAT  
CCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTGCGGCGAGCGGCGCGT  
GTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTGCTGTCCAAGGTGCG  
ACTGTGCGGGGGGCGGCCCGCGCGGCCGGACCGCGGGCCGGAGCCTCAGCTCAAAGGCATCGT  
CACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCGACGGAAGCATCCAGGG  
CACCCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCTGTGGGCCTCCGTGTGGT  
CACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGCTGAGGGACTGCTCTACAG  
TTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCTTTGAGAATTACTACGTCCT  
GTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCCTGGTACCTCGGCCTGGACAA  
GGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAAGGCAGCTGCCCCACTTTCTGCC  
CAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCCACAGTGTCCCCGAGGCCTCCCC  
TTCCAGTCCCCCTGCCCCCTGAAATGTAGTCCCTGGACTGGAGGTTCCCTGCACTCCCAGTGA  
GCCAGCCACCACCACAACCTGT

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**FIGURE 282**

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDRG  
PEPQLKGIVTKLFCRQGFYQLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHYMA  
MNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNRVKK  
TKAAAHFLPKLLEVAMYQEPSLHSVPEASPSSPPAP

**Important features:****Tyrosine kinase phosphorylation site:**

Amino acids 199-207

**N-myristoylation sites:**

Amino acids 54-60; 89-95; 131-137

**HBGF/FGF family signature:**

Amino acids 131-155

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**FIGURE 283**

**ATG**CCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTGG  
GACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACGGC  
AACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGGCGC  
CAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTTGCAA  
ATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCTTCAAC  
CTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTATATAGCC  
ATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTTTAAAGAA  
TCTGTTTTTGAATAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGGAATCTGGT  
AGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGAGTAAAGAAA  
ACCAAACCAGCAGCTCATTCTACCCAAGCCATTGGAAGTTGCCATGTACCGAGAACCATCT  
TTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAAGCACAAGTGCG  
TCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAAC**ATAG**

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**FIGURE 284**

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLRR  
QDPQLKGIVTRLYCRQGYLQMHPDGALDGTKDDSTNSTLFNLI PVGLRVVAIQGVKTGLYIA  
MNGEGYLYPSELF TPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNRVKK  
TKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

**Important features:****N-glycosylation sites:**

Amino acids 100-104, 242-246

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 28-32, 29-33

**Tyrosine kinase phosphorylation site:**

Amino acids 199-207

**N-myristoylation sites:**

Amino acids 38-44, 89-95, 118-124, 122-128, 222-228

**HBGF/FGF family proteins:**

Amino acids 104-155, 171-198



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**FIGURE 285**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCCAGGTTTTGCTTTGA  
TCCTTTTCAAAAAGTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCT  
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAGAGAC  
TCGGGAGTCGCTGCTTCCAAAGTGCCCGCCGTGAGTGAGCTCTCACCCAGTGCAGCCAAATGAGCCTCTTCGGGC  
TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC  
AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG  
GAAGTATTCACAGCCCAAGGTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG  
AGGAAATGTATGGATACAACCTTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT  
ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACCTATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG  
GAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCAGGGT  
TCTGCATCCACTACAACATTGTCTATGCCACAATTCACAGAAGCTGTGAGTCTTCAGTGCTACCCCTTCAGCTT  
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCCTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAG  
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAAGTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTTGGAA  
GAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTCT  
CAGTGTCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG  
GTGGGAAGTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC  
ACGAGGTCTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC  
ACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCA  
GAGCTGTGCAGTGCTGAGTGTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGTCT  
TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCAATCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA  
ACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAATGTTGTAT  
TAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCACCTAGCTGGGTTCTGTATTTTCAGTTCTTTC  
GATACGGCTTAGGGTAATGTGCTACAGGAAAAAAGTGTGCAAGTGAGCACCTGATTCCGTTGCTTGTCTTAAC  
TCTAAAGCTCCATGTCTGGGCTTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTCACAT  
ATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAAGTATGTTGCTATGAATTAACCTGT  
GTCATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAATTTCTGCCATTTAGAAGAAGAGAACTACA  
TTCATGGTTTGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG  
TTTCATTGTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCT  
ATTTTTACCAAAGGTATTTAATATCTTTTTTATGACAAGTATGATCAACTATTTTGTAGCTGGTAAATTTTTCT  
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA  
TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAAGTGAATTGGAATAGAATTGGTAAGTTGCAAA  
GACTTTTTGAAAATAATTAAATTATCATATCTCCATTCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGA  
AAGTAGACATTCAGATCCAGCCATTACTAACCTATTCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT  
AAAGCACCTTGAAAAGACTTGGCAGCTTCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCTATTTA  
TTGTGATGTTGTGGTTTTTATTATCTTAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTATGTACA  
GAAGTATGTCTCTTAACAGTTCACTTATTGTACTCTGGCAATTTAAAGAAAATCAGTAAATATTTTGTCTGT  
AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGATTGAATCATCAATAAAAGA  
ATGTGGCTATTTTGGGGAGAAAATTAATAAAAAAAAAAAAAAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

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**FIGURE 286**

MSLFGLLLLT SALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRF  
PHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGS  
GTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNA  
ITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNNLLTEEVRLYSCTP  
RNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKT  
GVRGLHKS LTDVALEHHEECDVCVRGSTGG

**Important features:****signal sequence:**

Amino acids 1-14

**N-glycosylation sites:**

Amino acids 25-29;55-59;254-258

**N-myristoylation sites:**

Amino acids 15-21;117-123;127-133;281-287;282-288;319-325

**Amidation site:**

Amino acids 229-233

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**FIGURE 287**

CAGCGCTGACTGCGCCGCGGAGAAAGCCAGTGGGAACCCAGACCCATAGGAGACCCGCGTCCC  
CGCTCGGCCTGGCCAGGCCCCGCGCT**ATG**GAGTTCCTCTGGGCCCCTCTCTTGGGTCTGTGCT  
GCAGTCTGGCCGCTGCTGATCGCCACACCGTCTTCTGGAACAGTTCAAATCCCAAGTTCCGGA  
ATGAGGACTACACCATACATGTGCAGCTGAATGACTACGTGGACATCATCTGTCCGCACTATG  
AAGATCACTCTGTGGCAGACGCTGCCATGGAGCAGTACATACTGTACCTGGTGGAGCATGAGG  
AGTACCAGCTGTGCCAGCCCCAGTCCAAGGACCAAGTCCGCTGGCAGTGCAACCGGCCAGTG  
CCAAGCATGGCCCGGAGAAGCTGTCTGAGAAGTTCAGCGCTTCACACCTTTACCCCTGGGCA  
AGGAGTTCAAAGAAGGACACAGCTACTACTACATCTCCAAACCCATCCACCAGCATGAAGACC  
GCTGCTTGAGGTTGAAGGTGACTGTCAGTGGCAAATCACTCACAGTCCTCAGGCCCATGACA  
ATCCACAGGAGAAGAGACTTGCAGCAGATGACCCAGAGGTGCGGGTTCTACATAGCATCGGTC  
ACAGTGCTGCCCCACGCCTCTTCCCCTTGCCTGGACTGTGCTGCTCCTTCCACTTCTGCTGC  
TGCAAACCCCG**TGA**AGGTGTGTGCCACACCTGGCCTTAAAGAGGGACAGGCTGAAGAGAGGGA  
CAGGCACTCCAAACCTGTCTTGGGGCCACTTTCAGAGCCCCCAGCCCTGGGAACCACTCCCAC  
CACAGGCATAAGCTATCACCTAGCAGCCTCAAACGGGTCAATATTAAGGTTTTCAACCGGAA  
GGAGGCCAACCAGCCCGACAGTGCCATCCCCACCTTCACCTCGGAGGGATGGAGAAAGAAGTG  
GAGACAGTCCTTTCCCACCATTCTTGCCTTTAAGCCAAAGAAACAAGCTGTGCAGGCATGGTC  
CCTTAAGGCACAGTGGGAGCTGAGCTGGAAGGGGCCACGTGGATGGGCAAAGCTTGTCAAAGA  
TGCCCCCTTCAGGAGAGAGCCAGGATGCCCAGATGAACTGACTGAAGGAAAAGCAAGAAACAG  
TTTCTTGCTTGGAAGCCAGGTACAGGAGAGGCAGCATGCTTGGGCTGACCCAGCATCTCCCAG  
CAAGACCTCATCTGTGGAGCTGCCACAGAGAAGTTTGTAGCCAGGTACTGCATTCTCTCCCAT  
CCTGGGGCAGCACTCCCCAGAGCTGTGCCAGCAGGGGGGCTGTGCCAACCTGTTCTTAGAGTG  
TAGCTGTAAGGGCAGTGCCCATGTGTACATTCTGCCTAGAGTGTAGCCTAAAGGGCAGGGCCC  
ACGTGTATAGTATCTGTATATAAGTTGCTGTGTGTCTGTCTGATTTCTACAACCTGGAGTTT  
TTTATACAATGTTCTTTGTCTCAAATAAAGCAATGTGTTTTTTCGG

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**FIGURE 288**

MEFLWAPLLGLCCSLAAADRHTVFWNSSNPKNEDYTIHVQLNDYVDIICPHYEDHSADAAM  
EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPQSAKHGPEKLSEKFQRFPTPFTLGKEFKEGHSYY  
YISKPIHQHEDRCLRLKVTVSGKITHSPQAHDNPQEKRLAADDPEVRVLHSIGHSAAPRLFPL  
AWTVLLLPLLLLQTP

**Important features:****Signal sequence:**

Amino acids 1-17

**N-glycosylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 118-127

**N-myristoylation site:**

Amino acids 10-16

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**FIGURE 289**

CGGACGCGTGGGCGGACGCGTGGGCGGCCCCACGGCGCCCGGGGCTGGGGCGGTGCTTCTTC  
CTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGGGC  
CTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGGCTC  
CAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTGCCGG  
GGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAGGTGGA  
AACACTGCCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTGGTAGAG  
GTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCTGAGTGAG  
GAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCGGACCTCTTCCAGTGGCTG  
TGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGCCCTCCTGCCTTCCCTGT  
CCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGGGACACGAGGG  
GGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCCAGTGTGGCCTT  
GGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGTTTTGGCCCCCTGT  
GCCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGGCTGGGCCCTGCAT  
CACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACTGTGGAGCTGACCAA  
TTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAGGCCTGCCTAGGCTGC  
ATGGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCAGCAGGTGGGCTCCAAG  
TGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGAACAAGCAGTGTGAAAAC  
ACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAGATGGAAGGCATCTGTGTG  
AAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGACAGAAGACGAGTTGGTGGTG  
CTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCACGCTGGCTGCTAAGGGCGAC  
TTGGTGTTACCGCCATCTTCATTGGGGCTGTGGCGGCCATGACTGGCTACTGGTTGTGAGAG  
CGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATAATCGCGGCCACCACCTGTAGGA  
CCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCCTCCTGCTGGACACTCAGGACAGC  
TTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTGCCTTACAGAGCAGCCCAGGTACCC  
AGGCCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGCCCTGAAGGTGGATACCATGAGCTCT  
TCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGAATTTCAAAGTTTTTCCTTAATGGTG  
GCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTGGTCCTCACAGGGGTGGGGCCATCACAG  
CTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGTTCTGTGTTACCCACATCCCCACACCCCA  
TTGCCACTTATTTATTCATCTCAGGAAATAAAGAAAGGTCTTGGAAGTTAAAAAAAAAAAAA  
AAAAAAAAAAAA

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**FIGURE 290**

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQSPPPQSSPPPQPHPCHTCRGLVDSFNKGLERT  
IRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQE  
APDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQCAGYGG  
EACGQCGLGYFEAERNASHLVCSACFGPCARCSGPESNCLQCKKGWALHHLKCVDIDECGTE  
GANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECETEVCP  
GENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFGIIICAL  
ATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

**Important features:****Signal sequence:**

Amino acids 1-29

**Transmembrane domain:**

Amino acids 342-392

**N-glycosylation sites:**

Amino acids 79-83;205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 290-294

**Aspartic acid and asparagine hydroxylation site:**

Amino acids 321-333

**EGF-like domain cysteine pattern signature:**

Amino acids 181-193

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**FIGURE 291**

CAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGACCCAC  
GCGTCCGAACACAGGTCCCTTGTTGCTGCAGAGAAGCAGTTGTTTTGCTGGAAGGAGGGAGTGC GCGGGCTGCCCC  
GGGCTCCTCCCTGCCGCTCCTCTCAGTGGATGGTTCCAGGCACCCTGTCTGGGGCAGGGAGGGACAGGCCTGC  
ACATCGAAGGTGGGGTGGGACCAGGCTGCCCTCGCCCCAGCATCCAAGTCTCCCTTGGGCGCCCGTGGCCCTG  
CAGACTCTCAGGGCTAAGGTCTCTGTTGCTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGTAGC  
TTGAAGGAGGCACCATGCAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCCTGGCTCAGGCCTGCCCTG  
AGCCCTGCGACTGTGGGGAAGATATGGCTTCCAGATCGCCGACTGTGCCTACCGCGACCTAGAATCCGTGCCGC  
CTGGCTTCCCGCCAATGTGACTACACTGAGCCTGTCAGCCAACCGGCTGCCAGGCTTGCCGGAGGGTGCCTTCA  
GGGAGGTGCCCTGCTGCAGTCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGAGCCCTGGCCT  
CTCTGAGCCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTGCCTGGAGCGACCTGCACAACC  
TCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGGACGCTTCCGCAGCCTCC  
GTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGACACATTGGCCGAGGGCACCTTCACCCGCTCACCG  
CGCTGTCCCACCTGCAGATCAACGAGAACCCCTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCC  
TGACCACGGCCGTGTCCATCCCGGAGCAGGACAACATCGCTGCACCTCACCCCATGTGCTCAAGGGTACACCGC  
TGAGCCGCTGCCGCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGGATGGTGCCG  
AGCTGCGGCCTGGTTTTGTGCTGGCACTGCACTGTGATGTGGACGGGCAGCCGGCCCTCAGCTTCACTGGCACA  
TCCAGATACCCAGTGGCATTGTGGAGATCACCAGCCCCAACGTGGGCACTGATGGGCGTGCCCTGCCTGGCACCC  
CTGTGGCCAGCTCCCAGCCGCGCTTCCAGGCCTTTGCCAATGGCAGCCTGCTTATCCCGACTTTGGCAAGCTGG  
AGGAAGGCACCTACAGCTGCCTGGCCACCAATGAGCTGGCAGTGCTGAGAGCTCAGTGGACGTGGCACTGGCCA  
CGCCCGGTGAGGGTGGTGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAAGGGCTGCTATA  
CGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCATCATCTACCTCAGCCGTGCTGGGAACC  
CTGAGGCTGCAGTCGAGAAGGGTCCCTGGGCAGCTGCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCC  
TCTTCTTCTCCTCACCTCCTTCTAGCCCCACCCAGGGCTTCCCTAACTCCTCCCCTTGCCCCACCAATGCCCC  
TTTAAGTGCTGCAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCTACCTCTCC  
TTCTAATCTCTTCTAGAGCACCTGCTATCCCCAATTCTAGACCTGCTCCAACTAGTGAAGTAGGATAGAATTTG  
ATCCCTAACTCACTGTCTGCGGTGCTCATTGCTGCTAACAGCATTGCCTGTGCTCTCCTCTCAGGGGCAGCATG  
CTAACGGGGCGACGTCTAATCCAATGGGAGAAGCCTCAGTGGTGAATTCCAGGCACTGTGACTGTCAAGCTG  
GCAAGGGCCAGGATTGGGGGAATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAG  
GAGGATGGGAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCTGCTCAAGCTCCTCCTGCTCCTTG  
CTGTTTTCTGATGATTTGGGGCTTGGGAGTCCCTTTGTCTCATCTGAGACTGAAATGTGGGGATCCAGGATGG  
CCTTCCTTCTCTTACCCTTCTCCTCAGCCTGCAACCTCTATCCTGGAACCTGTCTCCTTTCTCCCCAACT  
ATGCATCTGTTGTCTGCTCCTCTGCAAAGGCCAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTCTCTGATG  
CCAAAAAAGGGCGCCGCGACTCTAGAGTGCACCT

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**FIGURE 292**

MQELHLLWWALLLLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPPGFANVTTLSSLNRLP  
GLPEGAFREVPLLQSLWLAHNEIRTVAAGALASLSHLKSLDLSHNLISDFAWSDLHNLSALQL  
LKMDSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPFDCTCGIV  
WLKTWALTAVSIPEQDNIACTSPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELRPGFV  
LALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANGSLLIP  
DFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHGKAVEGKGCYTVDNEVQP  
SGPEDNVVIIYLSRAGNPEAAVAEGVPGQLPPGLLLLGQSLLLFFFLTSTF

**Important features:****Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 403-418

**N-glycosylation sites:**

Amino acids 51-55, 120-124, 309-313

**Tyrosine kinase phosphorylation site:**

amino acids 319-326

**N-myristoylation sites:**amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329, 334-340,  
350-356, 394-400**Amidation site:**

amino acids 355-359

**Leucine Rich Repeat:**

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

**Leucine rich repeat C-terminal domain:**

amino acids 180-230



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**FIGURE 293**

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCTCGCCTCCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCTGCC  
TCGCTTCCAGGCGCGGCGGCTGCAGCCTTGCCCCCTCTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCT  
GCTTTCTGCTGATCCTCGGACAGATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTACGTGGGAGGTCCATCT  
CTAGGGGCGAGACACGCTCGGACCCACCCGAGACGGCCCTTCTGGAGAGTTCTGTGAGAACAAGCGGGCAGACC  
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA  
TCTTGCAATTCTTGACATTGGTCCTGATGTCAACCCAGTGGGCCTGCTCCAATATGGCAGCACTGTCAAGAATG  
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG  
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGA  
GGGAGAATGTGCCACGGGTGATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGTGCTA  
AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCTTCTGTGGCCCAATTTAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG  
GCTCATACGTGTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGAGAATCCAGGATCTGT  
GTGCCATGGAGGACCACAACCTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGCTACAGTG  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACCCAGGATGTGAAC  
ATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTGCCATGAAGGATTGCTCTTAACCCAGATGAAAAA  
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAACCTGCAGCCGAGTGGACCACTGTGCAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCTTCGTCTGCCAGTGCTCAGAAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCCGGTGGATTACTGCCTGCTGAGTGACCATGGTTGTGAATACTCCT  
GTGTCAACATGGACAGATCCTTTGCCCTGTGAGTGTCTGAGGGACAGTGCTCCGCAGCGATGGGAAGACGTGTG  
CAAAATTGGACTCTTGTGCTCTGGGGGACCACGGTTGTGAACATTCTGTGTGAAGCAGTGAAGATTCTGTTGTG  
GCCAGTGCTTTGAAGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACAGTGCAGTGCTTGAGGGGATTCCGGCTCG  
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGCGAACACATTTGTGTTA  
ATAATGGGAATTCCTACATCTGCAATGCTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT  
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGAGAGAAGAAATTTGAGGTCG  
TGAAGCAGTTTGTCACTGGAATTATAGATTCTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT  
ATTCACACAGGTCCACACAGAGTTCACCTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAGCCGTGGCCC  
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTACCCAAG  
GAGAAGGGGGCCAGGCCCTTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTACCGACGGGACGGGCTCAGGATG  
ACGCTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG  
AGGAGGAACATAAGAGATTGCCTCTGAGCCCAACAACAGCATCTCTTCTATGCCGAAGACTTCAGCACAATGG  
ATGAGATAAGTGAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGGAAC TGCCAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT  
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAATGTGAAAACCTTATAATGT  
TCCAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC  
TGGAATAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT  
GAACGCAGTGACAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA  
GAAACCTGGTTTGCCACAGAACAAGACAAGAAGTATACACTAATTTGTATAAATTTATCTAGGAAAAAATCCT  
TCAGAATTCTAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC  
AACTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTTGCACAGTCTTACTT  
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG  
CATAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAAAATTCACCACTTCAG

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**FIGURE 294**

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHQPOTALLESSCENKRADLVFIID  
SSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAVKR  
MRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGI  
LIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHF  
CINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYALAEDG  
KRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINICALNKPGEHECVN  
MEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKTC  
SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTC AKLDSCALGDHGCEHSCVSSD  
SFVCQC FEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLAEDGKRCRRK  
DVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVIDGSKSLGEENF  
EVVKQFVTGIIDSLTISP KAA RVGLLQYSTQVHTEFTLRNFNSAKDMKKAVAHMKYMGKGSMT  
GLALKHMFERSFTQEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKA  
IEEELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALEDSDGRQDSPAGELPKTVQQPT  
ESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPLEEKHDQCKCENLIM  
FQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

**Important features:****Signal sequence:**

Amino acids 1-23

**N-glycosylation site:**

Amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 115-119;606-610;892-896

**N-myristoylation sites:**

Amino acids 133-139;258-264;299-305;340-346;453-459;494-500;  
639-645;690-694;  
752-758;792-798

**Amidation sites:**

Amino acids 314-318;560-564;601-605

**Aspartic acid and asparagine hydroxylation sites:**

Amino acids 253-265;294-306;335-347;376-388;417-429;  
458-470;540-552;581-593

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**FIGURE 295**

GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACCCGC  
**CATG**CGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCCGC  
GCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTTTAA  
CCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGCGGGAACACGGCTTGGGAGGAAAA  
GACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCTGGAGGGGCTGTGCGA  
GAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGCCTGGTG  
GCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACACTGAAAGT  
GTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCC  
CTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTCTGCCGGTG  
CCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCCG  
GAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGCTCGGGCCTGAC  
CAACAGAGACTGCGGCGAGTGTGAAGTGGGTGGGTGCTGGACGAGGGCGCCTGTGTGGATGT  
GGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGG  
CTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAAA  
CTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTG  
CTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTA  
CGTCTGTGTGTGCTCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGC  
TGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTG**TAA**TGTGCCGG  
ACTTACCCTTTAAATTATTCAGAAGGATGTCCCGTGAAAAATGTGGCCCTGAGGATGCCGTCT  
CCTGCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC  
TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTGTATATTTTGATACAGTTCTTTGT  
AATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAA

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**FIGURE 296**

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEK  
TLSEYSESEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLLK  
CCSPGTYGPDCLACQGGGSRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLR  
NETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPSPCSAAQFCKNANG  
SYTCEECDSSCVGCTGEGPGNCKEKCISGYAREHGQCADVDECSLAEKTCVRKNENCYNTPGSY  
VCVCPDGFEEETEDACVPPAEAEATEGESPTQLPSREDL

**Important features:****Signal peptide:**

Amino acids 1-24

**N-glycosylation sites:**

Amino acids 190-194;251-255

**Glycosaminoglycan attachment sites:**

Amino acids 149-153;155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 303-310

**N-myristoylation sites:**Amino acids 44-50;54-60;55-61;81-87;150-156;158-164;164-170;  
252-258;313-319**Aspartic acid and asparagine hydroxylation site:**

Amino acids 308-320

**EGF-like domain cysteine pattern signature:**

Amino acids 166-178

**Leucine zipper pattern:**

Amino acids 94-116

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**FIGURE 297**

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAGAAAGAGGAAG  
ATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGACCCTGGCATCATGCTGCTATTCTGCAAATACTGA  
AGAAGCATGGGATTTAAATATTTTACTTCTAAATAAATGAATTACTCAATCTCCTATGACCATCTATACATACTC  
CACCTTCAAAAAGTACATCAATATTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTT  
TTGGACAATGCAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAACTTTGTGGTTCTATGGCATTATCATTTT  
GACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTGTGGAATCCTTAAGGGC  
CCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACTCCGAATTCATGTGCTACTTGGCCTAGCTA  
TCACTACACTAGTACAAGCTGTAGATAAAAAAGTGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGT  
TTACACCCAGATCCATTTATATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCCAGCCA  
GATTGCCAGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAGACTTTC  
CAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAATATTAATGTAAAAAGATGC  
CTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACCTTACTGAACTGCCTGAAAAATGTCTGTCCGAACCTGAGCA  
ACTTACAAGAACTCTATATTAATCACAACTTGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATC  
TTCTTCGACTTCATCTCAATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAG  
AGATTCTGATGATTGGGGAATCCAATTATCAGAATCAAAGACATGAACTTTAAGCCTCTTATCAATCTTCGCA  
GCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTTGGACTGGAAAACTTAGAAAGCA  
TCTCTTTTTACGATAACAGGCTTATTAAAGTACCCCATGTTGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTGG  
ATCTAAATAAAAATCCTATTAATAGAATACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGA  
TAAATAATATGCCTGAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAG  
CTACTAACAACCCTAGATTGTCTTACATTACCCCAATGCATTTTTTCAGACTCCCCAAGCTGGAATCACTCATGC  
TGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTGCCAAACCTCAAGGAAATCAGCATAC  
ACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTGGATGAACATGAACAAAACCAACATTCGATTATGGAGC  
CAGATTCACTGTTTTGCGTGGACCCACCTGAATTTCAAGGTGAGAATGTTCCGGCAAGTGCATTTTCAGGGACATGA  
TGGAATTTGTCTCCCTCTTATAGCTCCTGAGAGCTTTCTCTTAATCTAAATGTAGAAGCTGGGAGCTATGTTT  
CCTTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTGGTCAAAAACCTTTGC  
CTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTAGATATAAATGGCGTAACTCCCAAAGAAG  
GGGTTTTATATACTTGTATAGCAACTAACCTAGTTGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGAT  
CTTTTCCACAAGATAACAATGGCTCTTTGAATATTAAAAAAGAGATATTACAGGCCAATTCAGTTTTGGTGTCTT  
GGAAAGCAAGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAATTCTCATGCTG  
CGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATCCATCAACTGAGTATAAAA  
TTTGATATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAATGTGTAAATGTCACCACCAAAGGTTTGCACC  
CTGATCAAAAAGAGTATGAAAAGAATAATACCACAACACTTATGGCCTGTCTTGGAGGCCCTTCTGGGGATTATTG  
GTGTGATATGTCTTATCAGCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACT  
TACAGAAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAAAGAAAAA  
GTACATCACTGAAAGTAAAGCAACTGTTATAGGTTTACCAACAAATATGTCCATAAAACCACCAAGGAAACCTA  
CTCCAAAAATGAAC

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**FIGURE 298**

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLTF  
PARLPANTQIILLQTNNAIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLEEN  
KLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDALPN  
LEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLEISFYDNRLIKVP  
HVALQKVVNLFKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPDLRKIE  
ATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISHSNPIRCDCVIRW  
MNMNKTNIRFMEPDSLFCVDPPEFQGGQNVVRQVHFRDMMEICPLIAPESFPSNLNVEAGSYVS  
FHCRTAEPEQPEIYWITPSGQKLLPNTLTDFYVHSEGTLDINGVTPKEGGLYTCIATNLVGA  
DLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFAVKTENSHAAQ  
SARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKEYEKNNTTTLM  
ACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKSTS  
LKVKATVIGLPTNMS

**Important features:****Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708**Cell attachment sequence.**

amino acids 277-280

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**FIGURE 299**

GCTGTGGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTT  
TGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCG  
CCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCAT  
ACCATGCCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGCCA  
GTCCTAGCTTACTCTGCCACCACTGCCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCA  
CAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAACAT  
ACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATGAACCT  
TCTTGCTTCCCATGTACAGTTTGTAATCAGATCAAAAACATAAAAGTTCCTGCACCATGACC  
AGAGACACAGTGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAAACCTCCCCAGAGATGTGC  
CGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAATTGTACGTCCTGGGATGAT  
ATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAAACCCCAGCTGCTGAAGAGACA  
ATGAACACCAGCCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCCAGGG  
ACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCCGGGGACTCCTGCCCCAGCTGCT  
GAAGAGACAATGACCACCAGCCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC  
AGCCCCGGGGACTCCTGCCTCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTA  
ATTGTGCTTCTGATTGTGTTTGTTGAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTG  
AAAGGTTTCAGGTAGGCGCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCT  
CTGCTGTGTTCCACAGACAGAAACGCCTGC

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**FIGURE 300**

MARIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVA PQQRHSFKGEECPAGSHRSEHT  
GACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCTMTRDTVCQCKEGTFRNENSPEMCR  
KCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGT  
PAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLI  
VLLIVFV

**Important features:****Signal peptide:**

Amino acids 1-29

**Transmembrane domain:**

Amino acids 240-259

**N-glycosylation site:**

Amino acids 77-81;140-144;156-160

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 126-130

**N-myristoylation sites:**

Amino acids 56-62;72-78;114-120;154-160;233-239



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**FIGURE 301**

CACAAGCATCTTAATTTGAATCCACAAAGTTTCATGTAATGAAAAGAAATACATAATTTTAAT  
TCAACCCGAGTGTTTTCCAAGAAGATTGTATTTGCTTAAATTGCTACAGTAATTCAGAGACA  
GCCCTGTCTGGACACAGAGTTACTGTGGATTTTTTAAGAGACTCAGTTAAAGAATTTAGGAATT  
TCTGATTCATTTAAAGGATTTACAAATTCATCAACCCCTGAAACTAAAGCAAATTGAACAGG  
AAAAAAAAAAGAAGATGGGTTTTTTAAGTCCAATATATGTTATTTTCTTCTTTTTTGGAGTC  
AAAGTACATTGCCAATATGAACTTATCAGTGGGATGAAGACTATGACCAAGAGCCAGATGAT  
GATTACCAAACAGGATTCCCATTTCTGTCAAAATGTAGACTACGGAGTTCCTTTTCATCAGTAT  
ACTTTAGGCTGTGTCTCAGTGAATGCTTCTGTCCAATACTTTCCATCATCAATGTACTGTGAT  
AATCGCAAACCAAGACTATCCCAAATATTCCGATGCACATTCAGCAACTCTACCTTCAGTTC  
AATGAAATTGAGGCTGTGACTGCAAATTCATTCATCAATGCAACTCATCTTAAAGAAATTAAC  
CTCAGCCACAACAAAATTAAATCTCAAAGATTGATTATGGTGTGTTTGCTAAGCTTCCAAT  
CTACTACAACCTTCATCTAGAGCATAATAATTTAGAAGAATTTCCATTTCTTCTCTAAATCT  
CTGGAAAGACTCCTTCTTGGTTACAATGAAATCTCCAACTGCAGACAAATGCTATGGATGGG  
CTAGTAACTTGACCATGCTTGATCTCTGTTATAATTATCTTCATGATTCTCTGCTAAAAGAC  
AAAATCTTTGCCAAAATGGAAAACTAATGCAGCTCAACCTCTGCAGTAACAGATTAGAATCA  
ATGCCTCCTGGTTTGCTTCTTCACTTATGTATCTGTCTTTAGAAAATAATTCAATTTCTTCT  
ATACCCGAAAAATACTTCGACAACTTCCAAACTTCATACTCTAAGAATGTCACACAACAAA  
CTACAAGACATCCCATATAATATTTTAACTTCCCAACATTGTAGAACTCAGTGTGGACAC  
AACAAATTGAAGCAAGCATTCTATATTCCAAGAAATTTGGAACACCTATACCTACAAATAAT  
GAAATAGAAAAGATGAATCTTACAGTGATGTGTCCTTCTATTGACCCACTACATTACCACCAT  
TTAACATACATTTCGTGTGGACCAAATAAACTAAAAGAACCAATAAGCTCATACTCTTCTTC  
TGCTTCCCTCATATACACTATTTATTATGGTGAACAACGAAGCACTAATGGTCAAACAATA  
CAACTAAAGACACAAGTTTTTCAGGAGATTTCCAGATGATGATGATGAAAGTGAAGATCACGAT  
GATCCTGACAATGCTCATGAGAGCCCAGAACAAGAAGGAGCAGAAGGGCACTTTGACCTTCAT  
TATTATGAAAATCAAGAATAGCAAGAACTATATAGGTATACACTTACGACTTCACAAAACCTA  
TACTTAATATAGTAAATCTAAGTAAACATGTATTACTCAAAGTAATATATTTAGAATTATGTA  
TTAGTATAAGATCAGAATTGAATTTAAGTTGTTGGTGACATCTGCATCATTTTCATAGGATTAG  
AACTTACTCAAAATAATGTAAATCTTTAAAAATATAAATTAGAATGACAAGTGGGAATCATAA  
ATTAAACGTTAATGGTTTCTTATGCTCTTTTAAATATAGAAATATCATGTAAAGAAAAAA  
AAAAAA

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**FIGURE 302**

MGFLSPIYVIFFFFGVKVHCQYETYQWDEDYDQEPDDDYQTGFPPFRQNVVDYGVPFHQYTLGCV  
SECFCTNFPSSMYCDNRKLKTIPNIPMHIQQLYLQFNEIEAVTANSFINATHLKEINLSHNK  
IKSQKIDYGVFAKLPNLLQLHLEHNNLEEFPPFLPKSLERLLLGYNIEISKLQTNAMDGLVNLT  
MLDLCYNYLHDSLLKDKIFAKMEKLMQLNLCSNRLESMPPGLPSSLMYLSLENNSSISSIPEKY  
FDKLPKLHTLRMSHNKLQDIPYNIFNLPNIVELSVGHNKLKQAFYIPRNLEHLYLQNNIEKM  
NLTVMCPSIDPLHYHHLTYIRVDQNKLEPISSYIFFCFPHIHTIYYGEQRSTNGQTIQLKTQ  
VFRFPDDDDDESEDHDDPDNAHESPEQEGAEGHFDLHYENQE

**Important features:****N-glycosylation sites:**

Amino acids 113-117;121-125; 187-191;242-246;316-320

**Tyrosine kinase phosphorylation sites:**

Amino acids 268-275;300-307

**N-myristoylation site:**

Amino acids 230-236

**Leucine zipper patterns:**

Amino acids 146-168;217-239

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**FIGURE 303**

GCCCCGGGACTGGCGCAAGGTGCCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTAGC  
TGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTACCA  
CGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCTGGT  
AGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTATGAT  
ACTGTGCTTTTCACTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGGGGTTT  
AAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGAAACAGT  
CTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAGGACCTCCA  
TCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCATGCCTTCAA  
AGGAGTAGCTGAAACCTTGCACTCTGGACTTGTCCGACAATCGGATTCAAAGTGTGCACAA  
AAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGCACTGCGACTG  
TACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCACAACGTGATCTG  
TAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGCCAACGACGCTGA  
CCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCATGTTTGGCTGGTT  
CACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAGGATGCCCCGAGACA  
CCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGAACCTGATGATATTAG  
CACTGTGGTATTAGTGTCCAACTGACTGTCAATTGAGAAAGAAAGAAAGTAGTTTGCGATTGCA  
GTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAACTTTGTATTTAGTTT  
TTTTTGAATTATGCCACTGCTGAACTTTTAAACAACACTACAACATAAATAATTGAGTTTAG  
GTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGTAAGCTACTATCTGAACATT  
AGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTTAATTTAAAGCAAATAAAAG  
CTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAAAAACA

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**FIGURE 304**

MNLVDLWLTRSLMCLLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCSNANLKEIPRDLP  
PETVLLYLDNSQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNRIQ  
SVHKNAFNNLKARARIANNPWCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFLNAA  
NDADLCNLPKKTDDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLSRQKKADEP  
DDISTVV

**Important features:****Signal sequence:**

Amino acids 1-33

**Transmembrane domain:**

Amino acids 204-219

**N-glycosylation sites:**

Amino acids 47-51;94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation sites:**

Amino acids 37-43;45-51;110-116

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**FIGURE 305**

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCCGCTCCTAGTGGTTTTTCCACTTTGTTGAATTGTTCCCT  
ATACTCAAAATTGCACCAAGACACCTTGCTCCCAAATGCAAAATGTGAAATACGCAATGGAATTGAAGCCTGCT  
ATTGCAACATGGGATTTTCAGGAAATGGTGTCACAATTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGT  
CCTGTGGCGAAAATGCTAATTGCACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCA  
GCAGTAACCAAGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATTTAG  
ATAATGTCTGTATAGCTGCAAAATTAATAAACTTTAACAAAAATCAGATCCATAAAAAGAACCTGTGGCTTTCGC  
TACAAGAAGTCTATAGAAATTCTGTGACAGATCTTTACCAACAGATATAATTACATATATAGAAATATTAGCTG  
AATCATCTTCATTACTAGGTTACAAGAACAACACTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTG  
AATTTGTAAAAACCGTGAATAATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATA  
GGAGAACACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCCAAAAGA  
CCACAGAGTTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTTCTTTTTGATTATATAACATGAACATA  
TTCATCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGAGAAAAGCTGCATATGATTCAAATG  
GCAATGTTGCAGTTGCATTTTTATATTATAAGAGTATTGGTCTTTGCTTTCATCATCTGACAACTTCTTATTGA  
AACCTCAAAATTATGATAATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTAGTCTCAATGAGCTCAA  
ACCCACCCACATTATATGAACCTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATAGGA  
GTCTATGTGCATTTTGGAAATTAACCTGATACCATGAATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACAT  
ACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTTGCAATTTTGATGTCTCTGGTCCCTT  
CCATTGGTATTAAAGATTATAATATTCTTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTG  
CCATATGCATTTTACCTTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCT  
GTAGCCTATTTCTTGCTGAACTTGTCTTTCTGTTGGGATCAATACAAATACTAATAAGCTCTTCTGTTCAATCA  
TTGCCGGAAGTGTACACTACTTCTTTTAGCTGCTTTGTCATGGATGTGCATTGAAGGCATACATCTCTATCTCA  
TTGTTGTGGGTGTCTCTACAACAAGGGATTTTGCACAAGAATTTTATATCTTTGGCTATCTAAGCCCGAGCCG  
TGGTAGTTGGATTTTCGGCAGCACTAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCGAAA  
ACAACTTTATTTGGAGTTTTATAGGACCAGCATGCCTAATCATTCTTGTTAATCTCTTGGCTTTTGGAGTCATCA  
TATACAAAGTTTTTCGTCACTGCAGGGTTGAAACCAGAACTTAGTTGCTTTGAGAACATAAGGTCTTGTGCAA  
GAGGAGCCCTCGCTCTTCTGTTCTCTCGGCACCACCTGGATCTTTGGGGTTCTCCATGTTGTGCACGCATCAG  
TGGTTACAGCTTACCTCTTCACAGTCAGCAATGCTTTCCAGGGGATGTTCAATTTTTTATTCCTGTGTGTTTTAT  
CTAGAAAGATTCAAGAAGAATATTACAGATTGTTCAAAAATGTCCCCTGTTGTTTTGGATGTTAAGGTAACAT  
AGAGAATGGTGGATAATTACAACCTGCACAAAAATAAAATTCAGCTGTGGATGACCAATGTATAAAAAATGACT  
CATCAAATTATCCAATTATTAACCTACTAGACAAAAAGTATTTTAAATCAGTTTTTCTGTTTATGCTATAGGAAT  
GTAGATAATAAGGTAAATTTATGTATCATATAGATATACTATGTTTTCTATGTGAAATAGTTCTGTCAAAAAATA  
GTATTGCAGATATTTGGAAAGTAATTGGTTTCTCAGGAGTGATATCACTGCACCCAAGGAAAGATTTTCTTTCTA  
ACACGAGAAGTATATGAATGTCCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTGCTTTGAACT  
AGTCCCCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAAACATAAGAGAATGAAGGGGAGAATATCAAA  
CAGTGAAGGGAATGATAAGATGATTTTGAATGAAGTGTTTTTCTGTAGACTAGCTGAGAAATTGTTGACAT  
AAAATAAAGAATGAAGAAACACATTTTACCATTTTGTGAATTGTTCTGAACCTAAATGTCCACTAAAACAACCTT  
AGACTTCTGTTTGCTAAATCTGTTTCTTTTCTAATATTCTAAAAAAGGTTTACCTCCACAAATTGA  
AA

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**FIGURE 306**

MKRLPLLVFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNECGNLTQSCGENANC  
TNTEGSIYCMCVPGFRSSSNQDRFITNDGTVCIEVNVNANCHLDNVCIANINKTLTKIRSIKEPVALLQEVYRNS  
VTDLSPTDIITYIEILAESSLLGYKNNTISAKDTLSNSTLTEFVKTVNNFVQORDTFVVWDKLSVNHRRLTKL  
MHTVEQATLRISQSFQKTTEFDTNSTDIALKVFFFDSDYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAF  
YYKSIGPLLSSSDNFLKPNYDNSEEEERVISVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAFWNY  
SPDTMNGSWSSEGCETYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLGIIISLICLAICIFTFW  
FFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIIAGLLHYFFLAFAWMCIEGILYLVVGVYIN  
KGFLHKNFYIFGYLSPAVVVGFSALGYRYYGTTKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVRHT  
AGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVLHVHVSVVTAFLTVSNAFQGMFIFLFLCVLSRKIQEEY  
YRLFKNVPCCFGCLR

**Important features:****Signal peptide:**

Amino acids 1-19

**Transmembrane domain:**

Amino acids 431-450;494-515;573-594;619-636;646-664

**N-glycosylation sites:**Amino acids 15-19;21-25;64-68;74-78;127-131;177-181;  
188-192;249-253;381-385;395-399**Glycosaminoglycan attachment site:**

Amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 360-364

**Tyrosine kinase phosphorylation sites:**

Amino acids 36-44;670-677

**N-myristoylation sites:**Amino acids 38-44;50-56;52-58;80-86;382-388;388-394;  
434-440;480-486;521-527**Aspartic acid and asparagine hydroxylation site:**

Amino acids 75-87

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**FIGURE 307**

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGT  
ATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCTGAGCAGCATGGC  
CCGGAGGAGCGCCTTCCCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGA  
GGCCGGGCGCCGCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGA  
AGAAGATATCCTGATTGTTTTAGAGGGGAAAATGGCACCTTTTACACATGATTTAGAAAAGCGCAACAGAGAAT  
GCCAGCTATTCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGA  
ATTCCTGTCCTTGCCTCCCTGGATAAAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGT  
GCCTCACAAGGCATCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTGGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCTTCTTTAAACATG  
TCAACAAGCTGAGTGCCCGAGGCGGGTGCCGAAATGGAGGCTTTTGTAAATGAAAGACGCATCTGCGAGTGTCTCTGA  
TGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATGGTGGACTTTGTGTGACTCC  
TGGTTTCTGCATCTGCCCACCTGGATTCTATGGAGTGAAGTGTGACAAAGCAAAGTCTCAACCACCTGCTTTAA  
TGGAGGGACCTGTTTCTACCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAA  
ATGCCACAACCTGTGCAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCAAAGGTTACCAGGG  
AGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAACAAATGCCA  
ATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCCTCATACTGCCCTGAGGCCAGC  
AGGCGCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTA  
CATCTGGTGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTTCATGTGTT  
GAATGTTCAAATAATGTTCACTTAAAGTAACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGC  
TGATATTTACTCTTCTTTTAAAGTTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCTTGTTTCAGTGCT  
TTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAAT  
TACAATGCATTTATGGTGTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAA  
GAATTTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAATTTTATTGTCAGATATTTAGATGTTTGTAC  
ATTTTTTAAATTTGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATTCA  
GTATTAAAAAATAAATTACACTGTGGTAGTGGCATTAAACAATATAATATATTCTAAACACAATGAAATAG  
GGAATATAATGTATGAACTTTTTGCAATTGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCT  
AATAAACATTTTATACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAATAAATAA  
AAAAA

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**FIGURE 308**

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGKM  
APFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLLGT  
VPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGCRNG  
GFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCSTTCFN  
GGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSPVCEPGCG  
AHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDPPESNYIW

**Important features:****Signal sequence:**

Amino acids 1-28

**N-glycosylation sites:**

Amino acids 88-92;245-249

**Tyrosine kinase phosphorylation site:**

Amino acids 370-378

**N-myristoylation sites:**

Amino acids 184-190;185-191;189-195;315-321

**ATP/GTP-binding site motif A (P-loop):**

Amino acids 285-293

**EGF-like domain cysteine pattern signatures:**

Amino acids 198-210;230-242;262-274;294-306;326-338



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**FIGURE 309**

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGGG  
TTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGACT  
CTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGATCATGGAATGAACCCGAGCAATGGAG  
ATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTGGCCG  
TGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTTCGATG  
ACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCGAGCGGAGGGG  
TTTTCTTTGAAGGCTCTGTAGCCCGATTTCCTGCGCAAGACGGATTCAAGCTGAAGGGCGCTA  
CAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGATAATTCCA  
TCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCAATAACAAGACAT  
ATAGACATGGAGAGAAGCTAATCATCACTTGTGATGAAGGATTCAAGATCCGGTACCCCGACC  
TACACAATATGGTTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCCCATCTGTCAAG  
GCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGCTCCAGACCTCCT  
TCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAACTTGATGGGTCTGCGT  
ATCTTGAGTGCTTACAAAACCTTATCTGGTTCGTCAGCCACCCCGGTGCCTTGCTCTGGAAG  
CCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGCTGCCACCCGCGGCCTT  
GTGAGCGCTACAACCACGGAACGTGGTGAGTGGTGGAGTTTTACTGCGATCCTGGCTACAGCCTACCA  
GCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTCTTATCAAGTCTACTGCA  
TCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCTCCTGACCACGTGGAAGATTGTGG  
CGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATCCTGGCCAGGATGTTCCAGA  
CCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAGTTCAGCAGTGACCCTGACT  
TTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCCTATGACGAAGCTGTGAGTGGCGGCT  
TGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAGGGCTGCCCCCTTACCCGTGGACG  
ACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGACACAGGCCAGGGGAGTCAGAAA  
CCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAAGTCTGTATTCACCTCCCAGGTGCC  
AAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATAATTGCCAGCACGGCAGAGGAGGTGG  
CATCCACCAGCCCAGGCATCCATCATGCCCCACTGGGTGTTGTTCCCTAAGAACTGATTGATTA  
AAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAAATACATGTTGATCTGTGGAGTTGATTC  
CTTTCCTTCTTGGTTTTAGACAAATGTAAACAAAGCTCTGATCCTTAAATTGCTATGCTG  
ATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTCTGTTTCTTCTTGACACAGACTGATTAAA  
AATTAAAAGNAAAAA

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**FIGURE 310**

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGIP  
ENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRIPQ  
IEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLASSNG  
YVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLPPMVS  
HGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQTWPSTH  
ETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVDGVPVML  
PSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDGPGESETCDSVSGSSEL  
LQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVFLRN

**Important features:****Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472**N-myristoylation site.**amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

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**FIGURE 311**

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGC**ATG**AGCGGCGGTTGGATGGCGCAGGTTGGAG  
CGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCTGG  
AGGCCGCCGCGAGCCCGCTTTCCACCCCGACCTCTGCCAGGCCGCGAGGCCCCAGCTCAGGCT  
CGTGCCCAACCACCAAGTTCCAGTGCCGCACCAAGTGGCTTATGCGTGCCCTCACCTGGCGCT  
GCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCCATGTA  
CCCAGAAAGGGCAATGCCCACCGCCCCCTGGCCTCCCCTGCCCTGCACCGGCGTCAGTGACT  
GCTCTGGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCAGGCGAGC  
TCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCACCCAGACT  
GTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAGGGGATGCCA  
CAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCCACAACCATGG  
GGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTCCTCTGCCGGAG  
ACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGCTCAGTGCAAGCC  
TGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGCCTCCGCCCCACTGG  
GGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGTCAGAACAGAAGACCTCGCTGCCCC**TGAG**  
GACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACAGGAGGAGAGCAGTGA  
TGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTTCTGGCCACGTGGAACC  
TCGAACCCGAGCTCCTGCAGAAAGTGGCCCTGGAGATTGAGGGTCCCTGGACACTCCCTATGGA  
GATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAGGGGCTGGCCCCAGGCAGC  
TCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTGCCCCGTCTGAGGGTGGCGA  
TTAAAGTTGCTTC

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**FIGURE 312**

MSGGWMAQVGAWRTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRT  
SGLCVPLTWRCRDLDCSDGSDEEECRIEPCCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKLRN  
CSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVTLES  
VTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLLLLSW  
LRAQERLRPLGLLVAMKESLLLSEQKTSLP

**Important features:****Signal sequence:**

Amino acids 1-30

**Transmembrane domain:**

Amino acids 231-248

**N-glycosylation sites:**

Amino acids 126-130;195-199;213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation sites:**Amino acids 3-9;10-16;26-32;30-36;112-118;166-172;212-218;  
224-230;230-236;263-269**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 44-55

**Leucine zipper pattern:**

Amino acids 17-39

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**FIGURE 313**

CGGACGCGTGGGCGTCCGGCGGTTCGACAGAGCCAGGAGGCGGAGGCGCGGGGCCAGCCTGGGCCCCAGCCCACAC  
CTTCACCAGGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTACTGCTGTTGCTGCCGCTGGCTGGCCAC  
TTGGCTCTGGGTGCCAGCAGGGTCGTGGGCGCCGGGAGCTAGCACCGGCTCTGCACCTGCGGGGCATCCGGGAC  
GCGGGAGGCCGGTACTGCCAGGAGCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTG  
GGCGCCATCTGTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTCTGC  
CTCGGCGTGCCACCCCTTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTATCCAGTCTTGGGAACG  
TACTGGGACAACGTGAACCGTTGCACCTGCCAGGAGAACAGGCAGTGGCATGGTGGATCCAGACATGATCAAAGC  
CATCAACCAGGGCAACTATGGCTGGCAGGCTGGGAACCACAGCGCCTTCTGGGGCATGACCCTGGATGAGGGGCAT  
TCGCTACCGCCTGGGCACCATCCGCCCATCTTCCTCGGTTCATGAACATGCATGAAATTTATACAGTGTGAACCC  
AGGGGAGGTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGACCAAGG  
CAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCTCAATCCATTCTCTGGGACA  
CATGACGCCTGTCTGTGCGCCCCAGAACCTGCTGTCTTGTGACACCCACCAGCAGCAGGGCTGCCGCGGTGGGCG  
TCTCGATGGTGCCTGGTGGTTCCTGCGTCGCGGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGA  
ACGAGACGAGGCTGGCCCTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGGCAAGCGCCAGGCCAC  
TGCCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTCCAA  
CGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGGTGCATGAGGACTTCTT  
CCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGGAGGCCAGAGAGATACCGCCGGCATGGGAC  
CCACTCAGTCAAGATCACAGGATGGGGAGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGC  
CAACTCCTGGGGCCCAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGC GCGGCGTCAATGAGTGC GACATCGA  
GAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCACTGAGGCTGCGGGCACACGC  
GGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATGGGGCGGTGACCCAGCCTCGCCCGA  
CAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAATCCCGCGCGGGTTCCGCTGACGCAGCGCCCCGCTGGG  
AGCCGCGGGCAGGCGAGACTGGCGGAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAG  
CACAGCTGCAGATCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGCCC  
CAATACCCCAACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTGTAGACAGGGTCTTGCTCCGTTGCCAGGTTGGAG  
TGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCAAGTGACCCTCCACCTCAGCCTCTCAAG  
TAGCTGGGACTACAGGTGCACCACCACACCTGGCTAATTTTTGTATTTTTTTGTAAAGAGGGGGGTCTCACTGTGT  
TGCCCAGGCTGGTTTCGAACTCCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTCTGGGATTGCAGG  
CATGAGCCACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAATAAAA  
CCAAAGTATTGATAAAAAAAA

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**FIGURE 314**

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDCA  
LPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPPFPIQGCMHGGRIYPVLGTYWDNCNRCT  
CQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

**Important features:****N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415**N-myristoylation site.**amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

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**FIGURE 315**

CGGACGCGTGGGCCCCTGGTGGGCCCAGCAAGATGGATCTACTGTGGATCCTGCCCTCCCTGT  
GGCTTCTCCTGCTTGGGGGGCCTGCCTGCCTGAAGACCCAGGAACACCCAGCTGCCCAGGAC  
CCAGGGAAGTGGGAAGCCAGCAAAGTTGTCCTCCTGCCCAGTTGTCCCGGAGCTCCAGGAAGTC  
CTGGGGAGAAGGGAGCCCCAGGTCCTCAAGGGCCACCTGGACCACCAGGCAAGATGGGCCCCA  
AGGGTGAGCCAGGCCCCAGAACTGCCGGGAGCTGTTGAGCCAGGGCGCCACCTTGAGCGGCT  
GGTACCATCTGTGCCTACCTGAGGGCAGGGCCCTCCCAGTCTTTTGTGACATGGACACCGAGG  
GGGGCGGCTGGCTGGTGTTCAGAGGCGCCAGGATGGTTCTGTGGATTTCTTCCGCTCTTGGT  
CCTCCTACAGAGCAGGTTTTGGGAACCAAGAGTCTGAATTCTGGCTGGGAAATGAGAATTTGC  
ACCAGCTTACTCTCCAGGGTAACTGGGAGCTGCGGGTAGAGCTGGAAGACTTTAATGGTAACC  
GTACTTTCGCCCCTATGCGACCTTCCGCCTCCTCGGTGAGGTAGACCACTACCAGCTGGCAC  
TGGGCAAGTTCTCAGAGGGCACTGCAGGGGATTCCCTGAGCCTCCACAGTGGGAGGGCCCTTTA  
CCACCTATGACGCTGACCACGATTCAAGCAACAGCAACTGTGCAGTGATTGTCCACGGTGCCT  
GGTGGTATGCATCCTGTTACCGATCAAATCTCAATGGTCGCTATGCAGTGTCTGAGGCTGCCG  
CCCACAAATATGGCATTGACTGGGCCTCAGGCCGTGGTGTGGGCCACCCCTACCGCAGGGTTC  
GGATGATGCTTCGATTAGGGCACTCTGGCAGCCAGTGCCCTTATCTCTCCTGTACAGCTTCCGG  
ATCGTCAGCCACCTTGCCTTTGCCAACCACCTCTGCTTGCCTGTCCACATTTAAAAATAAAAT  
CATTTTAGCCCTTTCA

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**FIGURE 316**

MDLLWILPSLWLLLLGGPACLKTQEHPSCPGPRELEASKVLLPSCPGAPGSPGEKGAPGPQG  
PPGPPGKMGPKGEPGPRNCRELLSQGATLSGWYHLCLPEGRALPVFCMDTEGGGWLVFQRRQ  
DGSVDFFRSWSSYRAGFGNQESEFWLGNENLHQLTLQGNWELRVELEDFNGNRTFAHYATFRL  
LGEVDHYQLALGKFSEGTAGDSLHSGRPFTTYDADHDSSNSNCAVIVHGAWWYASCYRSNL  
NGRYAVSEAAAHKYGIDWASGRGVGHPYRRVRMMLR

**Important features:****Signal peptide:**

Amino acids 1-16

**N-glycosylation site:**

Amino acids 178-182

**Glycosaminoglycan attachment site:**

Amino acids 272-276

**Tyrosine kinase phosphorylation site:**

Amino acids 188-197

**N-myristoylation sites:**

Amino acids 16-22;89-95;144-150;267-273

**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 242-255



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**FIGURE 317**

CCCAAGCCAGCCGAGCCGCCAGAGCCGCGGGCCGCGGGGGTGTGCGGGGCCCAACCCAGGAT  
GCTCCCCTGCGCCTCCTGCCTACCCGGGTCTCTACTGCTCTGGGCGCTGCTACTGTTGCTCTT  
GGGATCAGCTTCTCCTCAGGATTCTGAAGAGCCCGACAGCTACACGGAATGCACAGATGGCTA  
TGAGTGGGACCCAGACAGCCAGCACTGCCGGGATGTCAACGAGTGTCTGACCATCCCTGAGGC  
CTGCAAGGGGGAAATGAAGTGCATCAACCACTACGGGGGCTACTTGTGCCTGCCCCGCTCCGC  
TGCCGTCATCAACGACCTACATGGCGAGGGACCCCCGCCACCAGTGCCTCCCGCTCAACACCC  
CAACCCCTGCCCACCAGGCTATGAGCCCGACGATCAGGACAGCTGTGTGGATGTGGACGAGTG  
TGCCAGGCCCTGCACGACTGTGCGCCCAGCCAGGACTGCCATAACTTGCTGGCTCCTATCA  
GTGCACCTGCCCTGATGGTTACCGCAAGATCGGGCCCCGAGTGTGTGGACATAGACGAGTGCCG  
CTACCGCTACTGCCAGCACCGCTGCGTGAACCTGCCTGGCTCCTTCCGCTGCCAGTGCGAGCC  
GGGCTTCCAGCTGGGGCCTAACAACCGCTCCTGTGTTGATGTGAACGAGTGTGACATGGGGGC  
CCCATGCGAGCAGCGCTGCTTCAACTCCTATGGGACCTTCTGTGTCGCTGCCACCAGGGCTA  
TGAGCTGCATCGGGATGGCTTCTCCTGCAGTGATATTGATGAGTGTAGCTACTCCAGCTACCT  
CTGTGCTACCGCTGCGTCAACGAGCCAGGCCGTTTCTCCTGCCACTGCCCACAGGGTTACCA  
GCTGCTGGCCACACGCCTCTGCCAAGACATTGATGAGTGTGAGTCTGGTGCGCACCAAGTGTCTC  
CGAGGCCCAAACCTGTGTCAACTTCCATGGGGGCTACCGCTGCGTGGACACCAACCGCTGCGT  
GGAGCCCTACATCCAGGTCTCTGAGAACCGCTGTCTCTGCCCCGGCCTCCAACCCTCTATGTCG  
AGAGCAGCCTTCATCCATTGTGCACCGCTACATGACCATCACCTCGGAGCGGAGCGTGCCCCG  
TGACGTGTTCCAGATCCAGGCGACCTCCGTCTACCCCGGTGCCTACAATGCCTTTCAGATCCG  
TGCTGGAAACTCGCAGGGGGACTTTTACATTAGGCAAATCAACAACGTCAGCGCCATGCTGGT  
CCTCGCCCCGGCCGGTGACGGGGCCCCCGGGAGTACGTGCTGGACCTGGAGATGGTCACCATGAA  
TTCCCTCATGAGCTACCGGGCCAGCTCTGTACTGAGGCTCACCGTCTTTGTAGGGGCCTACAC  
CTTCTGAGGAGCAGGAGGGAGCCACCCTCCCTGCAGCTACCCTAGCTGAGGAGCCTGTTGTGA  
GGGGCAGAATGAGAAAGGCAATAAAGGGAGAAAGAAAGTCTTGGTGGCTGAGGTGGGCGGGTC  
ACACTGCAGGAAGCCTCAGGCTGGGGCAGGGTGGCACTTGGGGGGGCAGGCCAAGTTCACCTA  
AATGGGGGTCTCTATATGTTTCAGGCCAGGGGCCCCCATTTGACAGGAGCTGGGAGCTCTGCAC  
CACGAGCTTCAGTCACCCCGAGAGGAGAGGAGGTAACGAGGAGGGCGGACTCCAGGCCCCGGC  
CCAGAGATTTGGACTTGGCTGGCTTGCAGGGGTCCTAAGAACTCCACTCTGGACAGCGCCAG  
GAGGCCCTGGGTTCCATTCTAACTCTGCCTCAAACGTGACATTTGGATAAGCCCTAGTAGTT  
CCCTGGGCCTGTTTTTCTATAAAACGAGGCAACTGGAAAAAAAAAAAA

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**FIGURE 318**

MLPCASCLPGSLLLWALLLLLLLGSASPQDSEEPDSYTECTDGYEWDPDSSQHCRDVNECLTIPE  
ACKGEMKCIINHYYGGLCLPRSAAVINDLHGEGPPPPVPPAQHPNPCPPGYEPDDQDSCVDVDE  
CAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRQCCE  
PGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDECSSYSSY  
LCQYRCVNEPGRFSCHCPQGYQLLATRLCQDIDECESGAHQCSAQTCVNFHGGYRCVDTNRC  
VEPYIQVSENRLCPASNPLCREQPSSIVHRYMTITSESVPADVFQIQATSVYPGAYNAFQI  
RAGNSQGDIFYIRQINNVSAMLVLARPVTGPREYVLDLEMTMNSLMSYRASSVLRLTVFVGAYTF

**Important features:****Signal sequence:**

Amino acids 1-25

**N-glycosylation sites:**

Amino acids 198-202;394-398

**N-myristoylation sites:**Amino acids 76-82;145-151;182-188;222-228;290-296;305-311;  
371-377;381-387**Aspartic acid and asparagine hydroxylation sites:**

amino acids 140-152;177-189;217-229;258-270

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**FIGURE 319**

GCTGGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTCTGCCTCCTC  
TCAAAGGTGCGTACCCAGCTGTGCCCCGACACCATGTACCTGCCCCTGGCCACCTCCCCGATGC  
CCGCTGGGAGTACCCCTGGTGTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGGCGGGCTG  
GGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCTGCCAGCCCGGG  
GCAGGACCCGGTGGCCGGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGCAGCTGTGAGGTG  
AACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGCATCCGCTGCCGCTGC  
GAGGACGGCGGCTTACCTGCGTGCCGCTGTGCAGCGAGGATGTGCGGCTGCCAGCTGGGAC  
TGCCCCACCCCAGGAGGGTCGAGGTCCTGGGCAAGTGCTGCCCTGAGTGGGTGTGCGGCCAA  
GGAGGGGGACTGGGGACCCAGCCCCCTTCCAGCCCAAGGACCCAGTTTTCTGGCCTTGTCTCT  
TCCCTGCCCCCTGGTGTCCCCTGCCCAGAATGGAGCACGGCCTGGGGACCCTGCTCGACCACC  
TGTGGGCTGGGCATGGCCACCCGGGTGTCCAACCAGAACCGCTTCTGCCGACTGGAGACCCAG  
CGCCGCCTGTGCCTGTCCAGGCCCTGCCCACCCTCCAGGGGTGCGAGTCCACAAAACAGTGCC  
TTCTAGAGCCGGGCTGGGAATGGGGACACGGTGTCCACCATCCCCAGCTGGTGGCCCTGTGCC  
TGGGCCCTGGGCTGATGGAAGATGGTCCGTGCCAGGCCCTTGGCTGCAGGCAACACTTTAGC  
TTGGGTCCACCATGCAGAACACCAATATTAACACGCTGCCTGGTCTGTCTGGATCCCAGGTA  
TGGCAGAGGTGCAAGACCTAGTCCCCCTTCTCTAACTCACTGCCTAGGAGGCTGGCCAAGGT  
GTCCAGGGTCCTCTAGCCCACTCCCTGCCTACACACACAGCCTATATCAAACATGCACACGGG  
CGAGCTTTCTCTCCGACTTCCCCTGGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGC  
TGCAGCAGGTGCTGGGCTGGACTGGCCATTTTTCTGGGGGTAGGATGAAGAGAAGGCACACAG  
AGATTCTGGATCTCCTGCTGCCTTTTCTGGAGTTTGTAATAATTGTTCTGAATACAAGCCTAT  
GCGTGA

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**FIGURE 320**

MRGTPKTHLLAFSLCLLSKVRTQLCPTPCTCPWPPRCPLGVPLVLDGCGCCRVCCARRLGEP  
CDQLHVCDASQGLVCQPGAGPGGRGALCLLAEDDSSCEVNGRLYREGETFQPHCSIRCRCEG  
GFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPEWVCGQGGLGTQPLPAQGPQFSGLVSSLP  
PGVPCPEWSTAWGPCSTTCGLGMATRVSNQNRFCRLETQRRCLSRPCPPSRGRSPQNSAF

**Important features:**

Signal sequence:

Amino acids 1-23

**N-myristoylation sites:**

Amino acids 3-9;49-55;81-87;85-91;126-132;164-170;166-172;

167-173;183-189;209-215

**Insulin-like growth factor binding proteins signature:**

Amino acids 49-65

**von Willebrand C1 domain:**

Amino acids 107-124

**Thrombospondin 1 Homology Block:**

Amino acids 201-216

**IGF binding protein site:**

Amino acids 49-58

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**FIGURE 321**

[illegible]

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## **FIGURE 322**

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCFQYSHKPLPWTWVRSYEFTSNSCSQRAVI  
FTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-myristoylation sites.**

amino acids 3-9, 26-32

**Amidation site.**

amino acids 68-72

**Small cytokines (intecrine/chemokine).**

amino acids 23-88

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**FIGURE 323**

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGGGGCGTGAGGAGCA  
TGCCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCTGGGCTCAGTGCTGTCAGGCTCGGCCA  
CGGGCTGCCCCCGCTGCGAGTGCTCCGCCCAGGACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAG  
TCCCCGAGGGCATCCCCACCGAGACGCGCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACG  
AGTTCCGCCAGCTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCGCCT  
TCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATCCCGCTAGGCGTCTTCA  
CTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGATCGTTATCCTACTGGACTACATGTTTCAGG  
ACCTGTACAACCTCAAGTCACTGGAGGTTGGCGACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCC  
TCAACAGCCTGGAGCAGCTGACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGC  
ACGGCCTCATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGCTGTACC  
GACTCAAGGTCTTGAGATCTCCCACTGGCCCTACTTGAGACACCATGACACCCAACCTGCCTCTACGGCCTCAACC  
TGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCCCTACCTGGCCGTCCGCCACCTAGTCTATCTCC  
GCTTCCTCAACCTCTCCTACAACCCCATCAGCACCATTTAGGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGG  
AGATCCAGCTGGTGGGCGGGCAGCTGGCCGTGGTGGAGCCCTATGCCCTCCGCGGCCTCAACTACCTGCGCGTGC  
TCAATGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGGAGACACTCA  
TCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGCGCCGCTGGCGGCTCAACTTCA  
ACCGGCAGCAGCCACGTGCGCCACGCCCCGAGTTTGTCCAGGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTAC  
TGCCCCAACTACTTCACCTGCCGCCGCGCCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCC  
ACACGGTGCACTTGTGTGCCGGGCGGATGGCGACCCGCGCCCGCCATCCTCTGGCTCTCACCCCGAAAGCACC  
TGGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCTACGCCCAGGTAC  
AGGACAACGGCACGTACCTGTGCATCGCGCCAACGCGGGCGGCAACGACTCCATGCCCCGCCACCTGCATGTGC  
GCAGTACTCGCCCGACTGGCCCCATCAGCCCAACAAGACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAG  
AGGCCAACAGCACCCGCGCCACTGTGCCTTTCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCT  
TCATCTCTTCTGGGCGTCTCCTCTTCTGCCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACACAA  
AGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCGACGCGCCCCGCAAGT  
TCAACATGAAGATGATATGAGGCGGGGGCGGGGGCAGGGACCCCCGGGCGGCCGGGCAGGGGAAGGGCCTGGT  
CGCCACCTGCTCACTCTCCAGTCTTCCACCTCCTCCCTACCCTTCTACACAGTCTCTTTCTCCCTCCGCC  
TCCGTCCCTGCTGCCCCCGCCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCAGACCTGG  
GGACCCACCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCAATAAT  
TCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTTCAATAATTATGGATTTTATGAAAACCTTGAAATAA  
TAAAAAGAGAAAAAACTAAAAA

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**FIGURE 324**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCFVAVPEGIPTETRL  
LDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTLGLRSNRLKLIPLGVFTGLSNLTKQDI  
SENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRAFSGLSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHL  
NINAIIRDYSFKRLYRLKVLEISHWPYLDTMTNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRLNLSYNPIS  
TIEGSMHELLRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSGNLETILDSNPLACDC  
RLLWVFRRRWRLNFRNQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQVFVDEGHTVQFVCRADG  
DPPPAIWLSPRKHLVSAKSNRGLTVFPDGTLEVRYAQVQDNGTYLCIAANAGGNDSPAHLHVRSYSPDWPHQP  
NKTFAFISNQPGEGEANSTRATVPFPFDIKTLIIATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPR  
KSDAGISSADAPRKFNMKMI

**Important features:****Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345, 492-496,  
505-509, 526-530, 542-546**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353, 607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143, 262-268, 320-326,  
344-350, 359-365, 493-499, 503-509, 605-611**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43



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**FIGURE 325**

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGAG  
GCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGAGG  
AGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAGGAG  
GAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAACGGAG  
AGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGAGTAGG  
AAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCGGGAAAAGAGCAGAGGAAAGAGGAAAGAC  
ACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTGGCTGCTT  
TGGCATTGTTGGGGAAGTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCTTGAGGGAC  
AGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGGCAGGGGTCC  
CTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGCGCTGGTACTC  
TGGGCTGCACTGGGGGACAGCTCACATCGGACCAGCACCTGACCCCGAGGACTGGTGGAGC  
TACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGCCTGGTGAATGCA  
GCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGAGCTGAAGAGGGTT  
CTTTATGACCCCTTTCTGCCCCATTAAGGCTCAGCACTGGAGGAGAGAAGCTCCGGGGAACC  
TTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCTGTGGTCAATGTGTCT  
GGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCAGGCTGCTGTTTGGAGCTCGCGAC  
GGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTGAGGTGCAGCTCATTAC  
TTCAACCAGGAAGTCTACGGGAATTTACAGCGCTGCCTCCCGCGGCCCAATGGCCTGGCCATT  
CTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCATTCTCAGTCGCCTCCTTAACCGC  
GACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTCTTCAAGACCTGAGCCTGGAG  
CTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGCTCTCTCAGCACCCCGCCCTGC  
TCCGAGACTGTACCTGGATCCTCATTGACCGGGCCCTCAATATCACCTCCCTTCAGATGCAC  
TCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCTTCCAGAGCCTCAGCGGTAACAGC  
CGGCCCCCTGCAGCCCTTGGCCCCACAGGGCACTGAGGGGCAACAGGGACCCCGGCACCCCGAG  
AGGCGCTGCCGAGGCCCCAACTACCGCCTGCATGTGGATGGTGTCCCCATGGTCGCTGAGAC  
TCCCCTTCGAGGATTGCACCCGCCGTCTAAGCCTCCCCACAAGGCGAGGGGAGTTACCCCT  
AAAACAAAGCTATTAAAGGGACAGAATACTTA

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**FIGURE 326**

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCA  
VGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLY  
SHRLSELRLLEFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSLFVN  
VASTSNPFLSRLNLDITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSLTPPCSETVTW  
ILIDRALNITSLQMHSLRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGP  
NYRLHVDGVPHGR

**Important features:****Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 177-199

**N-glycosylation sites:**

Amino acids 118-122;170-174;260-264

**Eukaryotic-type carbonic anhydrases proteins:**

Amino acids 222-271;128-165;45-93

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**FIGURE 327**

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGTGTTGAAGGGTGT  
TTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACACAGTGTCTGAGAACATTTACATTATAGATAA  
GTAGTACATGGTGGATAAATTCTACTTTTAGGAGGACTACTCTCTTCTGACAGTCTTAGACTGGTCTTCTACACT  
AAGACACCAATGAAGGAGTATGTGCTCCTATTATTCCTGGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCTTCA  
ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATGATG  
ATGATGATGAGGACAACTCTCTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTCCATTTGATCTGTTTCCAA  
TGTGTCCATTTGGATGTGCTGCTATTACGAGTTGTACATTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCA  
ACATTCCATTTGATACTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAG  
GACTCACTTCACTTTATGGTCTGATCCTGAACAACAACAAGCTAACGAAGATTCACCCAAAAGCCTTTCTAACCA  
CAAAGAAGTTGCGAAGGCTGTATCTGTCCACAATCAACTAAGTGAATACCCTTAATCTTCCCAAATCATTAG  
CAGAACTCAGAAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACAG  
TTTTGGAATGAGTGCAAACCCTCTTGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGTGTTC  
ATATCAGAATTGCAGAAGCAAACTGACCTCAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAG  
ATTATAATAAAATTTCAACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAA  
ACAACAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATTTGGAAAACA  
ATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATAATCTTCCTTCATTCTAATTCAA  
TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCCAAAGATGAAGAAATCTTTATACAGTGCAATAAGTT  
TATTCAACAACCCGGTGAAATACTGGGAAATGCAACCTGCAACATTTTCGTTGTGTTTTGAGCAGAATGAGTGTT  
AGCTTGGGAACTTTGGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACAT  
TTGGAATACTTGAACCTCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCAAGTGGTAAAGTCC  
ACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAACTATTGATACATAAGGGGTTGAGAGAAACA  
AGCATCTATTGCAGTTTCCTTTTTGCGTACAAATGATCTTACATAAATCTCATGCTTGACCATTCCCTTCTTCAT  
AACAAAAAGTAAGATATTCCGTATTTAACACTTTGTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGG  
AATGCTTGACTTAGCAAAATTTGTGCTCTTTCATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGTGA  
AGAGTGCATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAATATTTTAAATCATCTTAAAGTATGA  
TTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGTCTTTATGTTTAAACTAATTTCTTAAAA  
TAAAGCCTTCAGTAAATGTTTATTACCAACTTGATAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATAT  
GCTTTTTTTTTTTAATTATTACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAAC  
CGCATTTTAAATGATCCGCTATTATAAGCTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCACTTCAA  
CTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGGAAGAGCCTGGACACTAACAAATCTACACC  
AAATTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCAT  
CAAATTAACAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAA  
CATATGTAAATCAGAAAACAGGGAAATTTTCATTAATAATATTGGTTTGAAAT

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**FIGURE 328**

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDNSLFPTREPRS  
HFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTS  
LYGLILNNNKLTKEHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDT  
FKGMNALHVLEMSANPLDNNGIEPGAEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI  
STVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLPPELKYLQI  
IFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQLGNFGM

**Important features:****Signal sequence.**

amino acids 1-15

**N-glycosylation site.**

amino acids 281-285

**N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

**Leucine zipper pattern.**

amino acids 154-176

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**FIGURE 329**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGCA  
TCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGTGT  
TTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGTGTT  
CAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACCAGCG  
GCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGCCTGCT  
GAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCCGCTCCC  
GCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACCTCAGTTTGA  
TTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCTCAATACCA  
TGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCATGCAGCAAAT  
GTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTCTTTACCAAC  
CTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTTCGGAATCTGGAGTCCACCCG  
TTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCATCCACACTGATGA  
AGCAGATTCAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAG  
AGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTGAAAAGGTGAAGGA  
CAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCTGGACAACGTGGCTGC  
CGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATCGAACA  
GAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGGGAAAGTCTTCAGATGGC  
AGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGC  
CCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTT  
AATGACCCTGGGGATTTTGTACCACAAATGGCCACCGTTTGCTGTTGACCTGACCATGGAACCT  
TTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTATTACCACGGGAAGGAGCAGGT  
GCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGTTCTTGAATGCCATGTCAGTTTA  
TACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAAACCTCAGGTGATGGAAGTTGGAAA  
TGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATTTTAAATAAAGTGCCTTTATACAATG

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**FIGURE 330**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVFRHGARSPLKPLPLEEQVE  
WNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIPFL  
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRRQTASLQ  
PGISEDLLKKVKDRMGIDSSDKVDFILLDNVAEEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMA  
VGPFLHILESNNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMTLGIFDHKWPPFAVDLTMELYQHLESKEWFVQ  
LYYHGKEQVPRGCPDGLCPLDMFLNAMSIVTSLPEKYHALCSQTQVMEVGNEE

**Important features:****Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

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**FIGURE 331**

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCAGTCTTGTGGCTACAACATTTTCCCTTTCCT  
AACAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTCTTCTTGGCTGGAGAAGAAAGGGCTGAGGGCAG  
AGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTGCCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGAT  
GCAGCGGAGTGAGGTGATGGAAGTCTAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGA  
CCTGGAGAGCCTGGGGGAGGGCCTGCCTAACAGCTTTCAAAAACAGGAGCGACTTCCACTGGGCTGGGATAAG  
ACGTGCCGCTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGGTGAACCTCAACAGCCT  
TTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAATAGAGATGCTTTGTAAATAAAATTTTAA  
AAAAAGCAAGTATTTTATAGCATAAAGGCTAGAGACCAAAATAGATAACAGGATTCCCTGAACATTCCTAAGAGG  
GAGAAAGTATGTTAAAAATAGAAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACC  
CTGGGTGACGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTTGCAGAA  
TCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCTCCTCACCGCCGCCCTCTC  
AGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCCTGCTCTCAGTGGTC  
TGGGTGCTGCTGGCCCCCAGCAGCCGGCATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACC  
TTCAACCACTTGACCGTCCACCAAGGGACGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACA  
GGCAACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCGCCCTCATC  
GTGCAGCCCTGCAGCGAAGTGCTCACCCTCACCAACAATGTCAACAAGCTGCTCATCATTGACTACTCTGAGAAC  
CGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTG  
GAGCCATCCCACAAGAAGGAGCACTACCTGTCCAGTGTCACAAGACGGGCACCATGTACGGGGTGATTGTGCGC  
TCTGAGGGTGAGGATGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCC  
AGCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCCTCT  
CTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTACGGCTTTGCTAGT  
GGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGACCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTC  
TTCTACACCTCACGCATCGTGCGGCTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGC  
TGCACCCGGGCCGGGGTGAATAACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCCAG  
GCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAGGGCAGAAGCAGTATCACCACCCG  
CCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTTGCAGATCAAGGAGCGCCTGCAGTCTGC  
TACCAGGGCGAGGGCAACCTGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGTGACGAAGGCGCCTGTCCCC  
ATCGATGATAACTTCTGTGGACTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTG  
TACACCACCAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTGTGGGG  
ACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTGAGATGCTCCAATGCCATTCACCTCCTCAGCAA  
GAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAGGCAACTTTATTTTCTTGGGGAACAAAGGTGA  
AATGGGGAGGTAAGAAGGGGTTAATTTTGTGACTTAGCTTCTAGCTACTTCCCTCAGCCATCAGTCATTGGGTAT  
GTAAGGAATGCAAGCGTATTTCAATATTTCCCAAACCTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAA

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**FIGURE 332**

MGTLGQASLFAPPGNYFWS DHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWPR  
ALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSEN RDWTFNHLTVHQGTGAVYVGAINRVYK  
LTGNLTIQVAHKTGPEEDNKSRYPP LIVQPCSEVLTLTNNVNKLLIIDYSENRL LACGSLYQG  
VCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFITAVD GKQDYFPTL  
SSRKLPRDP ESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYG FASGGFVYFLTVQPE  
TPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGDSL AQ  
AFNITSQDDVLF AIFSKGQKQYHHPDD SALCAFP IRAINLQIKERLQSCYQGEGNLELNWLL  
GKDVQCTKAPVPI DDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNGYSVV FVGT  
KSGKLLKVRVYEFRC SNAIHLLSKESSL EGSYWWRFNYRQLYFLGEQR

**Important features:****Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site. .**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509



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**FIGURE 333**

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAGG  
CCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCCAGAGCCCACACCATGCCGGGCACCTACGC  
TCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGGCCCTGAT  
GCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCCTGGTCCTAAGGCAGGTTTACCA  
GAAAGGGCTACAGGATGTTAACCTGCGCAATTTAGCTACGGCCAGACCAGCCTGGACAGGCT  
TAGAGATGGCCTCGTGGGCGCCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCG  
GGATGCCCTGCGCCTCACCCTGGAGCAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTC  
TGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCAT  
CGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCT  
GGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAA  
GGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGC  
AGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCG  
GGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGGTGTGTGCAA  
CAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGAT  
GGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGA  
TCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGA  
TGGGGCCGGCAAATTCCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGA  
GTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCG  
GGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTTGGAGGACAA  
GTTCCCGGATGAGCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACA  
GAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGC  
CAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAGTCCTTGCAGTTGTGGCCACCTT  
CCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCCTGCCAGATGTCACTGTAGCAAGC  
CACAGACACCCACAAAGTTCCTGTTGTGCAGGCACAAATATTTCTGAAATAAATGTTTT  
GGACATAG

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**FIGURE 334**

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYGQ  
TSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALNDTQ  
KLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGLTDF  
GEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQLLKK  
NGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLEDVSTY  
PVLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSSCHSDLS  
RLRQRQSLTSGQELTEIPIHWTAKLPKWSVSESSPHMAPVLAVVATFPVLILWL

**Important features:****N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

**N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

**Renal dipeptidase active site.**

amino acids 134-157

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**FIGURE 335**

[illegible]

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**FIGURE 336**

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEW  
KKLGRSVSVFVYYQOTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTV  
TLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSS  
YTMNTKTGTQLQFNTVSKLDTGEYSCEARNVSGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS  
VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAAGGSRGQEF

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

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**FIGURE 337**

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCGG  
CACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGAGGGCCA  
**TG**ATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTG  
CCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGCGG  
TGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGGAGGTGTCTTCATCCC  
AGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATCAGGTGT  
TGTCTACATCAATGGGGTCAACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCCATGCCCT  
CCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTACAGCTGCT  
CCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCTTAGAACTCA  
ATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCATGTGGGGGCAA  
ACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCAGTGGGATCGGC  
AGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCC  
TCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCA  
CTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAG  
CTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCC  
GGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCC  
TGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCG  
CACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCATTGACCCCCACGCCAGTC  
TCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCCACGACAGATGGGGCCCCACCCTCAACCAA  
TATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA  
TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTAT**TG**ATGACCCCACTCATTGGCTAAAG  
GATTTGGGGTCTCTCCTTCTATAAGGGTCACTCTAGCACAGAGGCCTGAGTCATGGGAAAG  
AGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAAACCATCTCA  
GTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGC  
CTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTACCAAGAGT  
GAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGATCTGTACCCACCCCTAT  
CTAACACCACCCCTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTTG  
GTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAAACTAACATGAAATATGTGTT  
GTTTTCATTTGCAAATTTAAATAAAGATACATAATGTTTGTATGAAAAA

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**FIGURE 338**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSS  
QPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPYSC  
SVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQWDR  
QLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAADVAG  
AVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTLSSVTS  
ARALRPPHGP RP GALTP T PSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSSGLSRMGAVPV  
MVPAQSQAAGSLV

**Important features:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

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**FIGURE 339**

CGGAGAACCTTTGCACGCGCACAAACTACGGGGACGATTTCTGATTGATTTTGGCGCTTTCGATCCACCCTCCT  
CCCTTCTC**ATG**GGACTTTGGGGACAAAGCGTCCCGACCGCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGCCA  
GGACAGCGTCGGGAACCCAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTCGTCTTTCATCGTCGCGGTTCT  
TGCTGCCGGTCCGGGTTGACTCTGCCACCATCCCCCGGCAGGACGAAGTTCGCCAGCAGACAGTGGCCCCACAGC  
AACAGAGGCGCAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTGTAACC  
CGTGCACAGAGGGTGTGGATTACACATTGCTTCCAACAATTTGCCTTCTTGCTGCTATGTACAGTTTGTAAAT  
CAGGTCAAACAAATAAAAGTTTCTGTACCACGACCAGAGACACCGTGTGTAGTGTGAAAAAGGAAGCTTCCAGG  
ATAAAACTCCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCAGAGGGATGGTCAAGGTCAAGTAATTGT  
CGCCCCGGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTTCCTGCGGAAAAACCCAGCAGCGGAGGAGA  
CAGTGACCACCATCTGGGGATGCTTGCCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTAGTCATCATTT  
TAGCTGTGGTTGTGGTTGGCTTTTCATGTGCGGAAGAAATTCATTTCTTACCTCAAAGGCATCTGCTCAGGTGGTG  
GAGGAGGTCCCGAACCTGTGCACAGAGTCCTTTTCCGGCGGCGTTTCATGTCTTCACGAGTTCCTGGGGCGGAGG  
ACAATGCCCGCAACGAGACCCCTGAGTAACAGATACTTGCAGCCACCCAGGTCTCTGAGCAGGAAATCCAAGTCT  
AGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTGCAGAGGAGCCACAGCGTCTGCTGGAACAGGCAGAAAG  
CTGAAGGGTGTGAGAGGAGGAGGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACATCAGCACCTTGCTGG  
ATGCCTCGGCAACACTGGAAGAAGGACATGCAAGGAAACAATTCAGGACCAACTGGTGGGCTCCGAAAAGCTCT  
TTTATGAAGAAGATGAGGCAGGCTCTGCTACGCTCTGCTG**TGA**AAGAATCTCTTCAGGAAACCAGAGCTTCCCT  
CATTTACCTTTTCTCTACAAAGGGAAGCAGCTGGAAGAAACAGTCCAGTACTTGACCCATGCCCAACAACT  
CTACTATCCAATATGGGCGAGCTTACCAATGGTCTAGAACTTTGTAAACGCACTTGGAGTAATTTTTATGAAAT  
ACTGCGTGTGATAAGCAACGGGAGAAATTTATATCAGATTCTTGGCTGCATAGTTATACGATTGTGATTAAGG  
GTCGTTTTAGGGCCACATGCGGTGGCTCATGCCTGTAATCCAGCACTTTGATAGGCTGAGGCAGGTGGATTGCTT  
GAGCTCGGGAGTTTGAGACCAGCCTCATCAACACAGTGAAACTCCATCTCAATTTAAAAAGAAAAAAGTGGTTT  
TAGGATGTCAATCTTTGCAGTCTTTCATCATGAGACAAGTCTTTTTTTCTGCTTCTTATATTGCAAGCTCCATCT  
CTACTGGTGTGTGATTTAATGACATCTAACTACAGATGCCGCACAGCCACAATGCTTTGCCTTATAGTTTTTTA  
ACTTTAGAACGGGATTATCTTGTTATTACCTGTATTTTCAGTTTCGGATATTTTGACTTAATGATGAGATTATC  
AAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTTACGAGGGTTCGACTTAGAGTTTTGAGCTTTAAGATA  
GGATTATTGGGGCTTACCCCCACCTTAATTAGAGAAACATTTATATTGCTTACTACTGTAGGCTGTACATCTCTT  
TTCCGATTTTTGTATAATGATGTAAACATGGAAAACTTTAGGAAATGCACTTATTAGGCTGTTTACATGGGTTG  
CCTGGATACAAATCAGCAGTCAAAAATGACTAAAAATATAACTAGTGACGGAGGGAGAAATCCTCCCTCTGTGGG  
AGGCACTTACTGCATTCCAGTTCTCCCTCCTGCGCCTGAGACTGGACCAGGGTTTGATGGCTGGCAGCTTCTCA  
AGGGGCAGCTTGTCTTACTTGTTAATTTTAGAGGTATATAGCCATATTTATTTATAAATAAATATTTATTTATTT  
ATTTATAAGTAGATGTTTACATATGCCAGGATTTTGAAGAGCCTGGTATCTTTGGGAAGCCATGTGTCTGGTTT  
GTCGTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGTCCACAGCAGATGAGGACAGTGAGAATTAAGTTAG  
ATCCGAGACTGCCAAGAGCTTCTCTTTCAAGCGCCATTACAGTTGAACGTTAGTGAATCTTGAGCCTCATTGGG  
CTCAGGGCAGAGCAGGTGTTATCTGCCCGGCATCTGCCATGGCATCAAGAGGGAAGAGTGGACGGTGCTTGGG  
AATGGTGTGAAATGGTTGCCGACTCAGGCATGGATGGGCCCCCTCTCGCTTCTGGTGGTCTGTGAAGTGAAGTCCCT  
GGGATGCCTTTTAGGGCAGAGATTCTGAGCTGCGTTTTAGGGTACAGATTCCCTGTTTGAGGAGCTTGGCCCT  
CTGTAAGCATCTGACTCATCTCAGAGATATCAATTCTTAAACACTGTGACAACGGGATCTAAATGGCTGACACA  
TTTGTCTTGTGTACGTTCCATTATTTATTTAAAAACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACCTCT  
TCTCCACAGTAGCCAGTCGTGGTAGGATAAATTACGGATATAGTCATTCTAGGGGTTTCAGTCTTTTCCATCTC  
AAGGCATTGTGTGTTTTGTTCCGGGACTGGTTTGGCTGGGACAAAGTTAGAAGTGCCTGAAGTTTCGCACATTCAG  
ATTGTTGTGTCCATGGAGTTTTAGGAGGGGATGGCCTTTCGGTCTTCGCACTTCCATCCTCTCCCACTTCCATC  
TGGCGTCCCACACCTTGTCCCCTGCACTTCTGGATGACACAGGGTGCTGCTGCCCTCCTAGTCTTTGCCCTTGGCTG  
GGCCTTCTGTGAGGAGACTTGGTCTCAAAGCTCAGAGAGAGCCAGTCCGGTCCCAGCTCCTTTGTCCCTTCTC  
AGAGGCCTTCTTGAAGATGCATCTAGACTACCAGCCTTATCAGTGTTTAAGCTTATTCTTTAACATAAGCTTC  
CTGACAACATGAAATGTGGGGTTTTTTGGCGTTGGTTGATTTGTTTAGGTTTTGCTTTATACCGGGCCAAAT  
AGCACATAACACCTGGTTATATATGAATACTCATATGTTTATGACCAAAATAAATATGAAACCTCATRTAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 340**

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQDEVPPQQTVAPOQQOR  
RSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRDTVCQCEKGSFQDKN  
SPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETVTTILGMLASPYHYLIIIVLVIIILAV  
VVVGFSCRKKFISYLKGICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQEL  
AELTGVTVESPEEPQRLLEQAEAGCQRRRLVPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKLFYE  
EDEAGSATSC

**Important features:****Transmembrane domains:**

amino acids 35-52, 208-230

**N-glycosylation sites.**

amino acids 127-131, 182-186, 277-281

**Glycosaminoglycan attachment site.**

amino acids 245-249

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 260-264

**N-myristoylation sites.**

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276, 297-303, 380-386

**ATP/GTP-binding site motif A (P-loop).**

amino acids 185-193

**TNFR/NGFR cysteine-rich region.**

amino acids 99-139



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**FIGURE 341**

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAGG  
CCATGCTTCGTTTCTTGCCAGATTTGGCTTTACGCTTCCTGTTAATTCTGGCTTTGGGCCAGG  
CAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCACCCC  
AGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTTCCAGGATCGCGAGGCAGCAGCGA  
CCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGTACTTC  
GCTTTCTCCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCTCCTGCC  
TGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACATTGGCCC  
AGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGAAGTGGCTC  
TGTTCTGGTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTAAAATGTTTG  
TGTTGCGGTGAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGATGTAGCTAAGG  
ATTGGAATGACAACCCCCGGAAAAATTTCTGGGTATTCTCTGGAGATACTGGTCAAAGAAGATA  
GAGACTCAGGGGTGAATTTTTCAGCCTGAAGACACCTGTGCCAGACTAAGATGCTCCCTTCATG  
CTTCCCTGCTGGTGGTGAAGTCTCAACCCTGATCAGTGCCACCCTTCTCGGAAAAGGAGAGCAG  
CCATCCCTGTCCCCAAGCTTTCTTGTAAAGAACCTCTGCCACCGTCACCAGCTATTCATTAACT  
TCCGGGACCTGGGTGGCACAAGTGGATCATTGCCCCCAAGGGGTTCATGGCAAATTACTGCC  
ATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAATTATGCTTTCATGCAAG  
CCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTATCCCCACCAAGCTGTCTC  
CCATTTCCATGCTCTACCAGGACAATAATGACAATGTCAATTCTACGACATTATGAAGACATGG  
TAGTCGATGAATGTGGGTGTGGGTAGGATGTCAGAAATGGGAATAGAAGGAGTGTCTTAGGG  
TAAATCTTTTAATAAAACTACCTATCTGGTTTATGACCACTTAGATCGAAATGTC

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**FIGURE 342**

MLRFLPDLAFSFLLILALGQAVQFQYVFLQFLGLDKAPSPQKFQVPVYILKKIFQDREAAAT  
TGVSRDLCYVKELGVRGNVLRFLPDQGGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQ  
LGLDLGPNSYYNLGPELELALFLVQEPHVWGQTTKPGKMFVLRVWPWPQGAVHFNLDDVAKD  
WNDNPRKNFGLFLEILVKEDRD SGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRKRAA  
IPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGECPFSLTISLNSSNYAFMQA  
LMHAVDPEIPQAVCIPTKLSPI SMLYQDNNNDNVILRHYEDMVVDECGCG

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 112-116, 306-310

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 96-100

**N-myristoylation site.**

amino acids 77-83

**TGF-beta family proteins.**

amino acids 264-299, 327-341, 345-364

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**FIGURE 343**

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCATTCTCTTTTCATTGACAACTGACTTTTTTTTATTTCT  
TTTTTTCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTGTGTTTTACACACATAAGGAT  
CTGTGTTTTGGGGTTTCTTCTTCCCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTGGGGAGGGAGACCAGTGG  
GCTCAGTGCTTGCTTGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC  
ATCGCTGGTGGTATCCTGGCGGCCCTTGCTCCTGCTGATAGTTGTCGTGCTCTGTCTTTACTTCAAATAACACAAC  
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAAGGTGTGGTGGGCCAAG  
AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGTCTGCCCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC  
AGTTTTGATTCCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA  
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG  
CTCCCCATCAGTTTCATGGAAAATAACTCAGTGCTGCTGGGAACAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGGCAACCCCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACAGTCA  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAACCTGACGTTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCCTATAAAAGCTGTCGGTCTTAAGGCTGCCAGCGCCTTGCCAAAATGAGAGCTTGTA  
AGAAGGCTCATGCCATTGACCCTCTTAATTCTCTCCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC  
AGTGAGAAGTGCACCTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTTTCTATGTCCAGCTT  
GATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCTTTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGG  
CAAGTCTGCAGTAAAAACGACTATGTTCCCTGATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT  
GACTCAGCAAGAATTCAAAGAAGTGTCTTTGCTTCTACTACTTCTTCTCTCCTAACATCTCTATTTCAAAGTGT  
GGCGGTTACCTGGATACCTTGGAGGATCCTTACCAGCCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT  
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAAACTTCAAAGAGATTTTCTAGAAAATAGAC  
AAACAGTGCAAAATTTGATTTTCTTGCCATCTATGATGGCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT  
GGCCGTGTGACTCCACCTTCGAATCGTCATCAAACCTCTCTGACTGTCTGTTGTCTACAGATTATGCCAATTCT  
TACCGGGGATTTTCTGCTTCTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCAACTAAAA  
GACCCAATTGCAGACCAAAATTATCAAATGTTGTGGAATTTTCTGTCCCTCTTAATGGATGTGGTACAATCAGA  
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC  
CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA  
GAAGATGATGTAATACAAAGTCAAATGCACTGGGCAAATATAACACCAGCATGGCTCTTTTTGAATCCAATTCA  
TTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAACTCTTTTTGTTCAAGTTAGTCTGCAC  
ACCTCAGATCCAAATTTGGTGGTGTCTTGTATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC  
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAAAGTGTATCCCTTATTTGGACACTATGGGAGA  
TTCCAGTTTAATGCCTTTAAATTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTTGATATGTGAT  
AGCAGTGACCACAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAATGG  
AAAACAGATTCCATCATAGGACCCATTCTGTGAAAAGGGATCGAAGTGCAAGTGGCAATTGAGGATTTAGCAT  
GAAACACATGCGGAAGAACTCCAACAGCCTTTCAACAGTGTGCATCTGTTTTCTTCATGGTTCTAGCTCTG  
AATGTGGTGAAGTGTAGCGACAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG  
CAGAAGTATTAACCTAACAGGTCCAACCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAAA

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**FIGURE 344**

MELVRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTIE  
RPNKSIRIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSSTLTFTQ  
IVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQVEKD  
YKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLSTDYA  
NSYRGFSASYTSIYAENINTTSLTCSSDRMRVLIISKSYLEAFNSNGNNLQLKDPTCRPKLSNV  
VEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNSTVEIIYI  
TEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPNLVVFLDT  
CRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYLQCKVLICD  
SSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFQHETHAEETPNQPFN  
SVHLFSFMVLALNVTVATITVRHFVNQRADYKYQKLQNY

**Important features:****Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423**Casein kinase II phosphorylation site.**amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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**FIGURE 345**

TGGGGGCCCCCAGGCTCGCGCGTGGAGCGAAGCAGCATGGGCAGTCGGTGCGCGCTGGCCCTGGCGGTGCTCTC  
GGCCTTGCTGTGTCTAGGTCTGGAGCTCTGGGGTGTTCGAAGCTGAAGCTGCAGGAGTTCGTCAACAAGAAGGGGCT  
GCTGGGGAACCGCAATTGCTGCGCGGGGGCGCGGGGCCACCGCCGTGCGCCTGCCGGACCTTCTTCCGCGTGTG  
CCTCAAGCACTACCAGGCCAGCGTGTCCCCGAGCCGCCCTGCACCTACGGCAGCGCGCTCACCCCGTGTCTGGG  
CGTCGACTCCTTCAGTCTGCCCCGACGGCGGGGGCGCGGACTCCGCGTTACAGCAACCCCATCCGCTTCCCTTCGG  
CTTCACCTGGCCGGGCACCTTCTCTGATTATTGAAGCTCTCCACACAGATTCTCCTGATGACCTCGCAACAGA  
AAACCCAGAAAGACTCATCAGCCGCTGGCCACCCAGAGGCACCTGACGGTGGGCGAGGAGTGGTCCCAGGACCT  
GCACAGCAGCGGCCGACGGACCTCAAGTACTCCTACCGCTTCGTGTGTGACGAACACTACTACGGAGAGGGCTG  
CTCCGTTTTCTGCCGTCCCCGGGACGATGCCTTCGGCCACTTCACCTGTGGGGAGCGTGGGGAGAAAGTGTGCAA  
CCCTGGCTGGAAAGGGCCCTACTGCACAGAGCCGATCTGCCTGCCTGGATGTGATGAGCAGCATGGATTTTGTGA  
CAAACAGGGGAATGCAAGTGCAGAGTGGGCTGGCAGGGCCGGTACTGTGACGAGTGTATCCGCTATCCAGGCTG  
TCTCCATGGCACCTGCCAGCAGCCCTGGCAGTGAAGTGCAGGAAGGCTGGGGGGGCTTTTCTGCAACCAGGA  
CCTGAAGTACTGCACACACCATAAGCCCTGCAAGAATGGAGCCACCTGCACCAACACGGGCCAGGGGAGCTACAC  
TTGCTCTTGCCGGCCTGGGTACACAGGTGCCACCTGCGAGCTGGGGATTGACGAGTGTGACCCAGCCCTTGTAA  
GAACGGAGGGAGCTGCACGGATCTCGAGAACAGTACTCCTGTACCTGCCACCCGGCTTCTACGGCAAAATCTG  
TGAATTGAGTGCCATGACCTGTGCGGACGGCCCTTGCTTAAACGGGGGTGCGTGTCTAGACAGCCCCGATGGAGG  
GTACAGCTGCCGCTGCCCGTGGGCTACTCCGGCTTCAACTGTGAGAAGAAAATTGACTACTGCAGCTCTTCACC  
CTGTTCTAATGGTGCCAAAGTGTGTGGACCTCGGTGATGCCTACCTGTGCCGCTGCCAGGCCGGCTTCTCGGGGAG  
GCACTGTGACGACAACCTGGACGACTGCGCCTCCTCCCCGTGCGCCAACGGGGGCACCTGCCGGGATGGCGTGAA  
CGACTTCTCCTGCACCTGCCCGCTGGCTACACGGGCAGGAAGTGCAGTGGCCCCGTGACGAGGTGCGAGCACGC  
ACCCTGCCACAATGGGGCCACCTGCCACGAGAGGGGCCACCGCTATGTGTGCGAGTGTGCCGAGGCTACGGGG  
TCCCAACTGCCAGTTCCTGCTCCCCGAGCTGCCCCGGGGCCAGCGGTGGTGGACCTCACTGAGAAGTAGAGGG  
CCAGGGCGGGCCATCCCCCTGGGTGGCGGTGTGCGCGGGGTATCCTTGTCTCATGCTGCTGCTGGGCTGTGC  
CGCTGTGGTGGTCTGCGTCCGGCTGAGGCTGCAGAAGCACGGGCCCCAGCCGACCCCTGCCGGGGGAGACGGA  
GACCATGAACAACCTGGCCAACTGCCAGCGTGAGAAGGACATCTCAGTCAGCATCATCGGGGCCACGCAGATCAA  
GAACACCAACAAGAAGGCGGACTTCCACGGGGACCACAGCGCCGACAAGAATGGCTTCAAGGCCCCGCTACCCAGC  
GGTGGACTATAACCTCGTGCAGGACCTCAAGGGTGACGACACCGCCGTGAGGACGCGCACAGCAAGCGTGACAC  
CAAGTGCCAGCCCCAGGGCTCCTCAGGGGAGGAGAAGGGGACCCCGACCACACTCAGGGGTGGAGAAGCATCTGA  
AAGAAAAGGCCGACTCGGGCTGTTCAACTTCAAAAGACACCAAGTACCAGTCGGTGTACGTATATCCGAGGA  
GAAGGATGAGTGCGTCATAGCAACTGAGGTGTAAAATGGAAGTGAGATGGCAAGACTCCCGTTTCTCTTAAATA  
AGTAAATTTCAAGGATATATGCCCCAACGAATGTGCTGAAGAGGAGGGAGGCCCTCGTGGACTGCTGCTGAGAA  
ACCGAGTTCAGACCGAGCAGGTTCTCCTCCTGAGGTCTCGACGCCTGCCGACAGCCTGTGCGGGCCCCGGCCGCC  
TGCGGCACTGCCTTCGTTGACGTGCGCGTTGCACTATGGACAGTTGCTCTTAAGAGAATATATATTTAAATGGGT  
GAACTGAATTACGCATAAGAAGCATGCACTGCCTGAGTGTATATTTTGGATTCTTATGAGCCAGTCTTTTCTTGA  
ATTAGAAACACAACACTGCCTTTATTGTCCTTTTGTATACGAAGATGTGCTTTTCTAGATGGAAAAGATGTGT  
GTTATTTTTTGGATTTGTAAAAATATTTTTTCATGATATCTGTAAAGCTTGAGTATTTTGTGATGTTCTGTTTTTA  
TAATTTAAATTTTGGTAAATATGTACAAAGGCACTTCGGGTCTATGTGACTATATTTTTTGTATATAAATGTAT  
TTATGGAATATTGTGCAAATGTTATTTGAGTTTTTACTGTTTTGTTAATGAAGAAATTCCTTTTTAAATATTT  
TTCCAAAATAAATTTTATGAATGACAAAAA

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**FIGURE 346**

MGSRCALALAVLSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGAGPPPCACRTFFRVC  
LKHYQASVSPPEPPCTYGS AVTPVLGVDSFSLPDGGGADSAFSPNPIRFPFGFTWPGTFSLII EA  
LHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGR TDLKYSYRFVCDEHY YGEGCS  
VFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLP GCDEQHGFCDKPGECKCRVGWQGR  
YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHK PCKNGATCTNTGQGSYTCS  
CRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPG FYGKICELSAMTCADGPCFNG  
GRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCD  
DNVDDCASSPCANGGTCTRDGVNDFSTCTPPGYTG RNC SAPVSRCEHAPCHNGATCHERGHRYV  
CECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGQGGPFPWVAVCAGVILVLM LLLGCAAVVV  
CVRLRLQKHRPPADPCRGETETMNNLANCQREKDISVSI IGATQIKNTNKKADFHGDHSADKN  
GFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPQ GSSGEEKGTPTTLRGGEASERKRPD  
SGCSTSKDTKYQSVYVISEEKDECVIATEV

**Important features:****Signal sequence:**

Amino acids 1-21

**Transmembrane domain:**

Amino acids 546-566

**N-glycosylation site:**

Amino acids 477-481

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 660-664

**Tyrosine kinase phosphorylation sites:**

Amino acids 176-185;252-261

**N-myristoylation sites:**

Amino acids 2-8;37-43;40-46;98-104;99-105;262-268;281-287;  
282-288;301-307;310-316;328-334;340-344;378-384;387-393;512-518;  
676-682;683-689;695-701

**Aspartic acid and asparagine hydroxylation sites:**

Amino acids 343-355;420-432;458-470

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 552-563

**EGF-like domain cysteine pattern signature:**

Amino acids 243-255;274-286;314-326;352-364;391-403;429-441;  
467-479;505-517

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**FIGURE 347**

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTTCGGTCAACA  
TCGTAGTCCACCCCCTCCCCATCCCCAGCCCCCGGGATTTCAGGCTCGCCAGCGCCCAGCCAG  
GGAGCCGGCCGGGAAGCGCGATGGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGCTGT  
TCGCCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGGACAT  
CTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGCTCAAGTGCCAAGTGAAAGATCACGAGG  
ACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGAGAGCCC  
TTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGCATCAGCA  
ATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGTGCGAACTG  
CCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTTATAAATCTT  
CATTACGGGAAAAAGACACAGCCACCCTAACTGTCAGTCTTCTGGGAGCAAGCCTGCAGCCC  
GGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCATACAGGAAGATC  
CCAATGGTAAACCTTCACTGTGACGAGCTCGGTGACATTCCAGGTTACCCGGGAGGATGATG  
GGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGACAGATCCACCTCTC  
AACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCCTCCCCATCCTCGTG  
AGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCCCCCAGCAGTACCTAT  
GGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGTGCCCTGATCTTCCCTT  
TCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAGCAACATGGGCAGCTACA  
AGGCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCCTCCTCCTCCAGCACCTACC  
ACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTGCTCATCATGCTCATCTTCC  
TTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACATGAGGCAAAAGGCTCCGACG  
ATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCGGGCAGTCAGGAGGGGACGACA  
AGAAGGAATATTTTCATCTAGAGGCGCCTGCCCCACTTCTGCGCCCCCAGGGGCCCTGTGGGG  
ACTGCTGGGGCCGTCACCAACCCGGACTTGTACAGAGCAACCGCAGGGCCGCCCTCCCGCTT  
GCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGCTTTGGGTGCGGTTTTGTACTCGGT  
TTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGGTTGCCCTCAGCCCTTTCCTGCGCTT  
CTCTGCATTTGGGTATTATTATTTTTTGTAAACAATCCCAAATCAATCTGTCTCCAGGCTGGA  
GAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACAAACAAAAACA

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**FIGURE 348**

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQWS  
NPAQQTLYFGEKRALRDNRILVTSTPHELSSISISNVALADEGEYTCSIFTMPVRTAKSLTV  
LGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFT  
VSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQKLLL  
HCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLN  
VNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIIFLGHYLI RHKGTYLTAEAKGSDDAPDADT  
AIINAEGGQSGGDDKKEYFI

**Important features:****Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



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**FIGURE 349**

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAGGACAGCAGCAAAG  
AGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTACCATACGCCCTCAGGACGTTCCCTCTA  
GCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGTCATTTTGATTTTGCTGTTATTTTTTTTTTCTTTTTCTT  
TTTCCCACCACATTGTATTTTATTTCCGTACTTCAGAAATGGGCGCTACAGACCACAAAGTGGCCCAGCCATGGGG  
CTTTTTTCTGAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAACTCCTGGCCTGCCCTA  
GTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTGCCTCTTGGGATCCCGG  
AGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGCTGGATTTCTGCAGAACTGCACAATGTAC  
AGTCGGTGCACACGGTCTACCTGTATGGCAACCAACTGGACGAATTCCTCATGAACCTTCCCAAGAATGTCAGAG  
TTCTCCATTTGCAGGAAAAACAATATTCAGACCATTTTACGGGCTGCTCTTGGCCAGCTCTTGAAGCTTGAAGAGC  
TGCACCTGGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCCTCAAAT  
TGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGACTTGCAAGAGCTGAGAGTGG  
ATGAAAATCGAATTGCTGTCATATCCGACATGGCCTTCCAGAATCTCACGAGCTTGAGCGTCTTATTGTGGACG  
GGAACCTCCTGACCAACAAGGGTATCGCCGAGGGCACCTTACGCCATCTCACCAAGCTCAAGGAATTTTCAATTG  
TACGTAATTGCTGTCCACCCCTCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACC  
AGATAAACCACATTCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCAACAACCAAC  
TGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCAACCTGAAGCAGCTCACTGCTCGGAATAACCCCTGGT  
TTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAAATATATCCCTTCATCTCTCAACGTGCGGGGTTTCA  
TGTGCCAAGGTCTGAACAAGTCCGGGGGATGGCCGTAGGGAATTAATATGAATCTTTTGTCTGTCCACCA  
CGACCCCGGCTGCTCTCTTACCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCACCCCTCTCTA  
TTCAAACCCCTAGCAGAAGCTACACGCCTCCAACCTCTACCACATCGAACTTCCCACGATTCTGACTGGGATG  
GCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATCCATTTTGTGAATGATACTTCCATTC  
AAGTCAGCTGGCTCTCTCTTACCCGTGATGGCATACAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAG  
GGGGCATCGTTCAGGAGCGCATAGTCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCA  
CCTATCGGATTTGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTAGAGGCCA  
CCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGACGTCCCACAGCATGG  
GCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGCGCGGTGATATTTGTGCTGGTGGTCTTGCTCAGCGTCTTTT  
GCTGGCATATGCACAAAAGGGGCGCTACACCTCCAGAAGTGGAATACAACCGGGGCGGGCGGAAAGATGATT  
ATTGCGAGGCAGGCACCAAGAAGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAATCGTCTCCTTAA  
ATAACGATCACTCCTTAAAGGAGATTTAGACTGCAGCCCATTTACACCCCAAATGGGGGCATTAAATTACACAG  
ACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGCACTGCCATACGTGACAGC  
CAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAACACACTCGTGTGTGCACATAAAGACACGCAG  
ATTACATTTGATAAATGTTACACAGATGCATTTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAA  
TGGGATTTAAAAAAGTGCTATCTTTCTATTTCAAGTTAATTACAAACAGTTTGTAACTCTTTGCTTTTTTAA  
TCTT

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**FIGURE 350**

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIPE  
GVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFFPMNLPKNVRVLHLQENNIQTISR  
AALAQLLKLEELHLDNDSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELRVDE  
NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPDLPGT  
HLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNNPWFCD  
CSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELMNLLSCPTTTPGLPLFTPAPSTAS  
PTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVNDTSIQVSW  
LSLEFVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPLDAFNRYRAV  
EDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVLLSVFCWHMH  
KKGRTSQKWYNRGRKDDYCEAGTKKDNSILEMTETSFOIVSLNNDQLLKGD FRLQPIYTP  
NGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Important features:****Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

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**FIGURE 351**

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA  
TGAAAGGGCTTCGCCGCCGGGAGTAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCGACGCGACCGC  
GAGGGCGGGCGTGCAACCTCGGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGA  
GACCTAGGCCGCTGGACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTGGGGCTGCTGCTGTGC  
GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGGTGCGGGGAACTCGGGCAGCCCTCTGGGGTAGCCGCC  
GAGCGCCCATGCCCCACTACCTGCCGCTGCCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGTCTT  
CCCCAGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCC  
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA  
GTCTCGGCAAAATATTACACTTCTCTCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTTGAAGCTTTGGACCTTAGCAGCAACAATATTTAGAGCTCCAAACTGCATTTCCAGCCCTACAG  
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAAACACA  
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAAGATGTTTAAACTGCCCAACTGCAA  
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGCTCTGAAGTCT  
CTGAAAATGCAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAAATTTTG  
CAGCTGGACCATAAACCTTAACAGAGATTACCAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCAT  
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA  
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCCTGGCCTAAGCTTACTAAATACACTGCACATTGGG  
AACAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAAC  
AATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTC  
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT  
GACAACGCAATCATGTCTTTTACAAGGCAATGCATTTTACAAATGAAGAACTGCAACAATTGCATTTAAATACA  
TCAAGCCTTTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGGTGGCGGAAAAACAATTTTCAAGCTTTGTA  
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTTGCTGTTAGCCAGATGGCTTTGTGTGT  
GATGATTTTCCCAAACCCAGATCAGGTTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC  
ATCTGCTCAGCTGCCAGCAGCAGTATTCCCAATGACTTTTGCTTGGAAAAAGACAATGAACACTACTGCATGAT  
GCTGAAATGGAAATTTATGCACACCTCCGGGCCAAAGGTGGCGAGGTGATGGAGTATACCACCATCCTTCGGCTG  
CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCCAATCACTTTGGTTTATCCTACTCTGTCT  
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCATGGATCTCACCATCCGAGCTGGGGCC  
ATGGCACGCTTGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC  
TTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCGAGGATGACGTGTTCTTTATCGTGGATGTGAAGATA  
GAGGACATTTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTAGCAAAATGCAACTCTGACTGTC  
GTAGAAACACCATCATTTTTTGGGCCACTGTTGGACCGAAGCTGTAACCAAGGGAGAAACAGCCGCTCCTACAGTGC  
ATTGCTGGAGGAAGCCCTCCCCCTAACTGAAGTGGACCAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCAC  
TTTTTTGAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGATGCTGGGAAATACACATGTGAG  
ATGTCTAACCCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCT  
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGTGT  
GTGGTGGGCACGTCACTCGTGTGGGTGGTCTCATATACCACAAAGGCGAGGAATGAAGATTGCAGCATTTACC  
AACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCTCTCAGGGAACGTTAGCTGACAGGCAG  
GATGGGTACGTGCTTTCAGAAAGTGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCA  
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGAAGCTGCCACAGATCTGTTT  
CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGATTTGAAGGGAAATGTGTATGGCTCAGATCCTTTTGAAACA  
TATCATACAGGTTGAGTCCCTGACCAAGACAGTTTAAATGGACCACTATGAGCCAGTTACATAAAGAAAAAG  
GAGTGTACCCATGTTCTCATCCTTCAGAAGAATCTTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT  
GTGAGGAAGCTACTTAACTACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC  
TCTTTAGATTTTAGTGAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTCATGGGTACCTTTTGAAAA  
GCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTGAGCCAAGAGCCTTTTAT  
TTGAAAGCTCATTTCTTCCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAA  
GAAATACATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTTCAGTCTTATGACTTGGAC  
ACATAGACTGAAATGAGACCAAGGAAAGCTTAACATACTACCTCAAGTGAAGTAACTTTTATTTAAAGAGAGAGAAT  
CTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTATACAGATGAACCAAAATTAC  
AAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTAAACTATTTTTTAACCTTG  
TTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTTATAATGCCAGA  
TTTCTTTTTATGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGATACCATTTTTTAAATAGAAGTT  
ACTTCATTATATTTTGCACATTATATTTAATAAATGTGTCAATTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 352**

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCCLGDLLDCSRKRLARLPEPLPSW  
VARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANITLLSLAGNRIVEILPEHLKEFQSLETL  
DLSSNNISELQTAFFPALQKLYLYLNSNRVTSMEPGYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLELNRN  
KIKNVDGLTFQGLGALKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNLTETITKGWLYGLLMLQELHLSQNAIN  
RISPDWFEFCQKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNNEISWTI  
EDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSOMKKLQQLHLNTSSLLCDC  
QLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASS  
SDSPMTFAWKKNELLHDAEMENY AHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFSSYSVKAKLTVN  
MLPSFTKTPMDLTIRAGAMARLECAAVGHAPQIAWQKDGDTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS  
CTAQN SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNWTKDDSPLVVTERHFFAAGNQ  
LLIIIVSDSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDGWATVGVVIIAVVCCVVGTSLV  
WVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGT LADRQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGT  
CHIDNSSEADVEAATDLFLCPFLGSTGPMYLGKNVYGSDFETYHTGCS PDRTVLM DHYEPSYIKKKECYPCSH  
PSEESCERSFNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHL  
DAYSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEEHNICTFKQTL ENYRTPNFQSYDLDT

**Important features:****Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939**Leucine zipper pattern.**

amino acids 58-80, 65-87

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**FIGURE 353**

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCTTTTCTTCTCCTTTCTGGCTTCGGACATTGG  
AGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTGTTACTTTGTGATGAGATCGGGGATGA  
ATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTTGCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTAC  
AGGGGACGTTTGCAAAGAGAAGATCTGTTCCCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAA  
GGGCTTCACAAGTCTGCAGCGTTTCACTGCCCCGACTTCCCAGTTTACCATTATTTCTGCATGGCAATTCCCT  
CACTCGACTTTTCCCTAATGAGTTCGCTAATCTTTATAATGCGGTTAGTTTGCACATGGAAAACAATGGCTTGCA  
TGAAATCGTTCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGGCTGCACATCAACAACAACAAGATCAAGTC  
TTTTCGAAAGCAGACTTTTCTGGGGCTGGACGATCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATAT  
AGACCCGGGGGCTTCCAGGACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTTACC  
TGCCAACGTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCCCTATGA  
GGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCCTGGGACTGCACCTGTGATCT  
GCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCCCTGATCGGCCGAGTGGTCTGCGAAGCCCCCAC  
CAGACTGCAGGGTAAAGACCTCAATGAAACCACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAG  
TCTCCCGGCGCCCCCTGCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCA  
AGAGGATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGATCAAAATCAG  
ACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCTTAGCTAACAGTTTACCCTGCCCTGGGGGCTG  
CAGCTGCGACCACATCCCAGGGTGGGTTTAAAGATGAACTGCAACAACAGGAACGTGAGCAGCTTGGCTGATTT  
GAAGCCCCAAGCTCTCTAACGTGCAGGAGCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTT  
TGTGGATTACAAGAACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAA  
GAACCTTTTGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGAGAAATTCGCGGG  
GCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCATCCTCCCGGGCATTTCATGCCAT  
GCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTGCTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGGTCTC  
GCTCTCTAAACTCAGCCTGCACAACAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTC  
CATCATCCAGATAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCAGA  
ACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGTGAACCTCTTTAGAAAGGATTTTCAT  
GCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCTCGCCACGTTAACTTCGCACAGTAAAAA  
CAGCACTGGGTTGGCGGAGACCGGGACGCACTCCAACCTCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTT  
GGTCCCGGGACTGCTGCTGGTGTGTTGTACCTCCGCCTTCACCGTGGTGGGCATGCTCGTGTGTTATCCTGAGGAA  
CCGAAAGCGGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCTACAGACAGTCTGTGACTC  
TTCCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCCACAGAGTGTATGACTGTGGCTCTCACTCGCTCTC  
AGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCGATACATCCTTCCCCACCGCAGGCACCCGGG  
GGCTGGAGGGGCGTGATCCCAAATCCCCGCGCCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTC  
GCACAACCGAAAGGGCCTGACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGA  
GCGCAGCCAGCTCGCTCTTTGCTGAGAGCCCCTTTTGACAGAAAGCCAGCAGACCCTGCTGGAAGAACTGACA  
GTGCCCTCGCCCTCGGCCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATACATATATACATATATCCACATC  
TATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAGCCCCGTGATGGCTCCCTGTTGGCTACGCAGGGAT  
GGGCAGTTGCACGAAGGCATGAATGTATTGTAAATAAGTAACCTTGACTTCTGAC

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**FIGURE 354**

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYHL  
FLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKKIKSFRKQTF  
LGLDDLEYLQADFNLLRDIDPGAFAQDLNKLEVLILNDNLISTLPANVFQYVPITHLDLRGNRL  
KTLPYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQGKDL  
NETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTKIPGNW  
QIKIRPTAAIATGSSRNKPLANSRPCPGGCSCDHIPGSGLKMNCNNRNVSSLADLKPKLSNVQ  
ELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNYLDTLSRE  
KFAGLQNLLEYLNVEYNAIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSLSKLSLHNN  
YFMYLPVAGVLDQLTSIIQIDLHGNPWECSTIVPFKQWAERLGSEVLMSDLKCETPVNFFRK  
DFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVLVPGLLLVFVT  
SAFTVVGMLVFILNRKRKRSDANSSASEINSLQTVCDSSYWHNGPYNADGAHRVYDCGSHS  
LSD

**Important features:****Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697**N-myristoylation site.**amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

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**FIGURE 355**

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTGACCCAGAATAACTCAGGGCTGCACCGGGCCTG  
GCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAAACTGTTGGCCGCTGGGCCCCGGGGGGATTCTTGG  
CAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGGAAGGGAGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAG  
GGCGGTGACCGCGCTCCAGACACAGCTCTGCGTCCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGC  
GGGGCCTCAGAGAAATGAGGCCGGCGTTGCGCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCGGGCGGCGG  
CGAACACCCCACTGCCGACCGTGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTGCACCACGCTACCATGAA  
GCGGCAGGCGGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTCAGCACCGTGCCTGCGGGCGCGGAGCTGCG  
CGCTGTGCTCGCGCTCCTGCGGGCAGGCCAGGGCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACT  
GGAGCGCAGGCGTTCCCACTGCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGG  
CGGTCTCGAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGCGGTACT  
CCAGGCCACCGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGCGCGCCAACGGCTACCTGTG  
CAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGGGCCGCTCTAACTTGAGCTATCGCGCGCCCTT  
CCAGCTGCACAGCGCCGCTCTGGACTTCAGTCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGGACAGCTCCC  
GATCTCAGTTACTTGCATCGCGGACGAAATCGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTG  
CCCCGGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGGCTTTGCCTG  
CGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCAGTGGGGAAGGACAGCCGACCCT  
TGGGGGGACCGGGTGCCCAACAGGCGCCCGCGGCCACTGCAACCAGCCCCGTGCCGCAGAGAACATGGCCAAT  
CAGGGTCGACGAGAAGCTGGGAGAGACACCACTTGTCCCTGAACAAGACAATTAGTAACATCTATTCTGAGAT  
TCCTCGATGGGGATCACAGAGCACGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCAC  
CCCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCTCTGCCACTCCTCAGGCTTTCGACTCCTCCTC  
TGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCTTGACCATGACAGTACTGGGGCTTGT  
CAAGCTCTGCTTTCACGAAAGCCCCCTCTTCCAGCCAAGGAAGGAGTCTATGGGCCCCGGGGCCTGGAGAGTGA  
TCCTGAGCCCGCTGCTTTGGGCTCCAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCT  
GCGGGACAGAGCAGAGGGTGCCTTGCTGGCGGAGTCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGACA  
TGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTACTTGTGTAACGACAA  
TTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAGGAGCTAAATCAGAACTGCACACTCCTTC  
CCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGATGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATT  
TTCTTATGTTTATTCGGAGAATTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATAT  
AATTTACATTAAAAATAATTTCTACCAAATGGAAGGAAATGTTCTATGTTGTTTCAGGCTAGGAGTATATTGG  
TTCGAAATCCCAGGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

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**FIGURE 356**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAEEEACILRGGALST  
VRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLESD  
TLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPPAPRPGAASN  
LSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPGRYLR  
AGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATATSPVP  
QRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITPSGSVIS  
KFNSTTSSATPQAFDSSSAVVVFIFVSTAVVVVLVILTMTVLGLVKLCFHESPSSQPRKESMGPP  
GLES DPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

**Important features:****Signal sequence:**

amino acids 1-16.

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274



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**FIGURE 357**

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGGGAAGA  
AGACTAAAAATGCTGTTTCCAATGTGGACACTGAAGAGACAAATTTCTATCCTTTTAAACATAATCCTAATTTCC  
AAACTCCTTGGGGCTAGATGGTTTCCCTAAAACTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG  
ATCGTGGACTGCACAGACAAGCATTGACAGAAATTECTGGAGGTATTTCCACGAACACCACGAACCTCACCCCTC  
ACCATTAACCACATACCAGACATCTCCCCAGCGTCCTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCAGA  
TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC  
TTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAACCCAGCTACTAGAGATACCGCAGGGCCTCCCG  
CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC  
AACATAGAAAATACTCTACCTGGGCCAAAACCTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAA  
GATGCCTTCCCTAAACTTGACAAAGTTAAAGTGCTCTCCCTGAAAGATAACAATGTCACAGCCGTCCCTACTGTT  
TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAATAAC  
CTCAACCAATTACAAATTTCTTGACCTAAGTGGAAATTGCCCTCGTTGTTATAATGCCCCATTTCCCTGTGCGCCG  
TGTAATAATAATTTCTCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAATTAAAGTTTACGTCTA  
CACAGTAACCTCTCTCAGCATGTGCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACCTGGATCTGTCC  
CAAACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCCAATTGGATCTG  
TCTTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG  
AAAATTTGCGGATCAGAGGATATGTCTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA  
AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAAATGCTAACCTCAGCATGTTTAAACAATTTAAAGA  
CTGAAAGTCATAGATCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAT  
GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCTTGAACAATTACATTATTTTCAGATATGATAAGTATGCA  
AGGAGTTGCAGATTCAAAAACAAGAGGCTTCTTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC  
TTGGATCTAAGTAAAAATAGTATATTTTTGTCAAGTCCTCTGATTTTCAGCATCTTTCTTCCCTCAAATGCCTG  
AATCTGTGAGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATCCAACCTTTAGCAGAGCTGAGATATTTG  
GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAGAGCTTCACAACTGGAAGTTCTGGAT  
ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAACTTTACCAAGAACCTAAAGGTT  
CTGCAGAACTGATGATGAACGACAATGACATCTCTTCCCTCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA  
ACTCTGGAAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG  
AATCTGCTAAATTAGAGGAATTAGACATCTCTAAAAATTCCTAAGTTTCTTGCTTCTGGAGTTTTTGATGGT  
ATGCCTCCAAATCTAAAGAATCTCTTTGGCCAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT  
CTAAGAACCTGGAAACTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAGAGATTATCCAACCTGTTCC  
AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTCTACAAGATGCCTTC  
CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCAGAAAATGTCTC  
AACAACTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG  
GTTAACCATACGGAGGTGACTATTCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC  
CAAAGTGTGATCTCCCTGGATCTGTACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA  
TCTGTATCTCTCTTTCTCATGGTGTGATGACAGCAAGTCACCTCTATTTCTGGGATGTGTGGTATATTTACCAT  
TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT  
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAAGAGAGAAA  
CATTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTTCCAGAGCATA  
CAGCTTAGCAAAAAGACAGTGTGTGTGATGACAGACAAGTATGCAAGACTGAAAATTTTAAGATAGCATTTTAC  
TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAG  
TCCAAGTTCTCCAGCTCCGGAAAAGGCTCTGTGGGAGTTCTGTCTTGTGAGTGGCCAAACAAACCCGCAAGCTCAC  
CCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA  
ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

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**FIGURE 358**

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGGI  
PTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFSGI  
TYLKSLEYLDGNQLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYYRNP  
YVYSIEKDAFLNLTKLVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNLNQLQ  
ILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWFKNINK  
LQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSLKILRIR  
GYVFKELKSFNLSPLHNLQNLEVLDTGNTFIKIANLSMFKQFKRLKVIDLSVNKISPSGDSSE  
VGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTLDSLKNS  
IFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLHSTAFEELHK  
LEVLDISSNSHYFQSEGITHMLNFTKNLKVLOKLMMNDNDISSSTSRTMESESLRTLEFRGNH  
LDVLWREGDNRYLQLFKNLLKLEELDISKNLSLPSGVFDGMPPNLKNLSLAKNGLKSFSWK  
KLQCLKNLETLDLSHNQLTTVPERLSNCSRLKNLILKNNQIRSLTKYFLQDAFQLRYLDLSS  
NKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWWVNHTVTPYLATDVTCVGPGA  
HKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVWYIYHFCKAKIKGYQ  
RLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCEERDWLPGQPVLENLSQ  
SIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIIILIFLEKPFQKSKFLQLRKRLC  
GSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

**Important features:****Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 840-860

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**FIGURE 359**

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTAC  
TGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGTGG  
AGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGAGAT  
GGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCACAACA  
AGGAGCGCGGGCGCCGCGGAGAACTCTGTTGCCATCACAGACGAGGGCATGGACGTGCCGC  
TGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCTGCAGCC  
CAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATCGGCTGTG  
GTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACTGGTGTGCA  
ACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTCCGTGCTCCC  
AATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGCCCGGAAGATG  
CTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGAAGCATCAGACT  
CTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCTTGGTAACAGAGG  
TCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCCCCAACTTCCTTAG  
CAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAACAACCTGAGGTCCCTT  
CCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTACCTTCCCCAAATCGA  
CCCATGTTCCCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACAAAAGTGCCCTCTAGGA  
GCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAGGGAACTCCTACCCCATG  
CCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTGAGGTCTTGGCCTCAGTTT  
TTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGACCACACGGGGCACACCTCCT  
CCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAATGCCACGGGTGGGCGTGCCC  
TGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACAAGCCTAGCGTTGTGTCAGGGC  
TGAACCTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGACTACTGCTCCTGCCTCCTCTGG  
TGTTGGCTGGAATCTTCTTGAATGGGATACCACTCAAAGGGTGAAGAGGTCAGCTGTCCTCCTG  
TCATCTTCCCCACCCTGTCCCCAGCCCCTAAACAAGATACTTCTTGGTTAAGGCCCTCCGGAA  
GGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCCATCCTGGAGGCACAAGGCCTGGCTG  
GCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACCGGGCCCACACCTCTCCTGCCCCTCCC  
TCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCTCACTGCCTACCTGGCCTGGGGCTGTCT  
GCCACACAGCATGTGCGCTCTCCCTGAGTGCCTGTGTAGCTGGGGATGGGGATTCTTAGGGG  
CAGATGAAGGACAAGCCCCACTGGAGTGGGGTTCTTTGAGTGGGGGAGGCAGGGACGAGGGAA  
GGAAAGTAACTCCTGACTCTCCAATAAAAACCTGTCCAACCTGTGAAA

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**FIGURE 360**

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEEL  
AAFAKAYARQCWVGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMC  
GHYTQVVWAKTERIGCGSHFCEKLQGVETNIELLVLCNYEPPGNVKGKRPYQEGTPCSQCPSG  
YHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRAEASDSRKMGTTPSSLATGIPAFLVTEVSGSL  
ATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKSTHVPI  
PKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLASVFPAQD  
KPGELQATLDHTGHTSSKSLPNFPNTSATA<sup>^</sup>NATGGRALALQSSLPGAEGPDKPSVVSGLNSGP  
GHVWGPLLGLLLLPLVLGIF

**Important features:****Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

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**FIGURE 361**

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTGG  
GGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAACT  
GGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACTGCG  
AGAGGACCCCGGCGTCCGGGGCTCCCGGTGCCAGCGCT**ATG**AGGCCACTCCTCGTCTGCTGCT  
CCTGGGCCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGCCCGGG  
GCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGGCCGCGATGG  
CCGCGACGGCCGCGACGGCGCGCCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGAGGCCGGG  
ACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGGCCCCACCGG  
GCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCCG  
GGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGGACA  
TTACGACGCCGTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCA  
TGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTC  
TTTCTTCCAGTTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCATGGTGAG  
GCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGC  
CAGCATCAAGACAGACAGCACCTTCTCCGGATTCTGGTGTACTCCGACTGGCACAGCTCCCC  
AGTCTTTGCT**TAG**TGCCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGA  
GGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCTGGAATATTGTGAATGACTAGGGAGG  
TGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCA  
GGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTGG  
CAAGTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTCTTCCTGGTC  
CTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGGGCCGGCCCTTTTCTCAGAGAT  
CACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 362**

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPG  
EKGEGRPGPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFD  
RVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFQFFGGWPKPA  
SLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

**Important features:****Signal sequence.**

amino acids 1-15

**N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

**Cell attachment sequence.**

amino acids 77-80

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**FIGURE 363**

[illegible]

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**FIGURE 364**

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGRE  
VAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDTYD  
TDRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATREELT  
AFLHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPWVQTERQQFRDF  
RDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFVGSQAT  
NYGEDLTRHHDEL

**Important features:****Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330



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**FIGURE 365**

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAAG  
GCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGGCA  
TTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCTGTG  
AAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCAAGGA  
GACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGGTGACC  
TTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATACACTTGT  
ATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGTGCTTGTG  
CCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTTGGGAACCGGGCAGTGCTG  
ACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTG  
ATGCCTACGAATCCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACA  
ACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCA  
CGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAAT  
GTGGGGGTTCATCGTGGCAGCCGTCTTGTAACCCTGATTCTCCTGGGAATCTTGGTTTTTGGC  
ATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGACTTCGAGTAAGAAG  
GTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCTG  
GTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACTCAGGTGCTACCGGACT  
CTGGCCCCCTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTCTACACCCCACAGGGCCC  
CCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCATCCTCCTTCATGCCCTC  
CCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAACCTGTTTTAAAGTGTTTATTCCCCATTTCT  
TTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCTTCTAAGTAGACAGCAAAAA  
TGGCGGGGGTTCGAGGAATCTGCACTCAACTGCCCACCTGGCTGGCAGGGATCTTTGAATAGG  
TATCTTGAGCTTGTTTCTGGGCTCTTTCCTTGTGTACTGACGACCAGGGCCAGCTGTTCTAGA  
GCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGGTGATGACACTGGGGTCCTTCCAT  
CTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTGCCACTGGGATCCCTCTGCCCTGTC  
CTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGTGGAAAATGGGAGCTCTTGTGTGGA  
GAGCATAGTAAATTTTTCAGAGAACTTGAAGCCAAAAGGATTTAAAACCGCTGCTCTAAAGAAA  
AGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTGTAATCCCAGAGGCTGAGGCAGGCGGAT  
CACCTGAGGTCTGGGAGTTCTGGGATCAGCCTGACCAACATGGAGAAACCCTACTGGAAATACAA  
AGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTCCCAGCTGCTCAGGAGCCTGGCAACAAGAG  
CAAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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**FIGURE 366**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRI PENNPVKLS CAYSGFSSPRVEWK  
FDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYTCMVSEEGNSYGEVKVKL  
IVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSEYTWFKDGIVMPTNPKSTRAFSNSSYV  
LNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLLILGI  
LVFGIWFAYS SRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Important features:****Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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**FIGURE 367**

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG  
AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTTAGACCCGCGGGGGTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCCTCC  
CCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCACAAAGAAAAAGTATGTTCATTTTCTC  
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT  
GGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA  
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTCTTCATCAACCTCCTTTTTTTAAAT  
TTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCACCTGGATTTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAAACAGGGCCCTATTTGACCCCTGCTTGTGGTGCT  
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGC GGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA  
CCAGTTCAGCAAGGTGATTTGTGTTTCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT  
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACCTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA  
ACTCTTTGACAATCGTCTTACTACCATCCGAATGGAGCTTTTGTATACTTGTCTAACTGAAGGAGCTCTGGTT  
GCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTTGCGCCGACTAGACTTAGG  
GGAATTGAAAAGACTTTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTGAGGTATTTGAACCTTGC  
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTTCTGGGAATCA  
TTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTTGATGCACCTTCAAAAACTGTGGATGATACAGTCCCAGAT  
TCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACATTTACATCACAACCTTGGAACCTG  
TAACCTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCGGTG  
TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCACATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGCGGGCCTCCACATC  
CCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGT  
GCTCAGTGATGGTACGTTAAATTTACAAATGTAACCTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA  
TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTTACTTTTC  
AACCCTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCCTCC  
AGTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTT  
CACCATCCCAGTGACTGATATAAACAGTGGGATCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT  
TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGCACCA  
TCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC  
CATGGAAGCCACCTGCCCATGCCTGCTATCGAGCATGAGCCTAAATCACTATAACTCATACAAATCTCCCTT  
CAACCACACAACAACAGTTAACACAATAAATTCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAAACAATCAAAAAAAA  
GACAGTTTATTAATAATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAA  
AAAAGAAAAGAAATTTATTTATTAATAATCTATTGTGATCTAAAGCAGACAAAA

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**FIGURE 368**

MLNKMTLHPQQIMIGPRFNALFDPLLVLALQLLVVAGLVRAQTCPSVCSCSNQFSKVICVRKNLREVPDGIS  
TNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKL  
KELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYNLAMCNLREIPNLTPLIKLDELD  
LSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHH  
NPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKC  
RASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTNLFTNVTQDTGMYTCMVSNVSGNTTASATLNVTAATTP  
FSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNTVTSLTPOSTRSTEKFTTIPVTDINSGIPGIDEVMKT  
TKIIIGCFVAITLMAAVMLVIFYKMRKQHRQNHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYS  
YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

**Important features:****Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438, 442-446,  
488-492, 606-610**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243, 391-397,  
422-428, 433-439, 531-537

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**FIGURE 369**

CAAACTTTCGCTCGCGGAGAGCGCCAGCTTGAATGGAAGGAGCCCCAGCCCGCGGAGCGCAGCTGAGAC  
TGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC  
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCCCTATCCCTCCTTTATATA  
GAAACCTTCCACACTGGGAAGGCAGCGGCGAGGCAGGAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAG  
GCGCACAGCATTCCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT  
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCCAGAGCCGGGTGCTGC  
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCCAGGATTGGCCGAA  
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGTGCTGGTACTGAGCCCTGAGG  
AGCCCGGGCCTGGCCAGCCGCGGTGAGCTGCCCCGAGACTGTGCCTGTTCCAGGAGGGCGCTGCTGGACTGTG  
GCGGTATTGACCTGCGTGAGTTCCCGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACCAACCAGC  
TGGAAGATCTACCTGAGGAGCTCTCCCGGTGCACCGGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA  
CTTCCCGAGGGCTCCAGAGAAGGCGTTTGAAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAGATCT  
ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACTGTCACAACAACAAGCTGGCAGACGCCGGC  
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCCTGTCCAGCAACTTCTGCGCCACGTGC  
CCAAGCACCTGCCGCCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT  
TCAGCGAGCTGAGCAGCTGCGCGAGCTATACCTGCAGAACAACCTACCTGACTGACGAGGGCCTGGACAACGAGA  
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGC  
CGCGCAGCCTGGTGTGCTGCACTTGAGAGAAGACGCCATCCGGAGCGTGGACGGAATGTGCTGACCCCATCC  
GCAGCCTGGAGTACCTGTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCACTGGCCTTCCAGGGCC  
TCAAGCGGTTGCACACGGTGCACCTGTACAACAACCGCTGGAGCGCGTGGCCAGTGGCCTGCCTGCGCGCTGC  
GCACCTCATGATCCTGCACAACCAGATCACAGGCATTGGCCGCGAAGACTTTGCCACCACCTACTTCTGGAGG  
AGCTCAACCTCAGCTACAACCGCATCACCAGCCCAAGGTGCACCGCGACGCTTCCGCAAGCTGCGCCTGCTGC  
GCTCGCTGGACCTGTCCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCTTGGCAGGAGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA  
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCGCTGCTGGGTGGACCTCGCCCATCTGCAGCTGCTGGACA  
TCGCGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACACA  
AGATTAGTGGGTGCCCGCAATGCCTTTCGACTCCACGCCCCAACCTCAAGGGGATCTTCTCAGGTTTAAACAAGC  
TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCACT  
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG  
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTCTTTTCTGC  
AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA  
TCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCACGGCGTGTCCACGGCCAGACACATGC  
ACACACATCACACCCTCAAACACCCAGCTCAGCCACACACAACCTACCCTCCAAACCACACAGTCTCTGTACAC  
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCTGCCCTGGCACACACAGGCACCCA  
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACACACACACATGCACAAGTATGTGCGAA  
CAGCCCTCCAAAGCCTATGCCACAGACAGCTCTTCCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT  
GTCCATCTGTCCGTCCGTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCCTCT  
GGAACCTACAAAAGCTGGCTTTTATTCTTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC  
TGGCCACCCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACTTTTCCAATGGGCAAGCCAGTGGAGGCAGGATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT  
GTTCTTCAGGCTGTGGGGGAAGTTCGGGTGCCTTTATTTTATTCTTTTCTAAGGAAAAAATGATAAAAT  
CTCAAAGCTGATTTTCTTGTATAGAAAACTAATATAAAGCATTATCCCTATCCCTGCAAAAAA

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**FIGURE 370**

MEGEEAEQPAWFHQWPWPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRSG  
GHSLSPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLPEH  
TNHLSLQNNQLEKIYPEELSRLHRLETLNLQNNRLTSRGLPEKA FEHLTNLNYLYLANNKLT  
APRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNVEVLI  
LSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTD EGLDNETFWK  
LSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSV DANVLTPIRSLEYLLLHSNQLREQG  
IHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTL MILHNQITGIGREDFATTYFLEELNLS  
YNRITSPQVHRDAFRKLRLRLSLDL SGNRLHTLPPGLPRNVHVLKVKRNELAALARGALAGMA  
QLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYLQNNKISAVP  
ANAFDSTPNLKGIFLRFNKLAVGSVVD SAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKEE  
EEEEEEEEEEETR

**Important features:****Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554**Leucine zipper pattern.**amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

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**FIGURE 371**

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGACCTCGGAGACCGCG  
CCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTACCGCCCCCACCCTCCTTCTTGAC  
TGCCGTCTCCGGAAGACCTTTTCCCCTGCTGTGTTTCTTACCGAGTCTGTGCATCGCCCCGGACCTGGCCGG  
GAGGAGGCTTGGCCGGCGGGAGATGCTCTAGGGGCGGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCCGGCAG  
GAAGATGGGCTCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCTTTGCCTCTGGCCTGGTCCT  
GAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGCCGTGCGCTCCGGACCA  
TGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAGGACCAGGGGCTCCCTGCTTCCCGGTGCTT  
GCGTGTGTGACCCCGGTACCTCCATGTACCCGGCGACCGCCGTGCCCGAGATCAACATCACTATCTTGAAAGG  
GGAGAAGGGTGACCGCGGAGATCGAGGCCTCCAAGGGGAAATATGGCAAACAGGCTCAGCAGGGGCCAGGGGCCA  
CACTGGACCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGCTTTTC  
GGTGGGCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCGACACGGAGTTCGTGAACCT  
CTACGACCACTTCAACATGTTTACCGGCAAGTTCTACTGCTACGTGCCCGGCCCTCTACTTCTTACGCTCAACGT  
GCACACCTGGAACCAGAAGGAGACCTACCTGCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTGCGCA  
GGTGGGCGACCGCAGCATCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACG  
CCTCTACAAGGGCGAAGCTGAGAAGGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCACTGGCTACCT  
GGTCAAGCACGCCACCGAGCCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCCACCTTCCACCCCTGCGCTGTGC  
TGACCCACCGCCTCTTCCCCGATCCCTGGACTCCGACTCCCTGGCTTTGGCATTCACTGAGACGCCCTGCACAC  
ACAGAAAGCCAAAGCGATCGGTGCTCCAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAG  
GGCGGGGCACCCGCGAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGG  
CGAGACGCGGTGGCGGCAGGGCGTCCCAGGGTGCGGCACCGCGGCTCCAGTCTTGGAAATAATTAGGCAAATT  
CTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGGTGTATTTTTGTCTTTCCAGCCAG  
CCTGCTGGCTCCCAAGAGAGAGGCCTTTTCACTTGAGACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGG  
GTCAGGGGAGGGGCCGGGGGCGAGGAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACCTTTCTGAGGG  
ATAGGTGGACCTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTCTGAGTCACAGCTGCGAGGTGA  
TGGGGGCTGGGGCCCCAGGGCTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGCTCCAGGTTGGTAGAA  
GCAGCCGAAGGGCTCCTGACAGTGGCCAGGACCCCTGGGTCCCCCAGGCCTGCAGATGTTTCTATGAGGGGCAG  
AGCTCCTTGGTACATCCATGTGTGGCTCTGCTCCACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATG  
CCTGCCACCTGGCATCGGCTTTTCTGTGCCCTCCCACACAAATCAGCCCCAGAAGGCCCCGGGGCCTTGGCTT  
CTGTTTTTTATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTTCCACG  
TGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCTCATCCAGGCCTCTGACCA  
GTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAGCTGGAAGGGGCTAGAAAGCTCCCGCTTGTCT  
GTTTCTCAGGCTCCTGTGAGCCTCAGTCTGAGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTCA  
GGATTCACTCTCAGGAGCTGGGTGGCAGGAGAGGCAATAGCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGG  
TTGCGGTGTCTCCAGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCCATAGCCCC  
TCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCCCCCAAACCCCCGCTGCCTCTC  
TTCCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGCTTCCCTCTCTGGGCTGGCTGCCGGGATCTGGGG  
TCCCTAAGTCCCTCTCTTTAAGAAGTCTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAG  
CAGAGCGCCACACTCGCTGCTTAAGCTCCCCAGCTCTTTCCAGAAAACATTAACTCAGAATTGTGTTTTCAA

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**FIGURE 372**

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRPS  
QDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGHTG  
PKGQKGSMSGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFYCYV  
PGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWVRLYK  
GERENAIFSEELDTYITFSGYLVKHATEP

**Important features:****Signal sequence.**

amino acids 1-25

**N-glycosylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

**Amidation site.**

amino acids 150-154

**Cell attachment sequence.**

amino acids 104-107



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**FIGURE 373**

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCCG  
TTCTAGACGCGGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGGA  
GCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAATAGAATGC  
ACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTTCAGAGG  
ATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACCCCAAAG  
ATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACTGTGACAAAGCAGAGTTCT  
TCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATGTGGTTAA  
TGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTGGTTCTTCC  
TTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAAAAAAGGATC  
CATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATATGTGGGTATGG  
AAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCTCAATATCCCAG  
AAAAGTGTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAACAGCTAGCAGTTT  
GCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGAAAAGATGTATTTA  
ATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCCCAACCAGGTAGTAG  
AAGGCTGTTGTTTCAGATATGGCTGTTACTTTTAATGGACTGACTCCAAATCAGATGCATGTGA  
TGATGTATGGGGTATACCGCCTTAGGGCATTGTTGGGCATATTTTCAATGATGCATTGGTTTTCT  
TACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCGTGAATATGATCTTTGTA  
TAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATACATATCCAATACAGCTGTATGTTTCTT  
TTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAGTCAGTAGTACATTTTAAA  
TGAGGGTGGTTTTTTTCTTTAAACACATGAACATTGTAAATGTGTTGGAAAAGTGTTTTA  
AGAATAATAATTTTGAAATAAACTATTAATAAATATTATATGTGATAAATTCTAAATTATGA  
ACATTAGAAATCTGTGGGGCACATATTTTGTGATTGGTTAAAAAATTTTAACAGGTCTTTA  
GCGTTCTAAGATATGCAATGATATCTCTAGTTGTGAATTTGTGATTAAAGTAAACTTTTAG  
CTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCTAAGCCTCCCCAAGTTCCAATGGAT  
TTGCCTTCTCAAAATGTACAATAAGCAACTAAAGAAAATTAAAGTGAAAGTTGAAAAAT

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**FIGURE 374**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERMELSKSFRVYCIILV  
KPKDVSLWAAVKETWTKHCDKAEFFSSSENVKVFESINMDTNDMWLMMRKAYKYAFDKYRDQYNWFFLARPTTFAI  
IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAV  
CLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFG  
HIFNDALVFLPPNGSDND

**Important features:****Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389, 399-403,  
409-413, 473-477, 729-733, 748-752**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550, 558-564,  
651-657, 657-663, 672-672**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

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**FIGURE 375**

GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACACAAT  
CTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGAAA  
AAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGG  
GCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAA  
AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAA  
CCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTG  
GTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCA  
GAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA  
GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATTTCTTCAGATAT  
CTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTAC  
GGTTACTTGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA  
AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGC  
CGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATACATTTCAGAAGCCAA  
GGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTC  
AGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGT  
GGAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAA  
CTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCC  
AGGCGCCGTCAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGGCTGCGTCTGGCTGCTGCC  
TCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAG  
GCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA  
TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAA  
GAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGACAGATATTTAGG  
TACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCACTGCA  
AGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCACAGA  
GTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAA  
CAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACG  
GCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAA

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**FIGURE 376**

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMD NVTVRQGESATLRCTIDNRV  
TRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPKTS  
RVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQ  
GITREQSGDYEC SASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGT LQCEASAVPSAE  
FQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGN YTCVASNKLGHTNASIMLFGPGA  
VSEVSNGTSRRAGCVWLLPLLVLHLLLKF

**Important features:****Signal peptide:**

amino acids 1-28

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**FIGURE 377**

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCTTTAGATTGTGAA  
**ATG**TGGCTCAAGGTCTTCACAACTTTCCTTTTCCTTTGCAACAGGTGCTTGCTCGGGGCTGAAG  
GTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTCCAC  
TATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCCACACA  
ATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTGACTTGGAATACCAACAC  
AAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTTGATGAA  
GGCAATTACATCGTGAAGGTCAACATTCAGGGAAAATGGAACCTCTATCTGCCAGTCAGAAGATA  
CAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTCATCCTCCCTCTGGGGCT  
GTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGGCTAGCTTAC  
CAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTCTCCCCAAAC  
AATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCTGCCTGGTGAGG  
AACCCTGTGAGTGAATGGAAGTGATATCATTATGCCCATCATATATTATGGACCTTATGGA  
CTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGTTGACCTTGGAGAG  
GCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACTCCTGGATTAGGAGG  
ACTGACAATACTACATATATCATTAAAGCATGGGCCCTCGCTTAGAAGTTGCATCTGAGAAAGTA  
GCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAACCGGCAGGCAAGATGAA  
ACTCATTTTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTGACACAGAAAGGAAAATCA  
TTGTCACCTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATTATATCCATGTGTCTTCTC  
TTCCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAACTAGAAGGCAGGCCAGAA  
ACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATGCTCTGGATGACTTCGGAATA  
TATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGGATTCCAAGCAGGTCTGTTCCA  
GCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGTGTATGAAGTTATTCAGCACATC  
CCTGCCCAGCAGCAAGACCATCCAGAG**TGA**ACTTTTCATGGGCTAAACAGTACATTTCGAGTGAA  
ATTCTGAAGAAACATTTTAAAGGAAAAACAGTGGAAAAGTATATTAATCTGGAATCAGTGAAGA  
AACCAGGACCAACACCTCTTACTCATTATTCCTTTACATGCAGAATAGAGGCATTTATGCAAA  
TTGAACTGCAGGTTTTTTCAGCATATACACAATGTCTTGTGCAACAGAAAAACATGTTGGGGAA  
ATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGGGGAGAACGAAAGTGACAGGGGTTTCCT  
CATAAGTTTTGTATGAAATATCTCTACAAACCTCAATTAGTTCTACTCTACACTTTCACTATC  
ATCAACACTGAGACTATCCTGTCTCACCTACAAATGTGGAACTTTACATTGTTTCGATTTTTT  
AGCAGACTTTGTTTTATTAAATTTTTATTAGTGTTAAGAATGCTAAATTTATGTTTTCAATTTT  
ATTTCCAAATTTCTATCTTGTTATTTGTACAACAAAGTAATAAGGATGGTTGTCACAAAAACA  
AACTATGCCTTCTCTTTTTTTTCAATCACCAGTAGTATTTTTTGAGAAGACTTGTGAACACTT  
AAGGAAATGACTATTAAAGTCTTATTTTTTATTTTTTTCAAGGAAAGATGGATTCAAATAAATT  
ATTCTGTTTTTGCTTTTAAAAAAAAAAAAAA

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**FIGURE 378**

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVGRQALYLPVHYGFHTPASDIQIIWLFERPHTMPKYLLGSVNKS  
VVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTSLASQKIQVTVDDPVTKPVVQIHPPSGAVEY  
VGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFSPQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPII  
YYGPYGLQVNSDKGLKVGVEVFTVDLGEAILEDSCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMD  
YVCCAYNNITGRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQKLEG  
RPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTVYEVIQHIIPAQQQDHPE

**Important features:****Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208, 276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237, 239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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**FIGURE 379**

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTCACATGGGCACAA  
TTTCACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTTGTT  
CTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCAAGC  
GCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCTTTAA  
TTAAGGGGTTACATCCAACCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCTGCGTC  
ACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGACATGTATAGACACAAAAACAGCTG  
GAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAACATTGAT  
TTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCAGCCCACAA  
GATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCT  
GCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAG  
GAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGG  
GCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCAGCA  
ATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAA  
ATAG

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**FIGURE 380**

MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLLS  
GATATAALPLEGGPTGRDSEHMQEAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVARR  
QEGAPPQQSARRDRMPCRNFFWKTFSSCK

**Important features:****Transmembrane domain:**

amino acids 51-69

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 35-39, 92-96

**N-myristoylation sites.**

amino acids 64-70, 75-81, 90-96

**Amidation site.**

amino acids 33-37



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**FIGURE 381**

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCGCC  
GCGCCGCCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCCGCGCCCCGCGC  
CCGCGCCCCAGGTGAGCGCTCCGCCCCGCGGAGGCCCGCCCCGGCCCCGCCCCGCCCCGCCCC  
CGGCCGGCGGGGGAACCGGGCGGATTCCTCGCGCGTCAAACCACCTGATCCCATAAAACATTC  
ATCCTCCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCGCCGCGCCCTCGCCCTG  
TGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCCAGCCAGAGCCGGGCGGAGCGGAGCG  
CGCCGAGCCTCGTCCCGCGGCCCGGGCCGGGGCCGGGCCGTAGCGGCGGCGCCTGGATGCGGAC  
CCGGCCGCGGGGAGACGGGGCGCCCCGCCCGAAACGACTTTCAGTCCCCGACGCGCCCCGCCCA  
ACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTGCTGTGGCTG  
CAGGCCTGGCAGGTGGCAGCCCCATGCCCAGGTGCCTGCGTATGCTACAATGAGCCCAAGGTG  
ACGACAAGCTGCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTGCTGCCAGCCAG  
CGCATCTTCTGACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTCCGTGCCTGCCGC  
AACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGCGGCTGCCTTCACT  
GGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCCGGTCTGTGGACCCT  
GCCACATTCCACGGCCTGGGCCCGCTACACACGCTGCACCTGGACCGCTGCGGCCTGCAGGAG  
CTGGGCCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTACCTGCAGGACAACGCG  
CTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCACACACCTCTTCTGAC  
GGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTGCACAGCCTCGACCGTCTC  
CTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCATGCCTTCCGTGACCTTGGCCGCCTC  
ATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCACTGAGGGCCCTGGCCCCCCTG  
CGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTGTGTGACTGCCGGGCACGCCCCA  
CTCTGGGCCTGGCTGCAGAAGTTCCGCGGCCTCCTCCTCCGAGGTGCCCTGCAGCCTCCCGCAA  
CGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATGACCTGCAGGGCTGCGCTGTGGCC  
ACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACCGATGAGGAGCCGCTGGGGCTTCCC  
AAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGTACTGGAGCCTGGAAGACCAGCTTCG  
GCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTGACAGCCCCGCCGGGCAACGGCTCTGGC  
CCACGGCACATCAATGACTCACCTTTGGGACTCTGCCTGGCTCTGCTGAGCCCCCGCTCACT  
GCAGTGCGGCCCCGAGGGCTCCGAGCCACCAGGGTTCCCCACCTCGGGCCCTCGCCGGAGGCCA  
GGCTGTTACGCAAGAACCGCACCCGCAGCCACTGCCGTCTGGGCCAGGCAGGCAGCGGGGT  
GGCGGGACTGGTGACTCAGAAGGCTCAGGTGCCCTACCCAGCCTCACCTGCAGCCTCACCCCC  
CTGGGCCTGGCGCTGGTGCTGTGGACAGTGCTTGGGCCCTGCTGACCCCCAGCGGACACAAGA  
GCGTGCTCAGCAGCCAGGTGTGTGTACATACGGGGTCTCTCTCCACGCCGCCAAGCCAGCCGG  
GCGGCCGACCCGTGGGGCAGGCCAGGCCAGGTCTCCTGATGGACGCTGCCGCCCGCCACC  
CCCATCTCCACCCCATCATGTTTACAGGGTTCGGCGGCAGCGTTTGTTCAGAACGCCGCCTC  
CCACCCAGATCGCGGTATATAGAGATATGCATTTTATTTTACTTGTGTAAAAATATCGGACGA  
CGTGGAATAAAGAGCTCTTTTCTTAAAAAA

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**FIGURE 382**

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAAASQRIE  
LHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPATF  
HGLGRLHTLHLDRCGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLELHGNER  
ISSVPERAFRGLHSLDRLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAPLRAL  
QYLRLNDNPWVCDRCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVATGP  
YHPIWTGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGNGSGPRH  
INDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQAGSGGGGT  
GDSESGALPSLTCSLTPLGLALVLWTVLGP

**Important features:****Signal peptide:**

amino acids 1-26

**Leucine zipper pattern.**

amino acids 135-156

**Glycosaminoglycan attachment site.**

amino acids 436-439

**N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

**VWFC domain**

amino acids 411-425

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**FIGURE 383**

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTCCTGAACCTTGTCTG  
AAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCGAGGGACCTTTTCGCTGCTTTTGTAGGG  
ACTTCTTTTCCTTGCTTCAGCAACATGAGGGCTTTTCTTGTGGAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGA  
TTGGGGCTTTGATCCCTGAACCAGAAGTGAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCA  
AAGGAGGGGATTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTCACA  
AACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGTTGGGACCAGGGCTTGA  
AAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCTCTGCTCTGGGCTATGGAAAAGAAGGAAAAGTA  
AAATTCCCCCAGAAAGTACACTGATATTTAATATTGATCTCCTGGAGATTGCAAATGGACCAAGATCCCATGAAT  
CATTCCAAGAAATGGATCTTAATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGT  
TTGAAAACATGGTGCCTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGTATAAAGAAGATG  
AAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTATAGAGATACATCTACCCCT  
TTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAAAGAACATTTTATTTTTATACAATGTTCTTTCT  
TGCTTTGTTTTTTATTTTTATATATTTTTCTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTT  
CTTTCTGATAAGTTATTGGGAAGAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTC  
ACAGATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACCACGACATGA  
GACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTCTCCAAGTTAGAGGTCAACATTT  
GAAAAGCCTTTTGCAATAGCCCCAAGGCTTGCTATTTTCATGTTATAATGAAATAGTTTATGTGTAAGTGGCTCTG  
AGTCTCTGCTTGAGGACCAGAGGAAAATGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGAT  
GTGCAATGCTGAAGTTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGA  
GGCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAACCCTATCTCTAC  
TAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCAGCTACCCAGGAAGGCTGAGGCGGCAGAA  
TCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAGATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAGAA  
AAGAACACGGTTAATACCATATNAATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGG  
CTCCTAGTGATTGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATGTA  
TCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGCTAGCGGAATATCCTT  
CCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACATTGTATCATAAGATAAAGTAGTAAACCA  
GTCTACATTTTCCCATTTCTGTCTCATCAAAAAGTGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAG  
CACTTTGGGGGCCAAGGAGGTTGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCT  
TGTCTCTACTAAAAATACAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAGGCTGA  
GACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCCACTGCACTCCAGCCTGGG  
TGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGCAGACCTACAGCAGCTACTATTGAATAAATACCTA  
TCCTGGATTTT

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**FIGURE 384**

MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSLF  
HSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPESTLI  
FNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVEDIFD  
KEDEDKDGFIAREFTYKHDEL

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 176-179

**Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

**Endoplasmic reticulum targeting sequence.**

amino acids 208-211

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

**EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

**S-100/ICaBP type calcium binding domain**

amino acids 183-203

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**FIGURE 385**

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCTC  
CCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGTCC  
CTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGTGGG  
ATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAATGAAG  
GGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGAACCTC  
ACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAGTCTTTA  
CTGATCTCTCTGTTTCGTCTTTCCAGGACCCTGCTGTCTCCCTCCCCTTCTCCCACCTTCCAG  
CCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCCCAGGATTG  
ACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGGGCTGAGGCC  
CCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACACAGGAACCTCT  
CCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCCATGCAGCTGGACTCCACC  
TCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGGGTGTCCATCCCG  
ATGGTCCGCATACTGGCCCCAGTCCCTGGTGTCTGCTGAGCCTTCTGTGAGCCGCAGGCCTGATC  
GCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCACGGAGACACAGAGG  
AACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCCCCCTTCCCAGGCCCT  
GAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGAGCTGGGCTTCTCGAAG  
TTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGTGAAGCAGTATGGCTGGC  
TGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAGTCCAGCTGCCCCGACTCC  
AGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGCATGTTCCAGCCTGACCTAGAAGCGTTT  
GTCAGCCCTGGAGCCAGAGCGGTGGCCTTGCTCTTCCGGCTGGAGACTGGGACATCCCTGAT  
AGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCAGCAGGGCCAGACAAGGCTCAG  
TGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGCCTCATGCCAGTGTGCGACCT  
GCCTTCTCTCCACTCCAGACCCACCTTGTCTTCCCTCCCTGGCGTCTCAGACTTAGTCCCA  
CGGTCTCCTGCATCAGCTGGTGTGAAGAGGAGCATGCTGGGGTGAGACTGGGATTCTGGCTT  
CTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCTGTGAAAAACGTGATTCTGGCCCCA  
CCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAGGACTCTGAATTCTAACAATGCCCAGT  
GACTGTGCACTTGAGTTTGAGGGCCAGTGGGCCTGATGAACGCTCACACCCCTTCAGGTTAG  
AGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCCCAATAGATCTGCTCTGTCTGCGACACCA  
GATCCACGTGGGGACTCCCCTGAGGCCTGCTAAGTCCAGGCCTTGGTCAGGTCAGGTGCACAT  
TGCAGGATAAGCCCAGGACCGGCACAGAAGTGGTTGCCTTTNCCATTTGCCCTCCCTGGNCCA  
TGCCTTCTTGCCCTTTGGAAAAAATGATGAAGAAAACCTTGGCTCCTTCCCTGTCTGGAAAGGG  
TACTTGCCTATGGGTTCTGGTGGCTAGAGAGAAAAGTAGAAAACCAGAGTGCACGTAGGTGT  
CTAACACAGAGGAGAGTAGGAACAGGGCGGATACCTGAAGGTGACTCCGAGTCCAGCCCCCTG  
GAGAAGGGGTCGGGGGTGGTGGTAAAGTAGCACAACTACTATTTTTTTTCTTTTTTCCATTATT  
ATTGTTTTTTAAGACAGAATCTCGTGCTGCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCA  
AACTCCGCCTCCTGGGTTCAAGTGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAG  
GCACGCACCACACACCTGGCTAATTTTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTG  
GCCAGGCTGGTCTTGAACCTCCTGACCTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCG  
GGATTACAGGCATGAGCCACTGTGTCTGGCCCTATTTCCCTTAAAAAGTGAAATTAAGAGTTG  
TTCAGTATGCAAACTTGGAAAGATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCA  
TAGTCTCACCAGAGACTATCATTATTTTCGTTTTGTGTACTTCCTTCCACTCTTTTCTTCTTC  
ACATAATTTGCCGGTGTCTTTTTTACAGAGCAATTATCTTGTATATACAACTTTGTATCCTGC  
CTTTTCCACCTTATCGTTCCATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTT  
ATAAATAAAATGTTTCATCAGCTGCATAAAAAAAAAAAAAA

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**FIGURE 386**

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCSG  
TIYAE EEGQETMKGRVSI RDSRQELSLIVTLWNLTLDAGEYWCGVEKRGPD ESSLISLFVFP  
GPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQ  
YGHERTSQYTGTSPHPATSPAPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRILAPV  
LVLLSLLSAAGLIAFCSHLLLWRKEAQQTETQ RNEKFWSRLTAE EKEAPSQAPEGDVISMP  
PLHTSEEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128

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**FIGURE 387**

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACATG  
GCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTCGGAGG  
CGCCCGGCCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATCGGG  
**ATG**TCCCTCCTCCTTCTCCTCTTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCACACT  
GAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGCTTCCA  
GAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAAGTGGTG  
ATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCGAGTGGCC  
TTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGAGATTGAACCTCTGAAGCCCAGTGAT  
GAGGGCCGGTACACCTGTAAGGTAAAGAATTCAGGGGCGCTACGTGTGGAGCCATGTCATCTTA  
AAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGACAGAAGGAAGT  
GACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATTACTGGCAGCGA  
ATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAATCTAGGATTGACTACAACCAC  
CCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTACCAGTGCACAGCA  
GGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGTATGTACAAAGCATC  
GGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTCTTGGTG  
TGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAAATT  
CGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCTCCTCTTCTCAGGCTCT  
CGGAGCTCACGCTCTGGTTCTTCTCCTCCTCGCTCCACAGCAAATAGTGCCTCACGCAGCCAG  
CGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCACCCAGGCATACAGCCTAGTG  
GGGCCAGAGGTGAGAGGTCTGAACCAAAGAAAGTCCACCATGCTAATCTGACCAAAGCAGAA  
ACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAAACGGTCT**TGA**ATTACAATGGAC  
TTGACTCCCACGCTTTTCTTAGGAGTCAGGGTCTTTGGACTCTTCTCGTCATTGGAGCTCAAGT  
CACCAGCCACACAACCAGATGAGAGGTGCTAAGTAGCAGTGAGCATTGCACGGAACAGATT  
CAGATGAGCATTTTCTTATACAATAACAAACAAGCAAAAGGATGTAAGCTGATTCATCTGTA  
AAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGGAAAGCAGGAGTCCAAATCTATTTGT  
TGACCAGGACCTGTGGTGAGAAGGTGGGGAAAGGTGAGGTGAATATACCTAAAACCTTTAAT  
GTGGGATATTTTGTATCAGTGCTTTGATTCACAATTTTCAAGAGGAAATGGGATGCTGTTTGT  
AAATTTTCTATGCATTTCTGCAAACCTTATTGGATTATTAGTTATTCAGACAGTCAAGCAGAAC  
CCACAGCCTTATTACACCTGTCTACACCATGTAAGTGAAGTAAACCTTCTAAGAACTCCAAA  
AAAGGAAACATGTGTCTTCTATTCTGACTTAACTTCATTTGTCATAAGGTTTGGATATTAATT  
TCAAGGGGAGTTGAAATAGTGGGAGATGGAGAAGAGTGAATGAGTTTCTCCACTCTATACTA  
ATCTCACTATTTGTATTGAGCCCAAATAACTATGAAAGGAGACAAAAATTTGTGACAAAGGA  
TTGTGAAGAGCTTTCCATCTTCATGATGTTATGAGGATTGTTGACAAACATTAGAAATATATA  
ATGGAGCAATTGTGGATTTCCCCTCAAATCAGATGCCTCTAAGGACTTCTCTGCTAGATATTT  
CTGGAAGGAGAAAATACAACATGTCATTTATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAA  
AAGGGATCTAGGAATGCTGAAAGATTACCCAACATACCATTATAGTCTCTTCTTTCTGAGAAA  
ATGTGAAACCAGAATTGCAAGACTGGGTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTA  
ATATGTCAAGGAAGGTAGCCGGGCATGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAG  
GTTGCAGTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

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**FIGURE 388**

MSLLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
ITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVIL  
KVLVRPSKPKCELEGELTEGSDLTLCESSTGTEPIVYYWQRIREKEGEDERLPPKSRIDYNH  
PGRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLIFLLV  
WLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANSASRSQ  
RTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

**Important freatures:****Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 232-251



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**FIGURE 389**

GCGGCACCTGGAAGATGCGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTCG  
CCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCTGT  
CCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCCCCA  
AAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTACTCA  
GCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGGAGAAC  
AGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGAATGTGA  
CAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAGTTTATTC  
AGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCACAAAGACTGA  
ATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACATGAAATTCA  
GGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATTCAGAGAGAAA  
AGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGAGATCCAGATAG  
AAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAATGTGTTCTGTATA  
AACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACAGCCCATATTTGAT  
GAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCAAATCTTGGTACGCA  
GTATTTTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGAACTAAAATGAATGG  
AAATTCTTAAAAAAAAA

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**FIGURE 390**

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQKC  
DHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTATRC  
FDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDKNAIEALGSKEIRNMKFRSSWV  
FIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

**Important features:****Signal sequence.**

amino acids 1-20

**N-glycosylation sites.**

amino acids 120-124, 208-212

**Glycosaminoglycan attachment site.**

amino acids 80-84

**N-myristoylation sites.**

amino acids 81-87, 108-114, 119-125

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**FIGURE 391**

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACCTGCCTCCAAGGACCGGCCTCGGAGGGGTGCGCGGGAAGGG  
AGGGAAGAAGGAAGGGCGGGGCGGGCCCCCTGCGCCCGCCCCGCGCCTCTGCGCGCCCTGTCCGCCCCGGCC  
AGCCAGCCCCAGCCCCGCGGGCCGGTCACACGCGCAGCCAGCCGGCCGCTCCCGCGCCCAAGCGCGCCGCTTG  
CTGTGCCCTGCGCCCTTGCCCCGCGCCAGCTTCTGCGCCCGCAGCCCGCCCGGCGCCCCGGTGACCGTGACCT  
GCCCTGGGCGCGGGGCGGAGCAGGCATGTCCCCCGGGGACCGCTACCCAGCGCTGGCCCTGGTGCTCCTGGC  
AGTGACCCTGGCCGGGGTTCGGAGCCCAGGGCGCAGCCCTCGAGGACCCTGATTATTACGGGCAGGAGATCTGGAG  
CCGGGAGCCCTACTACGCGCGCCCCGAGCCCGAGCTCGAGACCTTCTCTCCGCGCTGCCTGCGGGGCCCCGGGA  
GGAGTGGGAGCGGCGCCCGCAGGAGCCCAGGCCGCCAAGAGGGGCCACCAAGCCCAAGAAAGCTCCCAAGAGGGA  
GAAGTCGGCTCCGGAGCCGCTCCACCAGGTAAACACAGCAACAAAAAGTTATGAGAACCAAGAGCTCTGAGAA  
GGCTGCCAACGATGATCACAGTGTCCGTGTGGCCGTCGAGAGATGTGAGAGAGATTGCCACCTCTTGGTCTGGA  
AACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCTGGGGGCACATCGAGGGAG  
ACTCAACATCCAGGCGGGCATTAAATGAAAATGATTTTTATGACGGAGCGTGGTGCGCGGAAGAAATGACCTCCA  
GCAGTGGATTGAAGTGGATGCTCGGCGCCTGACCAGATTCACTGGTGTCTCACTCAAGGGAGGAACCTCCCTCTG  
GCTGAGTGACTGGGTGACATCCTATAAGGTGATGGTGAGCAATGACAGCCACACGTGGGTCACTGTTAAGAATGG  
ATCTGGAGACATGATATTTGAGGGAAACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCTACCCGTCGCCATGGT  
GGCCCGCTACATCCGCATAAAACCTCAGTCCCTGGTTTGATAATGGGAGCATCTGCATGAGAATGGAGATCCTGGG  
CTGCCCCTGCCAGATCCTAATAATTATTATCACCGCCGGAACGAGATGACCACCACTGATGACCTGGATTTTAA  
GCACCACAATTATAAGGAAATGCGCCAGTTGATGAAAGTTGTGAATGAAATGTGTCCCAATATCACCAGAAATTA  
CAACATTGGAAGAAAGCCACAGGGCCTGAAGCTGTATGCTGTGGAGATCTCAGATCACCTGGGGAGCATGAAGT  
CGGTGAGCCCGAGTTCCACTACATCGCGGGGGCCACGGCAATGAGGTGCTGGGCGGGAGCTGCTGCTGCTGCT  
GGTGCAATTCTGTGTGTCAGGAGTACTTGGCCCGGAATGCGCGCATCTCCACCTGGTGGAGGAGACCGGGATTCA  
CGTCTCCCTCCCTCAACCCCGATGGCTACGAGAAGGCCTACGAAGGGGGCTCGGAGCTGGGAGGCTGGTCCCT  
GGGACGCTGGACCCACGATGGAATTGACATCAACAACAACCTTCTGATTTAAACACGCTGCTCTGGGAGGCAGA  
GGATCGACAGAAATGCCCCAGGAAAGTTCCCAATCACTATATTGCAATCCCTGAGTGGTTTCTGTGCGAAATGC  
CACGGTGGCTGCCGAGACCAGAGCAGTCATAGCCTGGATGGAAAAATCCCTTTTGTGCTGGGCGGCAACCTGCA  
GGGCGGCGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGCGGTCCCCCTGGAAGACGAGGAACACACCCCCAC  
CCCCGATGACCACGTGTTCCGCTGGCTGGCCTACTCCTATGCCCTCCACACACCCGCTCATGACAGACGCCCGGAG  
GAGGGTGTGCCACACGGAGGACTTCCAGAAGGAGGAGGGCACTGTCAATGGGGCCTCTGGCACACCGTCTGCTGG  
AAGTCTGAACGATTTCACTACCTTCATACAACTGCTTCGAAGTGTCCATCTACGTGGGCTGTGATAAATACCC  
ACATGAGAGCCAGCTGCCCCAGGAGTGGGAGATAACCGGGAATCTCTGATCGTGTTCATGGAGCAGGTTCTATCG  
TGGCATTAAAGGCTTGGTGAGAGATTACATGGAAAAGGAATCCCAACGCCATTATCTCCGTAGAAGGCATTAA  
CCATGACATCCGAACAGCCAACGATGGGGATTACTGGCGCCTCCTGAACCTGGAGAGTATGGTCAAGCAAA  
GGCCGAAGGTTTCACTGCATCCACCAAGAAGTGTATGGTTGGCTATGACATGGGGGCCACAAGGTGTGACTTCAC  
ACTTAGCAAAACCAACATGGCCAGGATCCGAGAGATCATGGAGAAGTTTGGGAAGCAGCCCGTCAGCCTGCCAGC  
CAGGCGGCTGAAGCTGCGGGGGCGGAAGAGACGACAGCGTGGGTGACCCCTCTGGGCCCTTGAGACTCGTCTGGG  
ACCCATGCAAAATTAACCAACCTGGTAGTAGCTCCATAGTGGACTCACTCACTGTTGTTTCTCTGTAATTCAAG  
AAGTGCCTGGAAGAGAGGGTGCATTGTGAGGCAAGTCCCAAAAGGGAAGGCTGGAGGCTGAGGCTGTTTTCTTT  
CTTTGTTCCCATTTATCCAAATAACTTGGCAGAGCAGCAGAGAAAAGCTGATGGGAGTGAGAGAAGTCAAG  
CCAACCTGGGAATCAGAGAGAGAAGGAGAAGGAGGGGAGCCTGTCCGTTCAAGAGCCTCTGGCTGCATAGAAAAGG  
ATTCTGGTGTTCCTCTGTTTGGTGGCAGCAAGGGTTCCACGTGCATTGTCAATTTGCACAGCTAAATTTGCAG  
CATTTCCCGAGCTGGGCTGTCCCAATGTTACCATTTGAGATGCTCCAGGCGTCTAAGAGAATCCACCCCTCTC  
TGGCCCTGGGACATTGCAAGCTGCTACAAATAAATCTGTGTTCTTTTGACAATAGCGTCATTGCCAAGTGACACA  
TCAGTGAGCCTCTGAATCTGTTTAGTCTCCTTTTCAACAAAGGAGTGTGTTTCAAAAAGGAGAGAGAGGCTGA  
GATCATTCAGGAGTTTGTGGGAGCAAGCATGGAGCTTCTTGACAAAATCTGGGTCCATAAAACACCCCAAA  
GTCCCTGCTGATCCAGTAGCCCTGGAGGTTCCCGAGGTAGGAGAGCCAGAGGTGCCAGCCTTCTGAGGGGCCA  
GAAAATTTAGCCTGGATCTCCTCTTTTACCTGCTAGGACTGGAAAGAGCCAGAAGTGGGGTGGCCTGAAGCCCTC  
TCTCTGCTTGAAGTATTGCCCTGTGTGGAATTGAGTGCTCATGGGTGGCCTCATATCAGCCTGGGAGTTATTT  
TTGATATGTAGAATGCCAGATCTTCCAGATTAGGCTAAATGTAATGAAAACCTCTTAGGATTATCTGTGGAGCAT  
CAGTTTGGGAAGAATTATTGAATTATCTTGAAGAAAAAAGTATGTCTCACTTTTGTAAATGTTGCTGCCTCAT  
TGACCTGGGAAAAATGAAAAAATAAAGCAAATGGTAAGACCCTTAAAAAATAAAGAAAAAATAAAGAAAAA  
AAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAA

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**FIGURE 392**

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPLPA  
GPGEEWERRPQEPRPPKRAKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDHDSVR  
VAREDVRESCPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCAGRN  
DLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIFEGNS  
EKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLDPNNYYHRRNEMTTTDDL  
FKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEFHYIAGA  
HGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPBGYKAYEGGSELGGWS  
LGRWTHDGDIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLENATVAAETRAVIAW  
MEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSASTHRLMTDARR  
RVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHESQLPEEWENNR  
ESLIVFMEQVHRGIKGLVRDSHGKIPNAIISVEGINHDIRTANDGDYWRLNPGYVVTAKA  
EGFTASTKNCMVGYDMGATRCDFTLSTNMARIREIMEKFGKQPVSLPARRLKLRGRKRRQRG

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**FIGURE 393**

GTCCACATCCTGCTCAACTGGGTGAGTCCCTCTTAGACCAGCTCTTGTCATCATTGCTGAAGTGACCAAC  
TAGTTCCCAAGTAGGGGCTCTCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA  
TGGCCTTGCTTGGGGTCTGCTTGTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG  
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTT  
TCTGAATCTAGCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG  
CTACTTATTTCTTTAGGGGATTGTCAGGAGGTGACCACTCTCACGGTGAAATACCAAGTGTGAGAGGAAGTGCC  
ATCTGGTACAGTGATCGGGAAGCTGTCCAGGAACTGGGCCGGGAGGAGAGGCGGAGGCAAGCTGGGGCCGCTT  
CCAGGTGTTGACGCTGCCTCAGGCGCTCCCACTTACAGTGGACTCTGAGGAAGGCTTGTGCTCAGCACAGGCGG  
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGACTCCCTGCTGGTTTCTTGTGATGTGCTTGGCCACAGGGGATT  
GGCTCTGATCCATGTGGAGATCCAAGTGTGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCGAGCAGGA  
GCTGGAATCTCTGAGAGCGCTCTCTGCAACCCGGATCCCTTGGACAGAGCTCTTGACCCAGACACAGGCCC  
TAACACCTGACACCTACACTCTGTCTCCAGTGAGCACTTTGCCTTGGATGTGATTGTGGGCCCTGATGAGAC  
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCAATTTTTGATCTGGTGTTAACTGC  
CTATGACAATGGGAACCCCCCAAGTCAAGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAG  
CCCTGCGTTTGTGCTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAAAC  
GACCGCCACAGACCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCCTCCAGAGGT  
GCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCACTTCTGCGTCGACCTCTAGACTATGAAAAGAACCC  
TGCCTACGAGGTGGATGTTTCAAGGCAAGGACCTGGGTCCCAATCCTATCCAGCCCATGCAAAGTTCTCATCAA  
GGTTCTGGATGTCAATGACAACATCCCAAGCATCCACGTACATGGGCCTCCAGCCATCACTGGTGTGAGAAGC  
TCTTCCCAAGGACAGTTTTATTGCTCTTGTGATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG  
CTGGCTGAGCCAAAGAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCAACACATACATGTTTGGCTAACCAATGC  
CACACTGGACAGAGAGCAGTGGCCCAATATACCCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC  
AGCCAAGAAACAGCTCAGCATTGATCAGTACATCAACGACAATGCACCTGTGTTTGAAGAAAGCAGGTATGA  
AGTCTCCACGCGGGGAAAACAACCTTACCCTCTCTTACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGCAT  
TAATGGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA  
GGTCACTGCTCAGAGGTCACTGAATATGAAGAGATGGCCGGCTTTGAGTTCAGGTGATCGCAGAGGACAGCGG  
GCAACCCATGCTTGCATCCAGTGTCTGTGTGGGTGAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGT  
CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCC  
CATCGAGACTCCCAATGGCTTGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGTCCCGGCCATT  
CCTTTTGACAACCATTTGTGGCAAGAGATGCAGACTCGGGGGCAATGGAGAGCCCTCTACAGCATCCGCAATGG  
AAATGAAGCCACCTCTTCACTCAACCCCTCATACGGGGCAGCTGTTCTGTCATGTACCAATGCCAGCAGCCT  
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT  
GAGGGTCTATGTTTGTACCAAGTGTGGACCACTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGAT  
GCTGACGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTCCGGTTGATCTGGCTTTGTTTATGTCCATCTGCCG  
GACAGAAAAGAAGGACAACAGGGCTTACAACCTGTGCGGAGGCGGAGTCCACCTACCGCCAGCAGCCCAAGAGGCC  
CCAGAAACACATTGAGAAGGCAGACATCCACCTCGTGCCTGTGCTCAGGGGTGAGGCAGGTGAGCCTTGTGAAGT  
CGGGCAGTCCCAAGAGATGTGGACAAGGAGCGGATGATGAAGCAGGCTGGGACCCCTGCCTGACAGGCCCCCTT  
CCACCTCACCCCGAAGCTGTACAGGACGCTGCGTAATCAAGGCAACCAAGGAGCAGCGGCGGAGAGCGGAGGT  
GCTGCAAGACACGGTCAACCTCCTTTTCAACCATCCAGGCAGAGGAATGCCTCCCGGGAGAACCTGAACCTTCC  
CGAGCCCCAGCCTGCCACAGGCCAGCCAGCTTCCAGGCCTCTGAAGGTTGCAGGCAGCCCCACAGGAGGCTGGC  
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACAGCCTCCTCTGCAACCTGAGACGGCAGCGACATCT  
CAATGGCAAAGTGTCCCTGAGAAAGAATCAGGGCCCCGTGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGC  
TGCTTTCGCGAGCGGAACCCGTGGAGGAGCTCACTGTGATTCTCCTCTGTTTCAAGAAATCTCCAGCTGCT  
GTCCTTGTGCTGATCAGGGCCAATTCCAGCCCCAAACCAACCCAGGAGAAATAAGTACTTGGCCAAAGCCAGGAGG  
CAGCAGGAGTGCAATCCAGACACAGATGGCCCAAGTGCAAGGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA  
AGGGCCTTTGGATCCTGAAGAGSACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC  
CAGCACAGGTCTGGCCCTGGACCGCTGAGCGCCCCCTGACCCGGCCTGGATGGCGAGACTCTCTTGGCCCTCAC  
CACCACCTACCGTGACAATGTGATCTCCCCGGATGCTGAGCCACGGAGGAGCCGAGGACCTTCCAGAGCTTCGG  
CAAGGCAGAGGCACAGAGCTGAGCCCAAGGACAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT  
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCCGTGGAGGGCCCTCCGAGGCGCTGCCGCGGCTCTCGGT  
CTGCGGGAGGACCCTCAGTTTAGACTTGGCCACCAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGG  
AAAGACGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGGCTGCTGTAACATACCTCAGACGCCT  
CTGGATCCAAGAACCAGGGGCTGAGGATCTGTGGACAAGAGCTGGTTCTAAAATCTTGTAACTCACTAGCTAG  
CGGCGGCTGAGAACTTTAGGGTGAATGCTACCCCCACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC  
TGACCAAGACACCCCTTGTAAAGCAGCTCTGAGTCTTTTGGAGGACAGGACGCTTTGTGGCTGAGATAAGTGT  
TCCTGGCAAAACATATGTGGAGCACAAAGGGTCACTGCTTCTGGCAGAACAGATGCCACGGAGTACACAGGAGG  
AAAGGGTGGCCTTCTTGGGTAGCAGGAGTCAAGGGGCTGTACCCTGGGGGTGCCAGGAAATGCTCTCTGACCTAT  
CAATAAAGGAAAAGCAGTAAAAA

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**FIGURE 394**

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQAG  
AAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQVL  
DINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIVGPD  
ETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNDNSPAFAESSLALE  
IQEDAAPGTTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPLDYEKN  
PAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSFIALVMA  
DDLD SGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQDQGLQPLS  
AKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVSRYRIQDSPV  
AHLVAIDSNTGEVTAQRSLNYYEEMAGFEFQVIAEDSGQPMLASSVSVWVSLLDANDNAPEVVQ  
PVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTTIVARDADSGA  
NGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGSPPLQTRALLRV  
MFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEKKDNRAYNCREAE  
STYRQPKRPQKHIQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEAGWDPCLOAPFHLT  
PTLYRTLNRQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLEPPQPATGQPRSRPLKV  
AGSPTGRLAGDQGSEEPQRPPASSATLRRQRHLNGKVSPEKESGPRQILRSLVRLSVAFAE  
RNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEGSRSAIPDTDGPSARAGG  
QTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPDPAWMARLSLPLTTNYRD  
NVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSLLEMLLEQRSSMPVEAASE  
ALRRLSVCGRTLSLIDLATSAAAGMKVQGDPPGGKTGTGEGKSRGSSSSSRCL

**Important features:****Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 719-739

**N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

**Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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**FIGURE 395**

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAGG  
CTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAATC  
AGTAGGTGACCCCGCCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGTGCG  
GCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCACAG  
GAGGACAAGGTGCTGGGGGGTTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGGCCTTG  
TTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCCTTACAGCT  
GCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAATAAAGAT  
GGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACAGCAGCGAT  
GTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCCCTGGGGTCC  
AAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTGCACCGTCTCA  
GGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCCTGACACTCTCAACTGTGCAGAAGTA  
AAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACAGATGGCATGGTC  
TGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGGCCCCCTGGTGTGT  
GATGGTGCCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGAGGTCCGACAAACCT  
GGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATCATAGGCAGCAAGGGC  
TGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCTCTGGTTC

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**FIGURE 396**

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLV  
GGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSI PHPCYNSSDVEDHNNHDLMLLQL  
RDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFDTLNCAEVKIFPQKKCEDAYP  
GQITDGMVCAGSSKGADTCQGDSSGGLVCDGALQGITSWGS DPCGRSDKPGVYTNICRYLDWI  
KKIIGSKG

**Important Features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 51-71

**N-glycosylation site.**

amino acids 110-113

**Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

**Tyrosine kinase phosphorylation site.**

amino acids 182-188

**Kringle domain proteins motif**

amino acids 205-217



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**FIGURE 397**

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCCATGTCGGACCTGCTAC  
TACTGGGCCTGATTGGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGGGT  
ACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCACTG  
TGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGCTGCA  
GCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCCCCCTG  
ATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCCCTGAGC  
TCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGCCATGTGG  
TGACAGCCACCTTCCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCGTGTCCATC  
CTGCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGGAGATCTACC  
AGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTATGTGCCTGAGA  
TGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCAGGTGGATGGCA  
CAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCCCTGGCAGCCGGG  
AGACTTCAGCTGCCACACTGTCACCTGGGGCGAGCAGCCGTGGCTGGGATGACGGTGACACCC  
GCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGAGGAGCTGGACTTGG  
AGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGCCCCTGGGGACTACCA  
AGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAGTAACCCATGGCCTGCACCCTCC  
TGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCTCCAGCCCTCTTCCTCCT  
TCCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGCTCCAGGCCTCTTGCTAAG  
CCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCAGGGACTATTTTCTGCACCA  
GCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTCACAGTGGAGCTTCCAGGACC  
CAGAATAAAGCCAATGATTTACTTGTTTCACCTGGAAAAAAAAAAAAAAAAAAAA

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**FIGURE 398**

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGRL  
FTESCSISPKLRSIAVYYDNPHMVPPDKCRAVGSI SEGEESPSPELIDLYQKFGFKVFSFP  
APSHVVTATFPYTTILSIWLATTRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCP LARQGD  
FYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETS AATLSPGASSRGW  
DDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEKGKE



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**FIGURE 400**

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRRTSKDPEHEG  
CYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWLPL  
AHQLYTDVANNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTVGRI  
TGLDPAGPMFEGADIAHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDFQPGC  
GLNDVLGSIAYGTITEVVKCEHERAVHLEFVDSLQNQDKPSFAFQCTDSNRFKKGICLSCRKNR  
CNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

**Important features:****Signal peptide:**

amino acids 1-16

**Lipases, serine active site.**

amino acids 163-172

**N-glycosylation sites.**

amino acids 80-83 and 136-139

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**FIGURE 401**

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCTG  
CCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCTGT  
CAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGGCTC  
AACTCTCCTGCACGCTCAGCCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCTTGGTACC  
AGCAGCGGGCAGGCAGTGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCACCACC  
GGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCACAATGCCTGTGTCC  
TCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGCTACGGCT  
TTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTTCTGCCCCTGA  
CCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAAATGGGTTAATAATA  
TTCAACATGTCAACAAC

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**FIGURE 402**

MACRCLSFLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAGS  
APRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPEDDADYYCSVGYGFS

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**FIGURE 403**

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGAAAGCAGCGAGTTG  
GCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCTCACAACAAGATGCTCAAGGTGTCAGC  
CGTACTGTGTGTGTGTGCAGCCGCTTGGTGAGTCAGTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGG  
GCGGTCCGACGGCGGTAATTTTCTGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGG  
ACAGTGGAACAAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCTTTCGATCA  
GGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTATGCATTGCTCAAGATTC  
TCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATGAAAGAAGCAGGAGTAGACCATAGGCAGTG  
GAGGGGTCCCATATTATCCACCTGCAAGCAGTGCCAGTGGTCTATCCAGCCCTGTTTGTGGTTCAGATGGTCA  
TACCTACTCTTTTCAGTGCAAACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGG  
ACATTGCCCATGTCCTTCAGATAAGCCCACCACTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCTGGAGTT  
CAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAAGTCAAACAAGAAGACAAA  
AACATTGCTGAGGCCTGAGAGAAGCAGATTCGATACCAGCATCTTGCCAAATTGCAAGGACTCACTTGGCTGGAT  
GTTTAAACAGACTTGATACAACTATGACCTGCTATTGGACCAGTCAGAGCTCAGAAGCATTACCTTGATAAGAA  
TGAACAGTGACCAAGGCATTCTTCAATTCTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTG  
CTACTGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCAAGGGGTAAA  
GAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGCCAACACAATGTCATGGCAGTGT  
TGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTCATGGGATCCAGAATAAATGGTGTGTCAGATTGTGC  
TATAGATTTTGAGATCTCCGGAGATTTTGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGA  
CGATATTATGAATGATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTATGA  
CCATGATGTATACATTGATTGATGACAGTTGAAATCAATAAATCTACATTTCTAATATTTACAAAAATGATAG  
CCTATTTAAATATCTTCTTCCCAATAACAAAATGATTCTAAACCTCACATATATTTGTATAATTATTTGAA  
AAATTGCAGCTAAAGTTATAGAATTTTATGTTTAAATAAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACA  
AAAAGAAAATACATATGCAGTCTAGTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTCACGAGA  
ACAACTTTGTAAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAAGAT  
AATTCTAAGTGAAATTTAAATAAATAAATTTTAAATGACCTGGGTCTTAAGGATTTAGGAAAAATATGCATGCT  
TTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAGGATAACAGAGAGATACCACATGACTCCA  
AAAAAAAAAAAAAA

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**FIGURE 404**

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFRD  
EVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEAGV  
DHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPSPDK  
PTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLRPERSRFDTSILPICKDS  
LGWMFNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQRQQDP  
PCQTELSNIQKRQGVKKLLGQYIPLCEDGYYKPTQCHGSVGCWCVD RYGNV MGSRINGVA  
DCAIDFEISGDFASGDFHEWTDDEDDDDIMNDEDEIEDDDDEDEGDDDDGGDDHDVYI

**Important features:****Signal peptide:**

amino acids 1-16

**Leucine zipper pattern.**

amino acids 246-267

**N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

**Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352



**FIGURE 405**

[illegible]

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**FIGURE 406**

MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRCSQRNQTHRSSLHYKPTPDLRISIENSEE  
ALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLSDKASSLLCFQHQE  
ESLAQGPPLLATSVTSWWSPQNISLPSAASFSTFSFHSPHTAAHNASVDMCELKRDQLLSQF  
LKHPQKASRRPSAAPASQQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQDLHIH  
SRQEEEQSEIMEYSVLLPRTLQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGEKVLGI  
VVQNTKVANLTEPVVLTQFQHLQPKNVTLCVFWVEDPTLSSPGHWSSAGCETVRRETQTSCE  
CNHLTYFAVLMVSSVEVDVAVHKHYLSLLSYVGCVVSAALCLVTIAAYLCRVPLPCRKRPRDY  
TIKVHMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAIFLHFSLLTCLSWMGLEGYNLYRLV  
VEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIYPSMCWIRDS  
LVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLGLSLVLGLPWALIFFSF  
ASGTFQLVVLYLFSIITSFQGFLIFIWYSMRLQARGGPSPLKSNSDSARLPISSGSTSSSRI

**Important features:****Signal peptide:**

amino acids 1-25

**Putative transmembrane domains:**amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657**Microbodies C-terminal targeting signal.**

amino acids 691-693

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

**N-glycosylation sites.**amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344**G-protein coupled receptors family 2 proteins**

amino acids 475-504

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**FIGURE 407**

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGAG  
CCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTCGC  
TCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCTGGA  
CTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAAGCCC  
TGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAAAGCTC  
AGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAGCAGGGC  
TCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGCTCAGCTG  
CCTGCTACCCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTGCTACATGA  
CTTCGGGCTGGACGGATAACGGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGCTTATTTAC  
AAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACAACGGGATCTT  
CCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCGAACGTCCCCAACGTGTGCCGGAT  
GTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGCCATGAAGATAAC  
CCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCCAGGGAAAAGACCT  
CACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCACAGCAGGCTGGGAA  
ATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATAAAGGATGGTTGAACG  
TGAAA

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**FIGURE 408**

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALDY  
EADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYCSDLLNPNLKDTVICAMKITQEPQGLGYWE  
AWRHHCQGKDLTEWVDGCDF

**Important features:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 67-72

**Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

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**FIGURE 409**

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC  
CTCTTTTCAGCCCGGGATCGCCCCAGCAGGGATGCGGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTCTGGCC  
GCTCTGCCCTCCGGTGCTGCTGCCTGGGGCGCGGCTTACACCTTCCCTCGATAGCGACTTCACCTTTACCCCTT  
CCCCCGGGCCAGAAGGAGTGCTTCTACCAGCCCATGCCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTA  
GATGGAGCAGGATTAGATATTGATTTCCATCTTGCCCTCTCCAGAAGGCAAAACCTTAGTTTTTGAACAAAGAAAA  
TCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTTCAGCACCATT  
TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAAGATTGGAAAG  
AAATATATTACTGGCACAGATATATTGGATATGAAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC  
AGACTAAGCAAAAGTGGGCACATACAAATTTCTGCTTAGAGCATTGGAAGCTCGTGATCGAAACATACAAGAAAGC  
AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCATGGTGGTGGTGTGAGCCATTCAAGTTTAT  
ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAGTAGAACTTAAACTCCAACTAGAGTACGTAACATTGAAA  
AATGAGGCATAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAAATATTTTGAGATATA  
AAAGTAGGAAACAGGTATAATTTTAAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG  
TTGTACTTAAAGTGTTAACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATACTGCAT  
TTTCCTAACTTTTGAAGAAATTTTGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAATTGCAACACC  
AGTCTGTTTTTAAACAGGTTCTATTACCCAGAATTTTTTGTAAATGCGGCAGTTACAAATTAAGTGTGGAAGTTT  
TCAGTTTTTAAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCCAA  
CTTTTCTCTATTTACATATGCATCTCTCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG  
AGATTTTTTATAACCAAATACATTTTCAGTGTAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC  
CCAAAAGCTGACATTTTCACGATTCTTAAAAACACAAAGTTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG  
AAATGAAGAATATAGTTTAAAGCTTCTCTCCATAGGGACACATTTTCTCTAACCCTTAAGTAAAGTGTAGGA  
TTTTAAATTAATGTGAGGTAAAATAAGTTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA  
TAATCATGTTATGTTAATTTTAAACATGATTGCTGACTTGGATAATTCAATTATTACCAGCAGTTATGAAGGAAATA  
TTGCTAAAATGATCTGGGCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA  
AGAATTTAGAAAACTTGAGAAAACCTAATCCAAAATAAATTAACCTTAAGTAGAAGTATAAATAAATATCTAGA  
ATCTGACTGGCTCATCATGACATCCTACTCATACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG  
AACTTTTGGCTGTAGGTTTTTATTTTCTACAAGAATTCTGGTTGAATTATTTTGTAAAGCAGGTACATTTTATA  
AAATGTAAGCCCTACTGTAAGGTTTAGCACTGGGTGTACATATTTATTAATAAATTTTATTATAACAACCTTTTAT  
TAAATGGCCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTTAA  
CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGGTCTTAC  
TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAAATTTTAAAGTTATGCCCATTTATAACGTTGTTTAT  
GACTACATTGTGAGTTAGAAACAAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT  
CTTGATGAGCAATAATGATAACCAGAGAGTGATTTCACTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC  
TCTTAGGCCCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAATGCCGTAT  
ATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA  
AGGTCAATAAGATCCTTGCCATGAATACCCCTCCCTTTTGGCGCTGTTAAATTTGCAATGAGAAGCAAATTTACA  
GTACCATAACTAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTTCTATAAACTGTGATTAAGAATTCTA  
CCTCTCCTGTATGGCTGTTACTGTACTGTACTCTGACTCCTTACCTAACAATGAATTTGTTACATAATCTTCT  
ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACCTCTTACCATATAAAAACGATAATTGCTT  
TATTTGGAAGAAGATTTAGGAATACTAAGGACAATTATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG  
CATAACCAAAAAAGCAAACTTGTAAACAGAGTAAAAATCTTAAATTTCTAAAGACATACTGTTTATCTGCTT  
CATATGCTTTTTTTAATTTCACTATTCATTTCTAAATTTAAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTT  
AACAGCTCATTTTGTCTTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTTT  
CATAATGTAGCAGTTACCGTGTTCACCTCACACTAAGGCCTAGAGTTTGTCTGATATGCATTTGGATGATTAAT  
GTTATGCTGTTCTTTTATGTGAATGTCAAGACATGGAGGTTGTTGTAATTTTATGGTAAATTAATCCTTCTTA  
CACATAATGGTGTCTTAAATTTGACAAAAATGAGCACTTACAATTTGATGTCTCCTCAAATGAAGATTCTTTAT  
GTGAAATTTTAAAGACATTGATTCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACATCAGTGTG  
CTCAAACTGCTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATA  
AAATTATCAAAGGAAAA

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**FIGURE 410**

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLSDSDFTFTLPAQKECFYQPMPLKASLEIEYQ  
VLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFELIL  
DNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRNIQE  
SNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

**Important features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 195-217

**N-myristoylation site.**

amino acids 43-48

**Tyrosine kinase phosphorylation site.**

amino acids 55-62

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**FIGURE 411**

CCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAAACTTCCCAGGGGACCGCATTCCAGAGTCA  
GTACTCTGTGAAGCACCCACATCTACCTCTTGCCACGTTCCCACGGGCTGGGGGAAAGATGGTGGGGACCAAG  
GCTGGGTTTCTCCTTCTGCTGTGCTGGAAGTACATCTGTGTTGGGGAGACAGCAGTGTCTACCCAGTCACTA  
AGAAGAGTCCAGCCTGGGAAGAAAGAACCCAGCATCTTGCCAAAGCCTGCCGACACCCTGGAGAGCCCTGGTGAG  
TGGCAACATGGTTCAACATCGACTACCCAGGCGGGGAAGGCGCACTATGAGCGGCTGGAGCCCATTCGCTTCTAC  
TATGGGGACCGTGTATGTGCCCTCCCCCTCGGGCTAGAGGCTCGGACCACTGACTGGACACCTGCGGGCAGCACT  
GGCCAGGTTGGTCCATGGTAGTGTCCCCGTGAGGGTTTCTGCTGCTCAACAGGGAGCAGCGGCCTGGCCAGAAGTGC  
TCTAATTACACCGTAGCCTTCTCTGCCACAGGATCCCTCGCCCGAGACACAGAGCGCATCTGGAGCCCATG  
TCTCCTGGAGCAAGTGTCTACGCTGCTTGTTGTCAGACTGGGGTCCAGACTCGCACAGCATTTGCTTGGCAGAG  
ATGGTGTGCTGTGTCAGTAGGCCACGGAAGAGGGTACAGCATGCATGGGCCAGGAGTGTACAGCCTGTGACCTG  
ACTGTCCCAATGGGCCAGGTGAATGCTGACTGTGATGCTGCTGATGTGCCAGGACTTCATGCTTATGGGGCTGT  
TCCCTTCCCAGGAGGTGCCCCAGCCTCAGGGGCTGCTATCTACCTCCTGACCAAGACGCCGAAGCTGCTGACCCAG  
ACAGCAGTGTATGGGAGATTCCGAATCCCCCTGGCTTGTCCCTGATGGCAAAAGCATCCTGAAGATCAAAAGGTC  
AAGTTTGGCCCATTTGTACTCAATGCCCAGACTAGCCTGAAGGACGCCACCTCAAGGCAGAGTTTGTGAGG  
GCAGAGACTCCATACATGGTGATGAACCTGAGACAAAAGCACGGAGAGCTGGGCAGAGCGTGTCTCTGTGCTGT  
AAGGCCACAGGGAAGCCACAGGCCAGACAAAGTATTTTGGTATCATAAATGACAGTACTCTGGATCCTTCCCTCTAC  
AAGCATGAGAGCAAGCTGTGTCTGAGGAAACTGCAGACAGCAGGCTGGGAGTACTTTTGAAGGCCAGAGT  
GATGCTGGGGCTGTGAAGTCCGAAGTTGCCAGCTGATTTGTACAGCATCTGTATGAGACTCCTTGCAACCCAGTT  
CCTGAGAGCTATCTTATCCGGCTGCCCATGATTTGCTTTCAGAAATGCCACCACTCCTCTACTATGACGTGGGA  
CGCTGCCCTGTTAAGACTTGTGACGGGCAGCAGGATAATGGGATCAGGTGCCGTGATGCTGTGCAAGAACTGCTGT  
GGCATCTCCAAGACAGAGGAAAGGGAGATCCAGTGCAGTGGCTACACGCTACCCCAAGGTGGCCAAAGGATGCG  
AGCTGCCAGCGGTGTACGGAAACTCGGAGCATCGTGGGGCGGTGTCACTGTGCTGACAAATGGGGAGCCCATG  
CGCTTTGGCCATGTGTACATGGGGAACAGCCGTGTAAAGCATGACTGGCTACAAGGCACTTACCCTCCATGTCT  
CCCCAGGACACTGAGAGCTGGTGTCTACATTTGTGGACAGGCTGCAGAAGTTTGTCAACACCAAAAGTGTCTA  
CTTTTCAACAAGAAGGGGAGTGGCGTGTTCATGAATCAAGATGCTTCTGTGGAAGAGCCCATCACTTTGGAA  
GCCATGGAGACCAACATCATCCCCCTGGGGGAAGTGGTTGGTGAAGACCCCATGGCTGGAAGTGGAGATTCCATCC  
AAGAGTTTCTACAGGCAGAATGGGAGCCCTACATAGGAAAGTGAAGGCCGTGACCTTCTGGATCCCCGG  
AATATTTCCACAGCCACAGCTGCCAGACTGACCTGAAGTTCATCAATGACGAGAGACACTTTCCCCCTTCGG  
ACGTATGGCATGTTCTGTGGACTTCAGAGATGAGGTCACTCAGAGCCACTTAATGCTGGCAAAGTGAAGGTCT  
CACTTGTACTCGACCCAGGTGAGATGCCAGAGCACATATCCACAGTGAATCTGTGTCATCAATCAGACACA  
GGCTGTGGGAGGAGGAGGTGATTTCAAATTTGAAATCAAGAGGAGGAACAAAGAGAGACAGAACCTTCTGT  
GTGGGCAACCTGGAGATTCTGTGAGAGGAGGCTCTTTAACTGGATGTTCTGTAAAGCAGGCGGTGCTTTGTTAAG  
GTGAGGCGCTACCGGAGTGAGAGTTCTTGGCTAGTGAGCAGATCCAGGGGGTTGTGATCTCCGTGATTAACTGT  
GAGCTAGAACTGGCTTCTTGTCCAACCTTAGGCTGTGGGCGCTTTGACAGTGTATCACAGGCCCCAACGGG  
GCTGTGTGCTGCTGCTGTGTATGATGACGAGTCCCCGTGATGCTACTCTGCTTGTCTTGGCAAGCCTGGCTGGG  
GAGGAAGTCCAAGCATGTGGAGTCTTCTCTAAATTAACCCAAATGCAATTTGGCTCCCTCAGCCTATCTCAAC  
AAGCTCAACTACCGTTCGGACGGACCATGAGGATCCACGGGTTAAAAAGACAGCTTTCCAGATTAGCATGGCCAG  
CCAAGGCCCAACTCAGCTGAGGAGAGCAATGGGCCCATCTGATGCTTTGAGAACCCTCGGGCATGTGAAGAGGCA  
CCACCCAGTGCAGCCCACTTCCGGTTCTACAGGATGAGGGGATCGATATGACTACAACAGACTCCCCCTCAAC  
GAAGATGACCCTATGAGCTGGACTGAAGACTATCTGGCATGGTGGCCAAAGCCGATGGAATTACGGGCGCTGCTAT  
ATCAAGGTGAAGTTGTGGGGCCACTGGAAGTGAAATGTGCGATCCCCGAACATGGGGGGCATCATCGGGGACAT  
GTGGGGAAGCTGTATGGAATCCGAGATGTGAGGAGCACTCGGGACAGGGACAGGCCCAATGTCTCAGCTGCTGT  
CTGGAGTTCAAGTGCAGTGGGATGCTCTATGATCAGGACCGTGTGGACCGCACCTGGTGAAGGTGATCCCCAG  
GGCAGCTGCCGTGCAGCCAGTGTGAACCCATGCTGCATGAGTACCTGGTCAACCACTTGCCACTTGCAGTCAAC  
AACGACACCAAGTGAATACACCATGCTGGCACCTTGGACCACTGGGGCACAACTATGGCATCTACACTGTCACT  
GACCAGGACCTTCGACGGCGCAAGGAGATCGCGCTCGGCCGGTGTCTTGTATGGGCATCCGATGGCTCCTCAGA  
ATCATGAAGAGCAATGTGGGAGTAGCCCTCACTTCACTGTGTAGAGAGCAAGTAGGCCGCCAGAGTGCCTTCTC  
CAGTACCTCCAAGGACCCCGAGCTCCCTGCTCGAGGCACTGTCCAAGGAAGAGTGCCTCGAGGAGGCAG  
CAGCAGGACGAGCGGGGTGGCCACGCGCCAGGTTGGAGTGGTGGCCCTCTGATAGTTTCTAGAGTTGCTCAACAG  
CCCCGTCACTCACTAAGTTTGTGGTACTTCACTCTTCTGCCCTATTCTATGTGACAGCCATTGTGAGACTGA  
TGCACAAACTGTCACTTGGTTAATTTAAGCACTTCTGTTTTCTGTAATTTGCTTGTGTTTCTTTCATGCCTTTA  
CTTACTTTTGTCCATGCTACTGATTGGCACGTGGCCCCCAACATGGCCAAATAAAGCCCCCTTTGTGAAACTGTTT  
TTTAAATGAACACAAGAAATGGCCACTGGTAAAACTCTGACGCTTCAACTGTACTTCAATTTAATGCCATTAAT  
GCAAATATACTTCTCTTCTTTTTGCATGGTTTTGCCACCTCTGCAATAGTGATAATCTGATGCTGAAGATCAA  
ATAACCAATATAAGCATATTTCTTGGCCTGTCTCCACAGGACATAGGCAAGCCTTGATCATAGTTCTACATAT  
AAATGGTGGTGAATAAAGAAATAAAACAATACTTTTACTTGAATGTAAATAACTTATTTATTTCTTTGCTA  
AATTTGGAATCTTAGTGACATTCAAAGTTAAGCTATTAATATAGGTTGATCATAGTTCTCTTACCAAGTCTGG  
AAGAACAATCTCCTGGTATCCACAATTAACACAGGTTGCTAACTGTTATTTGTACATTTCCCTTTGCATTCGCTT  
TGTCTTGTCTAGAAACCCAGTGTAGCCAGGGCAGATGTCAATAAATGCATACTGTATTTTGGAAAAA

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**FIGURE 412**

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNID  
YPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQRP  
GQNCSNYTVRFLCPPGSLRRDTERIWSWPWSKCSAACGQTGVQTRTRICLAEMVSLCSEAS  
EEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTKTPKL  
LTQTDSDGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPYMVMNP  
ETKARRAGQSVSLCCATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRLKQQHQAGEYFCKA  
QSDAGAVKSKVAQLIVTASDETPCNVPESYLIRLPHDCFQONATNSFYDVGRCVPVKTCAGQQ  
DNGIRCRDAVQNCCGISKTEEREIQCSGYTLPTKVAKECSCQRCTETRSIVRGRVSAADNGEP  
MRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFVDRLQKFVNNTTKVLPFNKKGSASFHE  
IKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKVKASVTFLDPR  
NISTATAAQTDLNFINDGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHLDSTQVKMPEHI  
STVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLENLDVPESRRCFVKV  
RAYRSEFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNACVPAFCDDQSPDA  
YSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRRTDHEDPRVKKTAFQISMAKPR  
PNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPVFNEDDPMSWTEDYLAWW  
PKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRSTRDRDQPNVSAACLEF  
KCSGMLYDQDRVDRTLKVIPOGSCRRASVNPMLEHYLVNHLPLAVNNDTSEYTMLAPLDPLG  
HNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALTFCNVERQVGRQSAFYLO  
STPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVAQQPLIN



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**FIGURE 413**

GCCACGTTGTCTTCTTTCCTTCACCACCACCCAGGAGCTCAGAGATCTAAGCTGCTTTCCATC  
TTTTCTCCCAGCCCCAGGACACTGACTCTGTACAGGATGGGGCCGTCCTCTTGCCTCCTTCTC  
ATCCTAATCCCCCTTCTCCAGCTGATCAACCCGGGGAGTACTCAGTGTTCTTAGACTCCGTT  
ATGGATAAGAAGATCAAGGATGTTCTCAACAGTCTAGAGTACAGTCCCTCTCCTATAAGCAAG  
AAGCTCTCGTGTGCTAGTGTCAAAGCCAAGGCAGACCGTCCTCCTGCCCTGCTGGGATGGCT  
GTCAGTGGCTGTGCTTGTGGCTATGGCTGTGGTTCGTGGGATGTTTCAGCTGGAAACCACCTGC  
CACTGCCAGTGCAGTGTGGTGGACTGGACCACTGCCCCGCTGCTGCCACCTGACCTGACAGGGA  
GGAGGCTGAGAACTCAGTTTTGTGACCATGACAGTAATGAAACCAGGGTCCCAACCAAGAAAT  
CTAACTCAAACGTCCCACTTCATTTGTTCCATTCTGATTCTTGGGTAATAAAGACAACTTT  
GTACCTCAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 414**

MGPSSCLLLILIPLLQLINPGSTQCSLDSVMDKKIKDVLNSLEYSPSPISKKLSCASVKS  
QGRPSSCPAGMAVTGCACGYGCGSWDVQLETTCHCQCSVVDWTTARCCHLT

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**FIGURE 415**

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGTG  
AGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAGGA  
GTGTGTGGAACAGGACCCGGGACAGAGGAACCAATGGCTCCGCAGAACCTGAGCACCTTTTGCC  
TGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTGGGGG  
TGCCTCGAAGTGCCTCTATAAAGGATATTA AAAAGGCCTATAGGAACTAGCCCTGCAGCTTC  
ATCCCGACCGGAACCCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTGCTGCTT  
ATGAGGTTCTGTGAGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAAGGATTAA  
AAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTCACACTTCTTTGGGGATTTTGGTTTCA  
TGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATATTATTGTAG  
ATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTTAGAAACAAAC  
CTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGATGCGGACCACCC  
AGCTGGGCCCTGGGCGCTTCAAATGACCCAGGAGGTGGTCTGCGACGAATGCCCTAATGTCA  
AACTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTGAGAGACGGCATGG  
AGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGGAGATTTACGGTTCC  
GAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATTTGTACACAAATGTGA  
CAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACTCACTTGGATGGTCACA  
AGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCTATGGAAGAAAGGGGAAG  
GGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAATCACTTTTGATGTGGATT  
TTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAACAGCTACTGAAACAAGGGT  
CAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTGAATAAAATTGGACTTTGTTT  
AAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTTTTTGTGTGTGTTTTTGTTTTTA  
TTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGATCATCATGAAATGAATAAGAGG  
GCTTAAGAATTTGTCCATTTGCATTTCGAAAAGAATGACCAGCAAAGGTTTACTAATACCTC  
TCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCTGAGTTTCAAGAATTAAAGCTGCAAGAGG  
ACTCCAGGAGCAAAGAAACACAATATAGAGGGTTGGAGTTGTTAGCAATTTCAATTCAAAATG  
CCAACCTGGAGAAGTCTGTTTTTAAATACATTTTGTGTTATTTTTTA

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**FIGURE 416**

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYE  
VLSDSEKRKQYDITYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGT PRQQDRNIPRGSDIIVDLEVTLEEVYAGNF  
VEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQMTQEVVVCDECPNVKLVNEERTLEVEIEPGVRDGM EYPFI  
GEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAKLW  
KKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

**Important features:****Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 254-257

**Nt-dnaJ domain signature.**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

**N-glycosylation site.**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site.**

amino acids 253-260

**N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site.**

amino acids 164-168

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**FIGURE 417**

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGGA  
TGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGGCCAGCCCCGCGGGGCGAG  
GATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCTGCT  
GATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCTCTAG  
GCCGCACACGGGGCCCGCTGCCACGCCCCGGGCCGACAGGGACAGGGAGCTCACGGCCGA  
CTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGACCTTCC  
CAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGAGCATGGAGGAGAGCGTGAGAGGCTACGA  
CTGGTCCCCGCGCAGCCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAGCGGAGGAG  
CGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCGCGCATTCGA  
CGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGGCCATCTACTG  
CTACGTGCCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTGAGCGGAAGCCT  
GCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCACGTGCACAACGC  
CAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCTCCCGCCACCTCAT  
GAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCCTTCGTGCGCCTGAT  
CTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCGCAAGTTCGCCGTGCC  
CATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGCGCGAGGCCTTCCGCGC  
TGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGACCCGCACACGGAGAAGCT  
GGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCACCCGTGCCAGATCGACTA  
CGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGCAGCTGCTGCAGCTACTCCA  
GGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGGACCGCCAGCAGCTGGGAGGA  
GGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCTGTATAAACTCTACGAGGCCGA  
CTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCCGAGACTTGAAAGCTTTCGCGTTG  
CTTTTTCTCGCGTGCCTGGAACCTGACGCACGCGCACTCCAGTTTTTTTTATGACCTACGATTT  
TGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCCATTGAGTACTGTATCGATATTGTT  
TTTTAAGATTAATATATTTTCAGGTATTTAATACGA

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**FIGURE 418**

MTKARLFRLWLVLGSVFMILLIIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELTAD  
SDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAERRS  
VLRGFCANSSLAFTKERAFFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIIVLSGSL  
LHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPFVRLI  
SAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDPHTEKL  
APFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAQLLQLLQVDRQLRFPPSYRNRRTASSWEE  
DWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

**Important features:****Signal peptide:**

amino acids 1-31

**N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

**TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

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**FIGURE 419**

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAG  
GCTGCCAGGAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCCTTCTGGAAATCTTTGACT  
GTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGACCTCGCGGGACTGCTGA  
AGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATCATCA  
ACACCATTGAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAAGATCA  
ACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGTCGGGCA  
CGGAATGCACCATCTTACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAATGCCATCG  
TGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGAACGCTTTG  
GGCTGTTAGGGGGCTCCAAGTCTTGCCCAAGAAAGAGCTGGCCTATGTCCCAATTATCGGCT  
GGATGTGGTACTTCACCGAGATGGTCTTCTGTTGCGCAAGTGGGAGCAGGATCGCAAGACGG  
TTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTGATTCACTGTG  
AGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCCGGGCCAAGGGGC  
TGCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATCACCGTGAGGAGCT  
TGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTCAGAAATAATGAAAATCCAA  
CACTGCTGGGAGTCTAAACGGAAAGAAATACCATGCAGATTTGTATGTTAGGAGGATCCCAC  
TGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCACAAGCTCTACCAGGAGA  
AGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGAGACGCCCATGGTGCCCC  
CCCGGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCTCGCTGGTGCTCTACCCTTTCT  
TCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACGCTGGCCAGCTTCATCCTCG  
TCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGTGACGGAAATTGACAAGGGCT  
CTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACTGACTCAGGGAGGTGTCACCAT  
CCGAAGGGAACCTTGGGGAACTGGTGGCCTCTGCATATCCTCCTTAGTGGGACACGGTGACAA  
AGGCTGGGTGAGCCCCTGCTGGGCACGGCGGAAGTCACGACCTCTCCAGCCAGGGAGTCTGGT  
CTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTTTTTTCCCATGTGCTTTAGTGGGC  
TTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGCTGTGTGGTGAGTGTGAACCTTGTTT  
TGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAGGGCAGGGCTGGGGACCGAAGGGGACA  
AGTTCCTCTTTCATCCTTTGGTGCTGAGTTTTCTGTAACCCTTGGTTGCCAGAGATAAAGTGA  
AAAGTGCTTTAGGTGAGATGACTAAATTATGCCTCCAAGAAAAAAAATTAAAGTGCTTTTCT  
GGGTCAAAAAAAAAA

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**FIGURE 420**

MDLAGLLKSQFLCHLVFCYVFIA SGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLVM  
LLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHNKFEIDFLCGWSLSERFGLLGSKVLAKKEL  
AYVPIIGWMWYFTEMVFC SRKWEQDRKTVATSLQHRLDYPEKYFFLIHCEGTRFTEKKHEISM  
QVARAKGLPRLKHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVLNGKKYHAD  
LYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVNWLFWA  
SLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDSKQKLND



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**FIGURE 421**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCATC  
GCC**ATG**GACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGCCC  
TGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTCACC  
ACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGCGGCG  
CTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGGCGCTGGGTGCC  
CTGAAGGAGGAGGTGCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTGCAGACC  
ACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCTGCGGGAA  
CTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACGTCCGCACT  
GAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCTGCGAGCCGTGCCCCACG  
TCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGACGTGGGCGGCG  
GCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCCTGGATGAGCAG  
GGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGGGCTGTGCGCCAT  
CTGGGCAAGGTTACAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTTCAGCCACTGGAAC  
CAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCATGATGCTGCACACGGGGCTG  
TGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAGAAAAGGCACAACCTGC  
**TGA**CCCCGCCAGTGCCCTGGAGCCGCGCCCATTGCAGCATGTCGTATCCTGGGGGCTGCTCA  
CCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTTCTTCCTCATCCACCGCTGCTGAG  
TCTCAGAAACACTTGGCCCCAACATAGCCCTGTCCAGCCCAGTGCCTGGGCTCTGGGACCTCCA  
TGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACTAACCTCCACTAGCTCCAAAATCC  
CTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAACCAAGGTTAGGTGACTGAGG  
ACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGAAGCTGTTTTTGCAGCCTGAGG  
AAGCATCAATAAATATTTGAGAAATGAAAAA

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**FIGURE 422**

MDTTRYSKWGGSSSEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAAL  
LDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTTAEELGEAQAKLMEQESALREL  
RERVTOGLAEAGRGREDVRTELFRALAEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTWAAA  
QDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWGLRAVRHLGKVQGYQWVDGVSLSFHWNQ  
GEPNDAWGRENVMMLHTGLWNDAPCDSEKDGWICEKRHNC

**Important features:****Type II transmembrane domain:**

amino acids 31-54

**N-glycosylation sites.**

amino acids 73-76 and 159-162

**Leucine zipper pattern.**

amino acids 102-123

**N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

**C-type lectin domain signature.**

amino acids 264-287

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**FIGURE 423**

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGGC  
GAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCGGC  
GCCAACATGGCGGGTGGGCGCTGCGGCCCCGAGCTAACGGCGCTCCTGGCCGCCTGGATCGC  
GGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGGTCCA  
GCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTTTACGC  
CCCATGGTGTCCATCCTGCCAGCAGACTGATTGAGAATGGGAGGCTTTTGCAAAGAATGGTGA  
AATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTGGCCGCTT  
CTTTGTCAACACTCTCCACGATTTTTTTCATGCAAAGGATGGGATATTCCGCCGTTATCGTGG  
CCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATCAGTCGAGCC  
TCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTCTTTTATGAT  
CTCTGGCAAGATATGGCATCTTCACAACTATTTTACAGTGAATCTTGGAAATTCCTGCTTGGTG  
TTCTTATGTGTTTTTCGTCATAGCCACCTTGGTTTTTGGCCTTTTTATGGGTCTGGTCTTGGT  
GGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGCGTTCTGAGCAGAA  
TCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAGGAGGAAAAAGATGA  
TTCAAATGAAGAAGAAAACAAAGACAGCCTTGTTAGATGATGAAGAAGAGAAAGAAGATCTTGG  
CGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTGCTGGTGTGGATGAGGA  
GAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTGACCCGGGAGGAAGTAGA  
GCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGCTGACACAGAGGTGGTGA  
AGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGACTGTAGATTTAATGATGCGT  
TTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGGCCTGCAGTTTGTACCAAATC  
CTTAATTTTTCTGAATGAGCAAGCTTCTCTTAAAAGATGCTCTCTAGTCATTTGGTCTCATG  
GCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGTGACAATCAGGATATAGAAAAAC  
AAACGTAGTGTGAGGATCTGTTTGGGAGACTGGGATGGGAACAAGTTCATTTACTTAGGGGTCA  
GAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATCAGCACCTTCCAGAGACAAGGCTGC  
AGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCTCCTGAGCATCCCCAAAGTGTAACGT  
AGAAGCCTTGATCCTTTTTCTTGTGTAAAGTATTTATTTTTGTCAAATTGCAGGAAACATCAG  
GCACCACAGTGCATGAAAAATCTTTCACAGCTAGAAATTGAAAGGGCCTTGGGTATAGAGAGC  
AGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTGTGCTATGTTTTATTTCTTACCTTTAATT  
TTTCCAGCATTTCCACCATGGGCATTCAGGCTCTCCACACTCTTCACTATTATCTCTTGGTCA  
GAGGACTCCAATAACAGCCAGGTTTACATGAAGTGTGTTTGTTCATTCTGACCTAAGGGGTTT  
AGATAATCAGTAACCATAAACCCTGAAGCTGTGACTGCCAAACATCTCAAATGAAATGTTGTG  
GCCATCAGAGACTCAAAGGAAGTAAGGATTTTACAAGACAGATTAAAAAAAATTGTTTTGT  
CCAAAATATAGTTGTTGTTGATTTTTTTTTTAAGTTTCTAAGCAATATTTTCAAGCCAGAAG  
TCCTCTAAGTCTTGCCAGTACAAGGTAGTCTTGTGAAGAAAAGTTGAATACTGTTTTGTTTC  
ATCTCAAGGGGTCCCTGGGTCTTGAAGTACTTTAATAATAACTAAAAAACCTTCTGATTT  
TCCTTCAGTGATGTGCTTTTGGTGAAAGAATTAATGAAGTCCAGTACCTGAAAGTGAAAGATT  
TGATTTTGTTCATCTTCTGTAATCTTCCAAAGAATTATATCTTTGTAAATCTCTCAATACT  
CAATCTACTGTAAGTACCCAGGGAGGCTAATTTCTTT

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**FIGURE 424**

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAPW  
CPSCQQTDSWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRGPG  
IFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAWCSY  
VFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSERSEQNRRSEEAHRAEQLQDAEEEEKDDSN  
EENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPGEDGVTREEVEPE  
EAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

**Important features:****Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide  
isomerase)

amino acids 56-72

**Flavodoxin proteins**

amino acids 173-187

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**FIGURE 425**

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCCGTGCGCCGCGG  
CTGGGCGCGTCGGAGAGTGCCTGTGCTTCTCTCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGTCCGCGGCCA  
GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGCATGGCAAGGTATATTTTTGTGGAATGAAAAGGA  
AGTATTAGAAATGAGCTGAAGACCATTACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTACCCCT  
TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC  
TTAAATCAGAACTTGACATAAGAAAGAGAAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG  
GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTTACAGTTTACTTGG  
AGTGTCCAAAACGCAAGCAGTAGAGAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA  
AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA  
TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGGAACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA  
CTATTATCGTTATGATTTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGGAAAGAAGAGAATTTGATGC  
TGCTGTTAATTCTGGAGAAGTGTGGTTTGTAAATTTTTACTCCCCAGGCTGTTCACTGCCATGATTTAGCTCC  
CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTTACTTCGAATTGGAGCTGTTAACTGTGGTGATGATAGAAT  
GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCAGTCTCTTCAATTTTTCGGTCTGGAATGGCCCCAGTGAAATA  
TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTACAGAACTTTG  
GACAGGAAATTTTGTCAACTCCATACAACTGCTTTTTGCTGCTGGTATTGGCTGGCTGATCACTTTTGTCTAAA  
AGGAGGAGATTGTTGACTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCAACTCATTGGATGCTAA  
AGAAATATATTTGGAAGTAATACATAATCTCCAGATTTTGAACACTTTTCGGCAAACACACTAGAGGATCGTTT  
GGCTCATCATCGGTGGCTGTTATTTTTTCAATTTTGGAAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAAACT  
AAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGAAGTCTCTCTGCACCAGACATCTGTAGTAA  
TCTGTATGTTTTTTCAGCCGCTCTCTAGCAGTATTTAAAGGACAAGGAACCAAAGAATATGAAATTCATCATGGAAA  
GAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAATTCATGTTACCACGCTTGGACCTCAAAA  
TTTTCTGCCAATGACAAAGAACCATGGCTGTTGATTTCTTTGCCCCCTGGTGTCCACCATGTCGAGCTTTACT  
ACCAGAGTTACGAAGAGCATCAAATCTCTTTATGGTCAGCTTAAGTTGGTACACTAGATTGTACAGTTCATGA  
GGGACTCTGTAACATGTATAACATTCAAGCTTATCCAACAACAGTGGTATTCAACCAGTCCAACATTCATGAGTA  
TGAAGGACATCACTCTGCTGAACAAATCTTGAGTTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC  
ACCCACCACCTTCAACGAAGTGTACACAAAGAAACACAAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTG  
GTGTCATCCTTGCCAAGTCTTAATGCCAGAATGAAAAGAATGGCCCGGACATTAAGTGGACTGATCAACGTGGG  
CAGTATAGATTGCCAACAGTATCATTCTTTTGTGCCAGGAAAACGTTCAAAGATACCCTGAGATAAGATTTTT  
TCCCCCAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATTCCTGAGAAT  
CTGGGGTCTAGGATTTTTTACCTCAAGTATCCACAGATCTAACCTCAGACTTTTCAAGTGAAGAAAGTTCTACAAGG  
GAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGTCTCGAATTTGAGCT  
CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAGTAGACTGTCAAGCTTATGCTCAGACATGCCAGAA  
AGCTGGGATCAGGGCTATCCAAGTTAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAAGAAGAGCA  
GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAGAAATTTGAAACTCTCCGAAATCAAGGCAA  
GAGGAATAAGGATGAACCTTGAATAATGTTGAAGATGAAGAAAAGTTTAAAGAAATTTCTGACAGATGACATCAG  
AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA  
GAATTATCTACAGCACTGGTGTAAGGAAGGGTCTGCAAACTTTTTCTGTAAGGGCGGTTTATAAATATTTTA  
GACTTTGCAGGCTATAATATATGGTTCACACATGAGAACAAGAATAGAGTCATCATGTATTCTTTGTTATTTGCT  
TTTAAACACCTTTAAAAAATATTTAAACGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCAAGTCCATG  
GACCATAGATTGCTGTCCCCCTCGACGACTTATAATGTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT  
ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTCACGTTTTTTGGCTGACCTGAAAAGAGGTAAGT  
TAGTTTTTGGTCACTTGTTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTCTGTTTTAAAAACACCCAT  
GATGTGGCACAGTAAACAAACCCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTTTTCTTTCTCTCA  
AAGGTTGAAAAAATGCTTTTAATTTTTTACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC  
AAATTTGAGCAACAGTAAGTGCACAAATCTGTAGTTTGTGCTGATCATCCAGGAAAACCTGAGGGAAAAAATTA  
TAGCAATTAAGTGGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA  
TGTGTTTCATGTATTTTCTGAAATTGCTTTTATAGAAATTTTCCCACTGATAGTTGATTTTTTGAAGCATCTAATAT  
TTACATATTTGCTTCTGAACTTTGTGTTGACCTGTATCCTTTATTTACATTGGGTTTTTCTTTTCAATGTTTTGG  
TTTTTCACTCTGTCCAGTCTATTTATTTCAATAGGAAATTAATTTTACAGGTTGTTTTTACTGTAGCTTAT  
AATGATACTGTAGTTATTTCCAGTTACTAGTTTACTGTGAGAGGGCTGCCTTTTTTCAAGATAAATATTGACATAATA  
ACTGAAGTTATTTTTATAAGAAATCAAGTATATAAATCTAGGAAAGGATCTTCTAGTTTCTGTGTTGTTTGA  
CTCAAAGAAATCAAAATTTGTGCTAAGTATGATGTTTGTGTTTATTAATTCAGAGTGTACAGAAATGGTAAAAAT  
CCAATCAGTCAAAGAGGTCAATGAATTTAAAGGCTTGCAACTTTTTTCAAAAAA

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**FIGURE 426**

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKLH  
PDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKLEDNQGGQYESWNYYRYDFGIYD  
DDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNCGDD  
RMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNSIQTA  
FAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSANTLEDR  
LAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQPSLAVFK  
GQGTKEYEIHGKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWCPPCRALL  
PELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHSAEQILEFT  
EDLMNPSVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMARTLTGLINVGS  
IDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLGFLPQVSTDLT  
PQTFSEKVLQGNHVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDCQAYAQTCQKAG  
IRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGKRNKDEL

**Important features:****Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

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**FIGURE 427**

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGCA  
CGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTCTCCCTCTTGA  
GTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTCGCGATGGTAG  
CGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTCAATT  
CCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTCTGCAG  
TCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACAACTACC  
AGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGTCCCACCC  
GCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCTGCAGGAAGCGCCGAAAACGCTGCATGC  
GTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTTCTGATCAAA  
ATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGATCATAGCACCT  
TGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAAAGGACAAGAAG  
GTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTAGACACTTCTGGT  
CCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCATAGGAGAAAAGGCT  
CTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTCTTGCCGGATACAGA  
AAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGAGACACTTAAACCAGCT  
ATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACCTTTTATGACCTTCATC  
AACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCATTCCAATAACACCTTCCA  
AAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCCTGTGATTGCAGTAAATTACT  
GTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGAACTTTTAATTATTTTTCT  
AAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTTTGTACACATTGATTGTTAT  
CTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATTTTCAGCTTATAGTTCTTAAAAG  
CATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCAAGGATCTCTTGGAATGACAAAT  
GATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATTTTCTGAAATGTACTATCTTAATG  
CTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGAATAAAATTTAACATTTAAAAAA  
AAAAAA

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**FIGURE 428**

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSAA  
PGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRCMRHAM  
CCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEGSVC  
LRSSDCASGLCCARHFWSKICKPVLKEGVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQKDDH  
QASNSSLHTCQRH

**Important features:****Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 256-259

**Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126



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**FIGURE 429**

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCCC  
TTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGACCC  
CAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCT  
CCTGGTAACTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGAATAT  
AGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGTCTGTTT  
CAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATTTCCAAA  
TGAAAATCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATA  
CAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATA  
CAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAGTGACCCCAT  
TCAAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAAATATCATTGG  
ATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCGAATATTTTGCA  
TGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAGATATAGTGGCGA  
CAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACTTGGGAGCTATGAC  
AAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTTGTCGAGAAATAAC  
ATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCATACTCTTTCACATGAA  
AGAAGATACAGAAAGTTTAGAAATATTCAGAATGAAGTAGCTCGGCAATTAATAAGTGAAAA  
AGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACATCCTCTTCTGCACATACA  
GAAAACCTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAGGCATATGTATGTGTTTGG  
AGACTTCAAAGATGTATTAATTCCTGGAAAACCTCAAGCAATTCGTATTTGACTTACATTCTGG  
AAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACCTGATACAGCCCCAGGAGAGCAAGC  
CCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAACTAGCACCCAGTGAATATAG  
GTATACTCTATTGAGGGATCGAGATGAGCTTTTAAAAACTTGAAAAACAGTTTGTAAGCCTTTC  
AACAGCAGCATCAACCTACGTGGTGAAATAGTAAACCTATATTTTCATAATTCTATGTGTAT  
TTTTATTTTGAATAAACAGAAAGAAATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAA

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**FIGURE 430**

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQM  
LHPIFEEASDVKEEFNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYRGQ  
RSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILHDDC  
AFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNW IQDKCVPLVREITFEN  
GEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLHIQKTP  
ADCPVIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDLHSGKLHREFHHGPDPTDTAPGEQAQDV  
ASSPPESSFQKLAPSEYRYTLLRDRDEL

**Important features:****Signal peptide:**

amino acids 1-29

**Endoplasmic reticulum targeting sequence.**

amino acids 403-406

**Tyrosine kinase phosphorylation site.**

amino acids 203-211

**Thioredoxin family proteins**

amino acids 50-66

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**FIGURE 431**

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGCA  
GGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCGTG  
CAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGCGTG  
GACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGCAGTG  
CGGGGTTGCGGTTGCGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGCTTCTG  
GCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTCACCTCG  
CGGGCGCTCGACCCGGCAGGTAATGAGAGTGATACCCGCCCAACGGCGTGGAGTGCTACAGC  
TGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCGTGAGCTGCTACAAC  
GCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCAGCTAATGTG  
ACTGTGTCCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGATGGAGTAACA  
GGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAACCTCTGACCTCCGC  
AACAAGACCTACTTCTCCCCTCGAATCCCACCCCTTGTCCGGCTGCCCCCTCCAGAGCCACG  
ACTGTGGCCTCAACCACATCTGTCACTTCTACCTCGGCCCCAGTGAGACCCACATCCACC  
ACCAAACCCATGCCAGCGCCAACCAAGTCAGACTCCGAGACAGGGAGTAGAACACGAGGCCTCC  
CGGGATGAGGAGCCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGACCGCAGCAATTCAGGG  
CAGTATCCTGCAAAAGGGGGGGCCCCAGCAGCCCCATAATAAAGGCTGTGTGGCTCCCACAGCT  
GGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTTCTGTGAGCTTCTCCACCTGGA  
AATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCTCATCACTTCTGTTCCCA  
CCACTGGACTGGGCTGGCCCAGCCCTGTTTTTCCAACATTCCCCAGTATCCCCAGCTTCTGC  
TGCGCTGGTTTGCGGCTTTGGGAAATAAAATACCGTTGTATATATTCTGCCAGGGGTGTTCTA  
GCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTCTCCGCTTGTCTCTTGTGATG  
TTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTGAGAGAGAGGATGCTAAGCTTCC  
TACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGGGGTGGGTGGGACAATGGCTCCCC  
ACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGGGAATCGGTTCCCCATATGTCTTCC  
TTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTACCCAATTCGCCCTATAGTGAGTCGTA

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**FIGURE 432**

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGV DVCTE  
AVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNALNLT SRALDP  
AGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGC FDGNVTLTAA NVTVSLP  
VRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRI PPLVRLPPPEPTTVAST  
TSVTTST SAPVRPTSTTKPMPAPTSQT PRQGV EHEASRDEEPRLTGGAAGHQDRS NSGQYPAK  
GGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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**FIGURE 433**

CGGGACTCGGCGGGTCTCCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCCATGGAGTT  
GGTGCTGGTCTTCTCCTCTGCAGCCTGCTGGCCCCATGGTCCTGGCCAGTGCAGCTGAAAAGGA  
GAAGGAAATGGACCCTTTTCATTATGATTACCAGACCCTGAGGATTGGGGGACTGGTGTTTCGC  
TGTGGTCTCTTCTCGGTGGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTTTCAA  
TCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCCAGGTGGAGAACCTCATCACCGCCAATGC  
AACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAACCTGAG  
GCGGCTGCTTGAACCTTTGGATGCAAATGTCGATGCTTAAGAAAACCGGCCACTTCAGCAACA  
GCCCTTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCTATCCCCTCTAACACCATT  
CCTCCACCTGATGATGCAACTAACACTTGCCTCCCCACTGCAGCCTGCGGTCTGCCCACCTC  
CCGTGATGTGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTGGTCTTTGTGG  
CTACTTGTTTGTGGATGGTATTGTGTTTGTAGTGAAGTGTGGACTCGCTTTCCAGGCAGGG  
GCTGAGCCACATGGCCATCTGCTCCTCCCTGCCCCGTGGCCCTCCATCACCTTCTGCTCCTA  
GGAGGCTGCTTGTTGCCCGAGACCAGCCCCCTCCCCTGATTTAGGGATGCGTAGGGTAAGAGC  
ACGGGCAGTGGTCTTCAGTCGTCTTGGGACCTGGGAAGGTTTGCAGCACTTTGTCATCATTCT  
TCATGGACTCCTTTCACTCCTTTAACAAAAACCTTGCTTCCTTATCCCACCTGATCCCAGTCT  
GAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCCCAGCGTTGACGTCAGG  
CAGGCTATGCCCTTCCGTGGTTAATTTCTTCCCAGGGGCTTCCACGAGGAGTCCCCATCTGCC  
CCGCCCCCTTCACAGAGCGCCCGGGGATTCCAGGCCAGGGCTTCTACTCTGCCCTGGGGAAT  
GTGTCCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGGGACCCTACCCCTTCCAACC  
TTCCCTGCTTCTGAGACTTCAATCTACAGCCCAGCTCATCCAGATGCAGACTACAGTCCCTGC  
AATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCCGTTGGGGCCAGCACACCGGGA  
TGATGGAGGGAGAGCAGAGGCCTTTGCTTCTCTGCCTACGTCCCCTTAGATGGGCAGCAGAG  
GCAACTCCCGCATCCTTTGCTCTGCCTGTCGGTGGTCAGAGCGGTGAGCGAGGTGGGTGGAG  
ACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAGGTTGAAGGTCATAACGAGAGTGGG  
AACTCAACCCAGATCCCGCCCCCTCCTGTCCTCTGTGTTCCCGCGGAAACCAACCAAACCGTGC  
GCTGTGACCCATTGCTGTTCTCTGTATCGTGATCTATCCTCAACAACAACAGAAAAAGGAAT  
AAAATATCCTTTGTTTCCT

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**FIGURE 434**

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKC  
SFNQKPRAPGDEEAQVENLITANATEPQKQRTÉVQPSGGSLWNLRRLLEPLDANVDA

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**FIGURE 435**

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC  
TGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA  
TCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT  
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAACTAA  
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG  
AGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCAA  
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG  
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA  
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA  
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA  
GTGCAGGAGCACCACTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCACAGCCACCACCC  
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATCTGAGGAGAGT  
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC  
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT  
CATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCTTTTGCCAACAATTTTA  
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA  
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTCTTTTGTGTTGGAAAA  
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAAATAATCACG  
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAGAATTTTAAATTATTTAAT  
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA  
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 436**

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFH  
YDCGNKTVTPVSPLGKKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS  
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD  
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI



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**FIGURE 437**

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACCATGAAGCTCTTGTGGCAGG  
TAACTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTACCTCACGGCGCAAGTGTGGATTCTGT  
GTGCAGCCATCGCTGTGCCGCCTCAGCCGGGCCCCAGAAGTCCCCCTCCGTTTGCTCGTGCAGTAACCAGTTCA  
GCAAGGTGGTGTGCACGCGCCGGGGCCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCGGTACCTCAACC  
TCATGGAGAACAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGCAGTTGG  
GCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCTTCAACGGCCTGGCCAGCCTCAACACCCTGGAGCTGTTG  
ACAAGTGGCTGACAGTCATCCCTAGCGGGGCCTTTGAATACCTGTCCAAGCTGCGGGAGCTCTGGCTTCGCAACA  
ACCCCATCGAAAGCATCCCCTCTTACGCCTTCAACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCA  
AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAAGGGCTGTTCAACCTCAAGTATCTGAAGTTGGGCATGTGCA  
ACATTAAAGACATGCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACTTCCCTG  
AGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTGAAGTACAGGTCAGCCTGA  
TTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAGTCAACTTGGCCCACAATAACCTCTCTCTTTG  
CCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGCATCTACACCACAACCCTTGGAAGTGTGATTGTG  
ACATTCTGTGGCTAGCCTGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTCATGCTC  
CCATGCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCTTCATCATGG  
ACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGTGGACTCCCCCTATGTCCTCCG  
TGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGCCTCCCGCCACCAAGGATCTCTGTCTCTCAACGACG  
GCACCTTGAAGTTTTCCACGTGCTGCTTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCA  
ACTCCAACGCCTCGGCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAAGTACAGCTTCTTCACCACAG  
TAACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTTCTTACCACGTCCACTG  
GTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTGAGACTACCCGTGTGCCCAAGCAGGTGGCAGTAC  
CCGCGACAGACACCACTGACAAGATGCAGACCAGCCTGGATGAAGTCATGAAGACCACCAAGATCATCATTGGCT  
GCTTTGTGGCAGTGACTCTGCTAGCTGCCGCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGC  
GGAGTACAGTCACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCGCAG  
CAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCACAATTGATGACCATATTAAGT  
ACAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAACAGCCTGGGGAACTCTCTGCACCCACAGTCA  
CCACTATCTCTGAACCTTATATAATTCAGACCCATACCAAGGACAAGGTACAGGAACTCAAATATGAAGTCCCCT  
CCCCCAAAAACTTATAAAATGCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTT  
TTCTTGATATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAACAGATTATATTAATTTAAAGACAAAA  
AGTCAAAACA

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**FIGURE 438**

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCTR  
RGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLASLN  
TLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEYISE  
GAFEGLFNLKYLNLMCNKIDMPNLTPLVGLLEELEMSGNHFPFIRPGSFHGLSSLKKLWVMNS  
QVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHPWNCDCDILWLAWWL  
REYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAELKCRTPP  
MSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTVNAGNSNASAYLNV  
STAEINTSNYSFFTTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQTTRVPKQV  
AVPATDTTDMQTSLEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRSTVTAARTVE  
IIQVDEDI PAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHW TENS LGNSLHPT  
VTTISEPYIIQHTKDKVQETQI

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**FIGURE 439**

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCTG  
TCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCTGC  
CCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTCCAA  
GTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTGCACC  
GATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATTAGTAAAAAAT  
GTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTCAACGACACCCTGATC  
TTCATAAAAAATTGTAAAGGTTTCAACAGTTGCTTTAATAAATCACTTGCCCTGC

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**FIGURE 440**

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNQLQVAKLNPPPEALAAKLEVK  
HCTDQISFKKRLSLKKSWWK

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**FIGURE 441**

GAACATTTT TAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGATG  
GGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCACC  
ACCTCCGCCAGGAACTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCCAGG  
GACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCTCCAG  
CTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAA  
GCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGAAGGGGC  
AGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGTCAGGGGT  
TCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGGGAAGAGGC  
CAAAGAGGCCCCAGCCGACAAGTGATCGCCCACAAGCCTTACTCACCTCTCTAAGTTTAGA  
AGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTACAAGCTCAGG  
AGGCGAATAAATGTTCAAACCTGTA

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**FIGURE 442**

MPSPGTVCSELLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGG  
QAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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**FIGURE 443**

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTCG  
TGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGTTT  
CTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTGCTC  
CTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCTGAGT  
ATGTCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATCTTACA  
CCTCTACTTGAGTATGTCCCTAACCCTGAGCCCCCAGCCTGGGGCCAGAGTCTTTGTCCCC  
CGTGTGCGCATGTGTTTCAAGGTTCAGCCTCTCCCAGAAGTGAGATCATGGACAAAAAGGGCAA  
TCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAACTCACGCCG  
AGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTCAGAGACAATGGA  
ATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTTCCAAAAACAC  
AAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTACCCACTAACCAACAACCTGAAG  
CGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTGAGTCATGTTGCT  
GAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGTAACAACAACCTCC  
CTGCTCCTGGCACCAGCCGTTTTTGGTCATGGTGGGCCAGCTGCAAAGCGTCTTCCATTCTCTG  
GGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGACACGGGCAGCAGAGTG  
TGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCAACCCCTGGTCAGGGCA  
GAGGGAGTTGGGTGGGTTCAGGCTCTGGGCTCACCTCCATCTCCAGAGCATCCCCTGCCTGCAG  
TTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGAGCCTCCTTGTTCATAACC  
ACAGGTTACCCTACAAACCACTGTCCCCACACAACCCTGGGGATGTTTTAAACACACACCTC  
TAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGAATTTTTTTTAAATGAAAGTGC  
AATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAA

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**FIGURE 444**

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLS PRSPQGWV  
VRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQAQ  
QEAELTTPRPAGVVPGA



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**FIGURE 445**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGAAGTGGCCTCACAACCTGC  
TGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAAGA  
GGAAGGGGCAAGGGCGGCCTGGGCCCCTGGCCCCTGGCCCCTCACCAGGTGCCACTGGACCTGG  
TGTCACGGATGAAACCGTATGCCCCGATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGG  
CCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCTGTGGA  
TGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCCGTATCC  
CCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACCATGCAGG  
AGGACCGCAGCATGGTGAGCGTGCCGGTGTTACGCCAGGTTTCCTGTGCGCCGCCGCCTCTGCC  
CGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCT  
GCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCCGAGACCATCCTCCT  
TGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAG

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**FIGURE 446**

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEYE  
RNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCLGC  
VNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 75-78

**Homologous region to IL-17**

amino acids 96-180.

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**FIGURE 447**

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAGA  
TGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCTAT  
CACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGGTGC  
CCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTGGATG  
GAGATACCAACACATCCACCCAGGAGGTGGTACAATACTGGGAGACTGGGGATGACCGGT  
TCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAGAACCAG  
GGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAAGGACTAC  
TGGAAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAAGCGGTTGA  
TGGAGAAGGCTTCCCTCCCCCTCCCCTCCCCTTGGGGCTTTGTGGCAAAAATCCTATGGTTATCC  
CTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCTACTAACAGAC  
TTGCTACTCACTGGGAACCCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTGCTGTTTCCTCT  
GTCCTGTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTCTTCCAAGCGACT  
GTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAATTATGGCTGGGCCTTCTACATG  
GCCTGGCTCTCCTTCACCTGCTGCATGGCGTGGGCTGTCAACCACCTTCAACACGTACACCAGG  
ATGGTGCTGGAGTTCAAGTGCAAGCATAGTAAGAGCTTCAAGGAAAACCCGAACCTGCCTACCA  
CATCACCATCAGTGTTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCCACCCTGGGTCTTTGACC  
AGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGGGAGTCGACTTCTACTCC  
GAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTGAAAGAAGCAGTTAGGTCA  
TCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGAGTAGGCTTGAGCCCTACCT  
TACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCGTCTCTTGAGCATGGTTTTTA  
GAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTCCTAAGGGATTCTGGGTGCCA  
CTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTACCCACCCACATCTCACACATCCAGAA  
TTCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGCTAAACCATGGAGATAAAAAGAAG  
AGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

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**FIGURE 448**

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMPV  
SLDGD TNTSTQEVVQYNWETGDDRF SFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKRGE  
KGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQ LPPA  
TNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRL ETTCLELWLG  
LLHGLALLHLLHGVGCHHLQH VHQDGAGVQVQA

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**FIGURE 449**

CCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCC  
ACGCGTCCGGTGCAGCTCGCGCCGACACTGCCTGGTGGAGGGAAGGAGCCCGGGCGCCTCTCGCCGCTCCCG  
CGCCGCGCTCCGCACCTCCCCACCGCCCGCCGCCCGCCCGCCGCGCCGCAAAGCATGAGTGAGCCCGCTCTCT  
GCAGCTGCCCGGGGCGGAATGGCAGGCTGTTTCGCGGGAGTAAAAGGTGGCGCCGGTCACTGGTCTGTTTCAAT  
GACGGACATTAACCACTGTGAGATCCTGGGGAGTCGCGAGCCCCAGTTTGGAGTTTTTCCCCCACAACGT  
CACAGTCCGAACCTGCAGAGGGAAGGAAGGCGGCAGGAAGGCGAAGCTCGGGCTCCGGCACGTAGTTGGGAACT  
TGCGGGTCTAGAACTCGCCTCCCCGCTTGCCGCGCGCCCTTGACGCCCGGAGCCGAGCAGCAAAGTGAGACAT  
TGTGCGCCTGCCAGATCCGCGCGCGCGGACCGGGCTGCCTCGGAAACACAGAGGGGTCTTCTCTCGCCCTGCA  
TATAATTAGCCTGCACACAAAGGGAGCAGCTGAATGGAGTTGTCACTCTCTGAAAAGGATTTCTGACCGAGCG  
CTTCCAATGGACATTCTCCAGTCTCTCTGAAAAGATTCTCGTAATGGATTCTCTGCTGCTCGGTCTCTGTCTAT  
ACTGGCTGCTGAGGAGGCCCTCGGGGGTGGTCTTGTGTCTGCTGGGGGCTGCTTTCAGATGCTGCCCGCCGCC  
CCAGCGGGTGCCTGAGCTGTGCGGGTGCAGGGGCGGCTGCTGTACTGCGAGGCGCTCAACCTCACCGAGGCGC  
CCCACAACCTGTCCGCTGCTGGGCTTGTCCCTGCGCTACAACAGCCTCTCGGAGCTGCGCGCCGCGGCTGCA  
CGGGTTAATGCACTGACGTGGCTCTATCTGGATCAACATCACTCTGCTCCGTGCAGGGGACGCTTTTACA  
AACTGCGCGGAGTTAAGGAACCTCACGCTGAGTTCCAACAGATCACCAACTGCCAACACACCTTCCGGCCCA  
TGCCCAACCTGCGCAGCGTGGACCTCTCGTACAACAGCTGCAGGCGCTCGCGCCGACCTCTTCCAGGGCTGC  
GGAAGCTCACACGCTGCATATGCGGGCAACGCCATCCAGTTTGTGCGCGTGCAGATCTTCCAGGACTGCCGCA  
GCCTCAAGTTTCTCGACATCGGATACAATCAGCTCAAGAGTCTGGCGCGCAACTCTTTCGCGGGCTTGTTTAAGC  
TCACCGAGCTGCACCTCGAGCACAACGACTTGGTCAAGGTGAACCTTCGCCCACTTCCCGCGCCTCATCTCCCTGC  
ACTCGCTCTGCCTGCGGAGGAACAAGGTGGCCATTGTGTGCTGAGCTCGCTGGACTGGGTTTGGAACCTGGAGAAA  
TGGACTTGTGCGGCAACGAGATCGAGTACATGGAGCCCCATGTGTTGAGACCGTGCCGCACCTGCAGTCCCTGC  
AGCTGGACTCCAACGCTCACCTACATCGAGCCCGGATCCTCAACTCTTGAAGTCCCTGACAAGCATCACCC  
TGGCCGGAACCTGTGGGATTGCGGGCGCAACGTGTGTGCCCTAGCCTCGTGGCTCAGCAACTTCCAGGGGCGCT  
ACGATGGCAACTTGAGTGCCTGCGCCAGCCCGGAGTACGCACAGGGCGAGGACCTCTGGACGCGCTGTACGCTTCC  
ACCTGTGCGAGGATGGGGCGGAGCCACAGCGGCCACCTGCTCTCGGCCGTCAACACCGCAGTGATCTGGGGC  
CCCTGCCAGCTCGGCCACACGCTCGCGGACGGCGGGGAGGGGAGCAGCAGCGGCACATTCCAGCCTGCCACCG  
TGGCTCTTCCAGGCGCGAGCAGCGCGAGAAGCGCTGCAGATCCACAAGGTGGTACGGGCACCATGGCCCTCA  
TCTTCTCCTTCTCATCGTGGTCTCTGCTGTCTACGTGTCTGGAAGTGTTCACAGCCAGCCTCAGGCAGCTCA  
GACAGTGCTTTGTACGCGAGCGCAGGAAGCAAAAGCAGAAACAGACCATGCATCAGATGGCTGCCATGTCTGCC  
AGGAATACTACGTTGATTACAAACCGAACCACATTGAGGGAGCCCTGGTGATCATCAACGAGTATGGCTCGTGT  
CCTGCCACAGCAGCCCGGAGGGAATGCGAGGTGTGATTGTCCCAGTGGCTCTCAACCCATGCGCTACCAATA  
CGCTGGGACGCGCGGACCGGCGGCGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  
TGAAACTTTAAGGGGATCTCTCCAGAGACTTGACATTTTAGCTTTATTGTCTTAAACAAAGCGAATTAA  
AACACAACAAAAACCCCAACCTTCCAGGACAGTCTATCTTAAATTTTCAATGAGAACTCCTTCTCTCC  
TTTGAAGATCTGTCCATATTGAGGAATCTGAGAGTGTAAAAAAGGTGGCCATAAGACAGAGAGAGAATAATCGTG  
CTTTGTTTTATGCTACTCCTCCACCTGCCCCATGATTAAACATCATGTATGTAGAAGATCTTAAGTCCATACGC  
ATTTTATGAAGAACCATTGGAAGAGGAATCTGCAATCTGGGAGCTTAAGAGCAATGATGACCATAGAAAGCTA  
TGTTCTTACTTTGT  
AACGGGAATTTAGCTCACATCATTTTATGCCCCCTGTGCTCTAGCTCTGGAGATTGGTGGGGGGAGGTGGGGGA  
AACGGCAGGAATAAGGGAAAGTGGTAGTTTTAACTAAGGTTTTGTAACTTGAATCTTTTCTTCTCAAATTA  
ATTATCTTTAAGCTTCAAGAACTTGCTCTGACCCCTCTAAGCAAACTACTAAGCATTTAAAGAGAATCTAATT  
TTTAAAGGTGTAGACCTTTTTTTTTTATTCTTCCACAGAGGGTGCTAATCTCATTATGCTGTGCTATCTGAAA  
GACTTAAAGGCCAATTCAGGTCTCGTCTGGGATTTGTGATGGATTGACCTCCATTGTCAGTACCTTCCAG  
TGATTAAAGTTACGAGTGGTATTGAGGTTTTTCGAATATTTATATAGAAAAAAGTCTTTTACATGACAAAT  
GACACTCTCACACAGCTCTTAGCCCTAGTAGTTTTTTAGGTGGACCAGAGGAAGCAGGTTAAATGAGACCTGTC  
CTCTGCTGCACCTAGAAAAAATAGGCAGTCCCTGATGCTCAGATCTTAGCCTTGATATTAATAGTTGAGACCAC  
TACCCACAACCTGAGCTTACTCCCAAGACTACAAAGTTACCATCGCAAAGGAAAGGTTATTCCAGTAAAGGAA  
ATAGTTTTCTCAACCATTTAAAAATATTCTTCTGAACATCAAGTAGAAGAGCCCCAACCTTTTCTCTGTC  
CTTCAAGAAGGCAGACATTTGGTATGATTTAGCATCAACAACACATTTATGAGTATATGTAAGTAATCAGAGGG  
CAAATGCCACTTGTATTCTCTCCAAAGTTTTCCAAGCAAGTACACACAGATCTCTGGTAGGATTAGGGGCCACTT  
GTGTTTCCGGCTTATTTTAGTGCAGTTGTGACGAAGTTTGTATGCTAGTCTATCTGACATGGCCAGTAGAACAG  
GGCATTGATGGATCAGATGAGATGGTAGAAGGAACATCATCACATACCCCTCTCACAGAGAAAAATTATCAAAGAA  
CCAGAAATTATATCTGTTTTGGAGCAAGAGTGTCAATGTTTTAGGGTAGTCAAAATAAACATAAATTATCTCC  
TCTAGATGAGTGGCGATGTTGGCTGATTTGGGTCTGCCATTGACAGAATGTCAAATAAAAGGAATTAGCTAGAA  
TATGACCATTAATGTCTTCTGAAATATATTTGAGATAGGTTTAGAATGTCA

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**FIGURE 450**

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPHN  
LSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQIT  
QLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRI FQDCRSLKF  
LDIGYNQLKSLARNSFAGL FKLTELHLEHNDLVKVNFAHFPR LISLHSLCLRRNKVAIVVSSL  
DWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKS LTSITLAGNL  
WDCGRNV CALASWLSNFQGRYDGNLQ CASPEYAQGEDVLD AVYAFHLCEDGA EPTSGHLLSAV  
TNRSDLGPPASSATT LADGGEGQHDGT FEPATVALPGGEHAENAVQIHKVVTGT MALIFSFLI  
VVLVLYVSWKCFPASLRQLRQCFVTORRKQKQKQTMHQAAMSAQEYYVDYKPNHIEGALV I I  
NEYG SCTCHQQPARECEV

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**FIGURE 451**

TTGAGCGCAGGTGAGCTCCTGCGCGTTCGGGGGCGTTCCTCCAGTCACCCTCCCGCCGTTAC  
CCGCGGCGCGCCCCGAGGGAGTCTCCTCCAGACCCTCCCTCCCGTTGCTCCAAACTAATACGGA  
CTGAACGGATCGCTGCGAGGGTGGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACT  
ACCATCCATAGCCAGATAGATTATCTTACACTGAACTGATCAAGTACTTTGAAAATGAACTTCG  
AAATTTATCTTGGTGTCTTCATACTTGCTGCACTGAGTCTTTCAACCACCTTTTCTCTCCAA  
CTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACTTATATAAA  
GTTCCAACGCCCCATTTTCATTATATTATGAAATATGGTGTTCACGTGAAGCAAGTTACTAAT  
GTTTTTATTACAAAACCTACCCTAACCATTAATCTTTGGTAACTGGCCTCTTTGCAGAGAAT  
CATGGGATTGTTGCAAAATGATATGTTTGATCCTATTTCGGAACAAATCTTCTCCTTGGATCAC  
ATGAATATTTATGATTCCAAGTTTTGGGAAGAAGCGACACCAATATGGATCACAAACCAGAGG  
GCAGGACATACTAGTGGTGCAGCCATGTGGCCCCGGAACAGATGTAAAAATACATAAGCGCTTT  
CCTACTCATTACATGCCCTTACAATGAGTCAGTTTCATTTGAAGATAGAGTTGCCAAAATTGTT  
GAATGGTTTACGTCAAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCCTGATGAC  
ATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCATTTGAGATATTGACAAG  
AAGTTAGGATATCTCATACAAATGCTGAAAAAGGCAAAGTTGTGGAACACTCTGAACCTAATC  
ATCACAAGTGATCATGGAATGACGCGAGTGTCTGAGGAAAGGTTAATAGAAGTTGACCAGTAC  
CTGGATAAAGACCACTATACCCTGATTGATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAA  
GGTAAATTTGATGAAGTCTATGAAGCACTAACTCACGCTCATCCTAATCTTACTGTTTACAAA  
AAAGAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTCAACCAATCATAGCA  
GTGGCTGATGAAGGTGGCACATTTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACCAC  
GGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTTAGCCCATGGTCTCTGCCTTCAGA  
AAGAATTTCTCAAAAGAAGCCATGAACTCCACAGATTTGTACCCACTACTATGCCACCTCCTC  
AATATCACTGCCATGCCACACAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTCAGCA  
ATGCCAAGGGTGGTCCCTTATACACAGAGTACTATACTCCTCCCTGGTAGTGTTAAACCAGCA  
GAATATGACCAAGAGGGGTACATACCCTTATTTCATAGGGGTCTCTCTTGGCAGCATTATAGTG  
ATTGTATTTTTTTGTAATTTTCATTAAAGCATTAAATTCACAGTCAATACCTGCCTTACAAGAT  
ATGCATGCTGAAATAGCTCAACCATTATTACAAGCCTAATGTTACTTTGAAGTGGATTGTCAT  
ATTGAAGTGGAGATTCCATAATTATGTCAGTGTTTAAAGGTTTCAAATCTGGGAAACCAGTT  
CCAAACATCTGCAGAAACCATTAAAGCAGTTACATATTTAGGTATACACACACACACACACA  
CACATACACACACACGGACCAAAATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGT  
CTCCATTGTTCACTGTAGCATAGGGATAGATAAGATCCTGCTTTATTTGGACTTGGCGCAGAT  
AATGTATATATTTAGCAACTTTGCACTATGTAAAGTACCTTATATATTGCACTTTAAATTTCT  
CTCCTGATGGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGTCTTATAACTTGATTG  
AAAATGACAACTTTTTGCACCCATGTCACAGAATACTTGTTACGCATTGTTCAAACCTGAAGGA  
AATTTCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAA  
GGTGATAAGTGTGAAAATTAAATGTGATAACCTTTGAACCTTGAATTTGGAGATGTATTCC  
CAACAGCAGAATGCAACTGTGGGCATTTCTTGTCTTATTTCTTTCCAGAGAACGTGGTTTTCA  
TTTATTTTTTCCCTCAAAAGAGAGTCAAATACTGACAGATTCGTTCTAAATATATTGTTTCTGT  
CATAAAATTATTGTGATTTCTGATGAGTCATATTACTGTGATTTTCATAATAATGAAGACAC  
CATGAATATACTTTTTCTTCTATATAGTTTACGAATGGCCTGAATAGAAGCAACCAGGCACCAT  
CTCAGCAATGTTTTCTTCTTGTGTTGTAATTATTTGCTCCTTTGAAAATTAAATCACTATTAATT  
ACATTAAAAATCAAATTGGATAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 452**

MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVHVKQ  
VTNVFITKTPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIWIT  
NQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLYWED  
PDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEERLIEL  
DQYLDKDHYTLDQSPVAAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYNSRIQP  
IIA VADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTDLYPLLC  
HLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPPYFIGVSLGS  
IIVIVFFVIFIKHLSQIPALQDMHAEIAQPLLQA

**Important features:****Signal Peptide:**

amino acids 1-22

**Transmembrane Domain:**

amino acids 429-452

**N-glycosylation sites:**amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372,  
382-385, 389-392**Somatomedin B Domain:**

amino acids 69-85

**Sulfatase protein Region:**

amino acids 212-241



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**FIGURE 453**

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGAC  
**TATGG**CTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTGCT  
GATGGCCGCCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGACCAA  
CCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAAGCCGAGGAGGAGCTGGA  
TGCCGAAGTCCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGGCAGGC  
TGTCCCTGCAGGATCCCACGTACGGCTGAATCTTCAGACTGGGGAAAGAGAGGCCAAAACCTCCA  
ATATGAGGACAAGTTCCGAAATAATTTGAAAGGCCAAAAGGCTGGATATCAACACCAACACCTA  
CACATCTCAGGATCTCAAGAGTGCCTGGCAAAATTCAGGAGGGGGCAGAGATGGAGAGTTC  
AAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAGCGGCTCTTCCGCCCCATTGAGGAACTGAA  
GAAAGACTTTGATGAGCTGAATGTTGTCATTGAGACTGACATGCAGATCATGGTACGGCTGAT  
CAACAAGTTCAATAGTTCCAGCTCCAGTTTGGAAAGAGAAGATTGCTGCGCTCTTTGATCTTGA  
ATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGGTCTTCAAGTGGT  
GATCAATGGGCTGAACAGCACAGAGCCCCTCGTGAAGGAGTATGCTGCGTTTGTGCTGGGCGC  
TGCCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGAGCCCTGCAGAAGCT  
GCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGTCCTGTTTGCCTGTG  
CTCCCTGCTGCGCCACTTCCCCTATGCCAGCGGCAGTTTCTGAAGCTCGGGGGGCTGCAGGT  
CCTGAGGACCCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTGCGCGTGGTCACACTGCT  
CTACGACCTGGTCACGGAGAAGATGTTGCGCGAGGAGGAGGCTGAGCTGACCCAGGAGATGTC  
CCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAGGCCTGTGGGAACAGGGCTG  
GTGCGAGATCACGGCCCACCTCCTGGCGCTGCCCGAGCATGATGCCCGTGAGAAGGTGCTGCA  
GACACTGGGCGTCCTCCTGACCACCTGCCGGGACCGCTACCGTCAGGACCCCCAGCTCGGCAG  
GACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCAGCCTGGAGCTGCAGGATGGTGA  
GGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAACAGCTTGCTGAAGGAGCTGAGAT**TG**  
**AGG**CCCCACACCAGGACTGGACTGGGATGCCGCTAGTGAGGCTGAGGGGTGCCAGCGTGGGTG  
GGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCTTGGCCATTAAATGGAAACCTGAAGG  
CCAAA  
AAA

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**FIGURE 454**

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEELD  
AEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTY  
TSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMVRLI  
NKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYA AFVLGA  
AFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKLGGLQV  
LRTLQVEKGT EVLAVRVVTLTYDLVTEKMFAEEEAELTQEMSPEKLQQYRQVHLLPGLWEQGW  
CEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE  
DEGYFQELLGSVNSLLKELR

**Important features:****Signal peptide:**

amino acids 1-29

**Hypothetical YJL126w/YLR351c/yhcX family protein.**

amino acids 364-373

**N-glycosylation site.**

amino acids 193-197, 236-240

**N-myristoylation site.**

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

**Homologous region SLS1 protein.**

amino acids 68-340

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**FIGURE 455**

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAGT  
GGCCAGGAAGGCACAGGCCTGAGAAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCCACCCTTA  
CCTGGGGGACAGGGCAAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGGTGT  
CTGTGCGTCTTGACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCTAGAC  
TCCTATCTTCTGAATTCTATAGTGCCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCCGTCCTTG  
TGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCCCCTGGA  
TGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTTCTCGCCA  
ACAATGATGTTTCCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCAGGACCTGG  
GAGCTGGGGCCGGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCAATGGATCCG  
ACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAACCAGCTCTACT  
GCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCCCTGCAGGAAGAAAGTTT  
TCAGAGTCCGTCTCGGCCACTACTCCCTGTCACCAGTTTATGAATCTGGGCAGCAGATGTTCC  
AGGGGGTCAAATCCATCCCCCACCCTGGCTACTCCCACCCTGGCCACTCTAACGACCTCATGC  
TCATCAAACCTGAACAGAAGAATTCGTCCCACTAAAGATGTCAGACCCATCAACGTCTCCTCTC  
ATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAACCAAGAGCCCCCAAG  
TGCATTCCCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGTCAGAAAAGGTGCGAGG  
ATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGACAAAGCAGGTAGAGACT  
CCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCTCT  
GGGAGATTACCCTTGTGCCCCGCCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTCA  
CCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCATCCCAGGACTCAGCACACCGG  
CATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAGACCCTCATTCTTCCCAGAGA  
TGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCTCCTGGACTCAGGGTCTGCTTCC  
CCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCTGGGAACAATTTCCAAAAGTGTCCAG  
GGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGCTCAGGGCCCATCCCTT  
CTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGAAGTGGAAAAAAAAA

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**FIGURE 456**

MATARPPWMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDDS  
SSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLSPV  
YESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCP SAGTKCLVSG  
WGTTKSPQVHFPKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSCQGDSGGPVVCN  
GSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

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**FIGURE 457**

GCAGTCAGAGACTTCCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTTGCTTCCTGAACT  
AGCTCACAGTAGCCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCACCCTGTAGGAATCCAGATGCAGG  
CCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTG  
CCACAACTCGGCATCCAGAGCCCCGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGA  
CCCTGCTGACTTTGTGCTTGGTGTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACCAGC  
TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGTTGCAATCTC  
TTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAACTCTGTGCTGAGCTGTATAACA  
AAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATA  
AAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTGCCTTAGTGAAACTCTACCATGCTGAAGATAAACAAAC  
AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGGCC  
CTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCCATATTATAATAGATG  
TCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGA  
AGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCG  
AAGGTGACTGATTGCCCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAG  
ACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAATGGGTCTCGTGTTCCTGTT  
CAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAAGCTCACAAGAAGTCTTATTTACATGCCAC  
CAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAA  
TGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGGAAATAAGAACTTTTTGAAGTAGAGGAAA  
TACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTCCCAGATTGTAC  
CAGCAAATACACAAGGAATTCCTTTTGTGTTTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCC  
CATCTGCCTTGTCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA  
GCATTCCCTTCTGTGTCATTAAAGACTCTGATAATTGTCTCCCTCCATAGGAATTTCTCCCAGGAAAGAAATAT  
ATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCTTCAGAGAGATTAAAGACCAGAAAAAGT  
GAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAGGT  
ACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

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**FIGURE 458**

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLI  
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY  
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY  
SEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEL  
KRCVCERRAGMVKPESLHVPPETLGEGD

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**FIGURE 459**

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCCAC  
TGGCGGCCCCGCAACACTCCGTCTCACCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCTGT  
GAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGTGGT  
CAGCTGGGTCAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAGGGAA  
GTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCTTCACCTGGACAGGATGA  
GAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGATGTTTA  
TTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCAGCCTCGC  
CCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCAGCCAACT  
ACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCTGGGCCCTACTATGTGCTTTGAAG  
ACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATCGCCCTGGTGA  
ATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGGAGATGTTATGC  
ACCTAGTGAAATTCTTAAAGAAATTCCGGGGGGTGCCTGGTGTGGTGGCCTCCTACGACG  
ATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTGGGGAGTTCTTACG  
CAAAACAACCTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGACCTCAGGGGTAAAA  
GCCCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAATAACGAGGGATGGCCAGAGC  
TGCTGGAGATGGAGGGCTGCATGCCCCCGAAGCCATTTTAGGGTGGCTGTGGCTCTTCCTCAG  
CCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCGGCAGGGGCTGAGGAGGA  
GGAGCAGGGGGTGTGCTGCGTGGAAGGTGCTGCAGGTCCTTGACGCTGTGTGCGCCTCTCCTC  
CTCGGAAACAGAACCCTCCCACAGCACATCCTACCGGAAGACCAGCCTCAGAGGGTCCTTCT  
GGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGGACTGCTGACGGCTGGTCCTG  
AGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTATTTTGTGGTTTTGAAAAAA  
AAAAAAAAAAAAA

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**FIGURE 460**

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCPA  
NYFAFKICSGAANVVGPPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSGDV  
MHLVKFLKEIPGGALVLVASYDDPGTKMNDESRLKLFSDLGSSYAKQLGFRDSWVFIGAKDLRG  
KSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

**Important features:****Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110



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**FIGURE 461**

AAACTCAGCACTTGCCGGAGTGGCTCATTTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGGA  
AACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCCTC  
TAGAACCCGACCCACCACCATGAGGTCTTGCCTGTGGAGATGCAGGCACCTGAGCCAAGGCGT  
CCAGTGGTCTTGCTTCTGGCTGTCTGGTCTTCTTTCTCTTCGCCTTGCCCTCTTTTATTAA  
GGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCTCTACA  
GTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTATGCAGA  
GCCAGCGCCAGAGAACAAATGCCCTCAACACACAAACCCAGCCCAAGGCCCACACCACCGGAGA  
CAGAGGAAAGGAGGCCAACCAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCACACAGCACA  
GAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAAAACCATGGTGAACACACTGTCACCCAGAGG  
GCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCCAGGACACAAA  
GACGACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACGGTGTGAGAGAA  
GCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTCCCAAAAGTCAGCACAGAATGCT  
GGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCACAGCAGTCATCCC  
ACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCCCTGCCCCCTTCCAGAGCCCCACGACGCA  
GAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTGGGATTTTGAGGAAAA  
ATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGCCCTGACTCTGTGAAGATCAAAGCCTC  
CAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCCAACCTCACTCTCTTCCCTGGACTCCAGACA  
CTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACCCTTTGGCTTCATGGAGCT  
CAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAGTGCCCCAGCAGCAGCTGCT  
CCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGTGCCGTGGTGGGCAACGGGGG  
CATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCACGACTACGTGTTCCGATTGAG  
CGGAGCTCTCATTAAGGCTACGAACAGGATGTGGGGACTCGGACATCCTTCTACGGCTTTAC  
CGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAATCGGGGTTTCAAGAACGTGCCTCT  
TGGGAAGGACGTCCGCTACTTGCACTTCCTGGAAGGCACCCGGGACTATGAGTGGCTGGAAGC  
ACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTTTCTGGTTCAGGCACAGACCCAGGA  
AGCTTTTCCGGGAAGCCCTGCACATGGACAGGTACCTGTTGCTGCACCCAGACTTTTCTCCGATA  
CATGAAGAACAGGTTTCTGAGGTCTAAGACCCTGGATGGTGCCCACTGGAGGATATACCGCCC  
CACCCTGGGGCCCTCCTGCTGCTCACTGCCCTTCAGCTCTGTGACCAGGTGAGTGCTTATGG  
CTTCATCACTGAGGGCCATGAGCGCTTTTCTGATCACTACTATGATACATCATGGAAGCGGCT  
GATCTTTTACATAAACCATGACTTCAAGCTGGAGAGAGAAGTCTGGAAGCGGCTACACGATGA  
AGGGATAATCCGGCTGTACCAGCGTCCTGGTCCCGGAACTGCCAAAGCCAAGAACTGACCGGG  
GCCAGGGCTGCCATGGTCTCCTTGCTGCTCCAAGGCACAGGATACAGTGGGAATCTTGAGAC  
TCTTTGGCCATTTCCCATGGCTCAGACTAAGCTCCAAGCCCTTCAGGAGTTCCAAGGGAACAC  
TTGAACCATGGACAAGACTCTCTCAAGATGGCAAATGGCTAATTGAGGTCTGAAGTTCTTCA  
GTACATTGCTGTAGGTCTTGAGGCCAGGGATTTTAAATTAAATGGGGTGATGGGTGGCCAATA  
CCACAATTCTGCTGAAAAACACTCTTCCAGTCCAAAAGCTTCTTGATACAGAAAAAAGAGCC  
TGGATTTACAGAAACATATAGATCTGGTTTGAATTCCAGATCGAGTTTACAGTTGTGAAATCT  
TGAAGGTATTACTTAACTTCACTACAGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTC  
TAGAAGGTCTATACTTGTCTTGTCTTAAAGCTATTTGACAACTCTACGTGTTGTAGAAAAC  
TGATAATAATACAAATGATTGTTGTCCATGGAAAGGCAAATAAATTTTCTACAGTGAAAAAAA  
AAAAAAA

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**FIGURE 462**

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKPK  
SQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAWKS  
PEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGGQTRKLTASRTVSEKHQGKAA  
TTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIPPEKKPQATPPPAPFQSPTTQRNQRK  
AANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHFNQSEW  
DRLEHFAPPFGFMELNYSLVQKVVTFRPPVPQQQLLASLPAGSLRCITCAVVGNGGILNNSH  
MGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATFSLTQSLILGNRGFKNVPLGKD VRY  
LHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLLHPDFLRYMKNRFL  
RSKTL DGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSWKRLIFYINH  
DFKLEREVWKRLHDEGIIRLYQRP GPGTAKAKN

**Important features:****Cytoplasmic Domain:**

amino acids 1-10

**Type II Transmembrane Domain:**

amino acids 11-35

**Lumenal catalytic Domain:**

amino acids 36-600

**Ribonucleotide Reductase small subunit Signature:**

amino acids 481-496

**N-glycosylation Sites:**

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

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**FIGURE 463**

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGGCGCAAGGGTGAGGGCGGCCCCAGAAC  
CCCAGGTAGGTAGAGCAAGAAGATGGTGTCTTCTGCCCCCTCAAATGGTCCCTTGCAACCATGTC  
ATTTCTACTTTCCTCACTGTTGGCTCTCTTAACCTGTGTCCACTCCTTCATGGTGTGAGAGCAC  
TGAAGCATCTCCAAAACGTAGTGATGGGACACCATTTCCTTGGAATAAAATACGACTTCCTGA  
GTACGTCATCCCAGTTCATTATGATCTCTTGATCCATGCAAACCTTACCACGCTGACCTTCTG  
GGGAACCACGAAAGTAGAAATCACAGCCAGTCAGCCCACCAGCACCATCATCCTGCATAGTCA  
CCACCTGCAGATATCTAGGGCCACCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGGAAGAACC  
CCTGCAGGTCCCTGGAACACCCCCCTCAGGAGCAAATTGCACTGCTGGCTCCCCGAGCCCCCTCT  
TGTCGGGCTCCCGTACACAGTTGTCACTTACTATGCTGGCAATCTTTCGGAGACTTTCACGG  
ATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAAGTGGGATACTAGCATCAACACAATT  
TGAACCCACTGCAGCTAGAATGGCCTTTCCTGCTTTGATGAACCTGCCTTCAAAGCAAGTTT  
CTCAATCAAATTAGAAGAGAGCCAAGGCACCTAGCCATCTCCAATATGCCATTGGTGAAATC  
TGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTTGATGTCACTGTGAAGATGAGCACCTA  
TCTGGTGGCCTTCATCATTTTCAGATTTTGAGTCTGTGCAAGATAACCAAGAGTGGAGTCAA  
GTTTTCTGTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGCACTGGATGCTGCGGT  
GACTCTTCTAGAATTTTATGAGGATTATTTTCAGCATACCGTATCCCCCTACCCAAACAAGATCT  
TGCTGCTATTTCCGACTTTCAGTCTGGTGTATGGAAAACCTGGGACTGACAACATATAGAGA  
ATCTGCTCTGTTGTTTATGATAAGGGAGCTTCTTGCATCAAGTAAGCTTGGCATCACAGTGAC  
TGTGGCCCATGAAGTGGCCACCAGTGGTTTGGGAACCTGGTCACTATGGAATGGTGGATGA  
TCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTGTCTGTGAGTGTGACCCATCC  
TGAAGTGAAGTTGGAGATTATTTCTTTGGCAAATGTTTTGACGCAATGGAGGTAGATGCTTT  
AAATTCCTCACACCCTGTGTCTACACCTGTGAAAATCCTGCTCAGATCCGGGAGATGTTTGA  
TGATGTTTTCTTATGATAAGGGAGCTTGTATTCTGAATATGCTAAGGGAGTATCTTAGCGTGA  
CGCATTTAAAAGTGGTATTGTACAGTATCTCCAGAAGCATAGCTATAAAAATACAAAAACGA  
GGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAGATGGTGTAAAAGGGATGGATGGCTT  
TTGCTCTAGAAGTCAACATTCATCTTCATCCTCACATTGGCATCAGGAAGGGGTGGATGTGAA  
AACCATGATGAACACTTGGACACTGCAGAGGGGTTTTCCCTAATAACCATCACAGTGAAGGG  
GAGGAATGTACATGAAGCAAGAGCACTAGATGAAGGGCTCTGACGGCGCCCGGAGTGG  
GTACCTGTGGCATGTTCCATTGACATTCATCACCAGCAAATCCAACATGGTCCATCGATTTTT  
GCTAAAACAAAAACAGATGTGCTCATCCTCCCAGAAGAGGTGGAATGGATCAAATTTAATGT  
GGGCATGAATGGCTATTACATTGTGCATTACGAGGATGATGGATGGGACTCTTTGACTGGCCT  
TTTAAAAGGAACACACAGCAGTCAGCAGTAATGATCGGGCAAGTCTCATTAACAATGCATT  
TCAGCTCGTCAGCATTGGGAAGCTGTCCATTGAAAAGGCCTTGGATTTATCCCTGTACTTGAA  
ACATGAAACTGAAATTATGCCCGTGTTCAGGTTTGAATGAGCTGATTCCTATGTATAAGTT  
AATGGAGAAAAAGAGATATGAATGAAGTGGAACTCAATTCAAGGCCTTCCTCATCAGGCTGCT  
AAGGGACCTCATTGATAAGCAGACATGGACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCG  
GAGTGAAGTACTACTCCTCGCCTGTGTGCACAACTATCAGCCGTGCGTACAGAGGGCAGAAGG  
CTATTTTCAGAAAGTGAAGGAATCCAATGGAACTTGAGCCTGCCTGTGACGCTGACCTTGGC  
AGTGTGTTGCTGTGGGGGGCCAGAGCACAGAAGGCTGGGATTTTCTTTATAGTAAATATCAGTT  
TTCTTTGTCCAGTACTGAGAAAAGCCAAATTTGAATTTGCCCTCTGCAGAACCCAAAAATAAGGA  
AAAGCTTCAATGGCTACTAGATGAAAGCTTTAAGGGAGATAAAAATAAAACTCAGGAGTTTCC  
ACAAATTTCTTACACTCATTGGCAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAG  
GAAAACTGGAACAACTTGTACAAAAGTTTGAAGTGGCTCATCTTCCATAGCCACATGGT  
AATGGGTACAACAAATCAATTCTCCACAAGAACACGGCTTGAAGAGGTAAAAGGATTCTTCAG  
CTCTTTGAAAGAAAATGGTTCTCAGCTCCGTTGTGTCCAACAGACAATTGAAACCATGAGA  
AAACATCGGTTGGATGGATAAGAATTTTGATAAAATCAGAGTGTGGCTGCAAAGTGAAAAGCT  
TGAACGTATGTAAAAAATTCCTCCCTTGCCCGGTTCTGTTATCTCTAATCACCAACATTTTGT  
TGAGTGTATTTTCAAAGTAGAGATGGCTGTTTTGGCTCCAAGTGGAGATACTTTTTTCCCTTC  
AACTCATTTTTTGAATATCCCTGTGAAAAGAATAGCTGTTAGTTTTTCATGAATGGGCTTTTT  
CATGAATGGGCTATCGCTACCATGTGTTTTGTTTCATCACAGGTGTTGCCCTGCAACGTAAACC  
CAAGTGTGGGTTCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

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**FIGURE 464**

MVFLPLKWSLATMSFLLSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVHY  
DLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLEHP  
PQEQIALLAPEPLLVLGTPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTAARM  
AFPCFDEPAFKASFSEIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVAFIIS  
DFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLFEFYEDYFSIPYPLPKQDLAAIPDFQ  
SGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDLWLNELF  
AKFMEFVSVSVTHPELKVGDFYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFDDVSYDKG  
ACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDFGFCRSQHS  
SSSSHWHQEGVDVKTMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPDTGYLWHVPL  
TFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSLTLGLLKGTHTA  
VSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIPMYKLMEKRD MN  
EVETQFKAFILRLRLDIDKQTTWTDEGSVSEQMLRSELLLLACVHNYQPCVQRAEGYFRKWKE  
SNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALCRTQNKEKLQWLLD  
ESFKGDKIKTQEFQILTLIGRNPVGYPLAWQFLRKNWNKLVQKFELGSSSIAHMVMGTTNQF  
STRTRLEEVKGGFFSSLKENGSQLRCVQQTETIETIENIGWMDKNFDKIRVWLQSEKLERM

**Important features:****Signal peptide:**

amino acids 1-34

**N-glycosylation sites:**

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

**Neutral zinc metallopeptidases, zinc-binding region signature:**

amino acids 350-360

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**FIGURE 465**

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACT  
GCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGA  
CCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACAC  
GTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGC  
CAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTA  
CACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGC  
CCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGGAAGGCTG  
TCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCT  
CAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGG  
TTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGAACTGCAATAG  
GAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAACTTGGCTCAAGA  
ACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGAC  
GCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGT  
TGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGGGTGCTTGTGGCCTC  
CTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAA  
CTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCTACCTGTGTGCAGCC  
CCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTA  
TGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTTCAGGGCTGCGT  
GGCCCAACCTTCCAGCTTCTTGTGTAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGA  
GAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC  
TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGGCCCTTC  
CTGCTTAACTCTATTACCCCCACGATTCTTACCCTGCTGACCACCCACACTCAACCTCCCTC  
TGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTCCCATCTGTCCATGAATCATCTT  
CCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATC  
CGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGATAATACAGAC  
CCTGTCCTTTCA

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**FIGURE 466**

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLIE  
SGPQVSLVLSKGCTEAKDQEPRVTEHRMGPLSLISYTFVCRQEDFCNNLVNSLPLWAPQPPA  
DPGSLRCPVCLSMEGCLEGTTEEICPKGTTTHCYDGLLRRLRGGGIFSNLRVQGCMPPQPGCNLLN  
GTQEIGPVGMTENCNRKDFTLCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETLLLID  
VGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLNCSASSSSVLLNSLPPQ  
AAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSS  
FLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

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**FIGURE 467**

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTTG  
AGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAGGATGATGGTGGCCCTTCG  
AGGAGCTTCTGCATTGCTGGTTCTGTTCCTTGCAGCTTTTCTGCCCCCGCCGCACTGTACCCA  
GGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGGAAAA  
ATGTACCCAAGCAACGAGGGGCATACATTCAAGAATTCCAAGAGTTCTCAAAAAATATATCTGT  
CATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAAGTTGGCACT  
GAGAGTTGAACGTGCCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGCTGACGAGTG  
CATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAAGAGAAAAA  
GATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTCTTTGAAAAT  
AGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAAGATGCTGTCTATAACTCTCCAAA  
GGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAACATACGGGCATT  
CATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTCCTGGCAGGGAAC  
AGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTTCATAACCAAGCAACTTCTAATGAGATAAT  
CAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCAGGAGGGGTAGGCCG  
AGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGTGGATGAGCATGGGCT  
CTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCACAAAGATTGAGCCGGG  
CACACTGGGAGTGGAGCATTCTATGGGATACCCCATGCAGAAGCCAGGATGCTGAAGCCTCATT  
CCTCTTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCAGGGCCCTCATCGCATCAC  
CTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGCCCAACTTGTTCTTCCCCAA  
GAGACCAAGAAGTCACTCCATGATCCATTACAACCCCAAGAGATAAGCAGCTCTATGCCTGGAA  
TGAAGGAAACCAGATCATTTACAACTCCAGACAAAGAGAAAGCTGCCTCTGAAGTAAATGCAT  
TACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTCTACAGGACAGTGAGGCTATAGC  
CCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAGAGTGTGTAGAAGTGGAATACGT  
ATGCCTCCTTTCCCAAATGTCACTGCCTTAGGTATCTTCCAAGAGCTTAGATGAGAGCATATC  
ATCAGGAAAGTTTCAACAATGTCCATTACTCCCCCAAACCTCCTGGCTCTCAAGGATGACCAC  
ATTCTGATACAGCCTACTTCAAGCCTTTTGTCTTACTGCTCCCCAGCATTTACTGTAAGTCTG  
CCATCTTCCCTCCCAATTAGAGTTGTATGCCAGCCCCTAATATTCACCACTGGCTTTTCTC  
TCCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTCAAATGTCTATTGATATTCTCCCATTTT  
CACTGCCCCAACTAAAATACTATTAATATTTCTTTCTTTTCTTTTCTTTTCTTTTGGAGACAAGGT  
CTCACTATGTTGCCAGGCTGGTCTCAAACCTCCAGAGCTCAAGAGATCCTCCTGCCTCAGCCT  
CCTAAGTACCTGGGATTACAGGCATGTGCCACCACACCTGGCTTAAAATACTATTTCTTATTG  
AGGTTTAAACCTCTATTTCCCTAGCCCTGTCTTCCACTAAGCTTGGTAGATGTAATAATAAA  
GTGAAAATATTAACATTTGAATATCGCTTTCCAGGTGTGGAGTGTGTCACATCATTTGAATTC  
TCGTTTACCTTTGTGAAACATGCACAAGTCTTTACAGCTGTCATTCTAGAGTTTAGGTGAGT  
AACACAATTACAAAGTGAAAGATACAGCTAGAAAATACTACAAATCCCATAGTTTTTCCATTG  
CCCAAGGAAGCATCAAATACGTATGTTTGTTCACCTACTCTTATAGTCAATGCGTTCATCGTT  
TCAGCCTAAAAATAATAGTCTGTCCCTTTAGCCAGTTTTCATGTCTGCACAAGACCTTTCAAT  
AGGCCTTTCAAATGATAATTCCTCCAGAAAACAGTCTAAGGGTGAGGACCCCAACTCTAGCC  
TCCTCTTGTCTTGCTGTCTCTGTTTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTG  
AGCAAAAAAAAAAAAAA

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**FIGURE 468**

MMVALRGASALLVLFLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQEF  
SKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLLQE  
AEEKKIRTLLNASCDNMLMGIKSLKIVKKMMDTHGSMKDAVYNSPKVYLLIGSRNNTVWEF  
ANIRAFMEDNTKPAPRKQILTLSWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVEDRMLL  
PGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGLGVEHSWDTPCRSQ  
DAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIHYNPRDK  
QLYAWNEGNQIIYKLQTKRKLPLK



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**FIGURE 469**

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGGC  
AGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCCTC  
CTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGTGGG  
GCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCTGGGG  
CGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCAAGCAC  
CACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTACCGCTGC  
TCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCCTGGTCTCAGGATACCCACCATCCT  
TTTCCTGAGCACAGCCTGGATTTTTTATTTCTGCCATGAAACCCAGCTCCCATGACTCTCCCAG  
TCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAGGCAGACATA  
CCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGGCTGTGGTGTG  
AAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTAAATGGCAGAAA  
GGACATTCCCCCTCCCCCTCCCAGGTGACCTGCTCTCTTTCCTGGGCCCTGCCCTCTCCCCA  
CATGTATCCCTCGGTCTGAATTAGACATTCCCTGGGCACAGGCTCTTGGGTGCATTGCTCAGAG  
TCCCAGGTCCCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGGACCAATTTGTGGGT  
AGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGACTCAAGATTGGCTCTT  
CCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCAGGGAGGCCAATCAGCC  
CCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGACCTGTGACCTTCTGCCA  
GAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGTTAACCCTGAAGCCCCCA  
ATTCCACAGCTTTTCCATTAAATGCAAATGGTGGTGGTTCAATCTAATCTGATATTGACAT  
ATTAGAAGGCAATTAGGGTGTTTCCTTAAACAACTCCTTTCCAAGGATCAGCCCTGAGAGCAG  
GTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGGTGGGAGCAAGGGACAGGGAGC  
AGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGGCAACTACACACCAACATGCTGG  
CTTTAGAATAAAAGCACCAACTGAAAAA

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## **FIGURE 470**

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAI SLWLRGLRMCTPLGREGE ECHPG  
SHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

**Important feratures:**

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 88-95

**N-myristoylation sites:**

amino acids 33-39, 35-41, 46-52

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**FIGURE 471**

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGTCTTTCC  
TCCAGGACCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGCTG  
CTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGGCCC  
TGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAAGCAA  
AGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTTCCTCT  
GTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCGTCCCCC  
TCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTATTTCAAAG  
GAGAAATCTTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGATGATGTTTA  
TGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAGGCTTCTCTG  
GAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTTCGTGGTGGGATCAGGAAAGCAGG  
GCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACTTTCTGTTCTGG  
AAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAATGATTGTGTGAACTG  
CCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATTGTTTCCACTCGTG  
TCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTATTAATGTATTTTAA  
TATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAAA  
CTAATGAGGATTATTAAGCTAAACCTGGGAAATAGGAGGCTTAAATTGACTGCCAGGCTGG  
GTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAG  
GTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTCTCTACTAAAAATACAAAA  
ATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCGGGAGGCTGAGGCAGGAGAA  
TCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCACACCACTGTATTCCAGCCTG  
GGTGA CTGAGACTCTAACTAA

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**FIGURE 472**

MSFLQDPSFFTMGMWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKTLEKEPRT  
FKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQP  
YFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGFILGGVFVVG  
GKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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**FIGURE 473**

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTTT  
TGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATTGTTGGT  
ATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATC  
AAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTAC  
CAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTT  
AATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATGATTGTA  
AATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATATATACAA  
TAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACTTTATTAAT  
TTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGATCATATAAT  
TTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAAATGCGATACA  
GTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAAAGAAGGGAAAA  
TGTTGCCAAGGAAAAA

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**FIGURE 474**

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKG  
IVKGRNLDSRGLILGAEAWGRGVKKNT



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**FIGURE 476**

MAPLALHLLVLPILLSLVSQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRVI  
VVGAGVAGLVAAKVLS DAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRILHK  
LCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLG YALRPQEKGHSPEDIYQMALNQ  
ALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMS EDGFFYLSFAEALRAHSC  
LSDR LQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNLKV LKA  
DVVLLTASGPAVKRITFS PPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEG GHSNTDR  
PSRMIFYP PPREGALLLASYTWS DAAAAFAGLSREEALRLALDDVAALHGPVVRQLWDGTGVV  
KRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHG WVETAVKSALRAAIKI  
NSRKG PASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQNTTHTRTSH

**Important features:****Signal peptide:**

amino acids 1-21



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**FIGURE 477**

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAAGTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT  
GGACGCTCTGAAGCCACCCTGTCTCTGGAGGAACACGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA  
GAACCTCAGAGCCCGGAAGCCCCATTCACTAGAAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCT  
GCTGCTGTTCCACAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCCCACTTCCGACCCCGGCGTTGATCTGCAT  
CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA  
CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGGTTTTCCAGAAGAACAATGACCTAACAAAGTTGCTG  
CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG  
ATATAGAAAACCAACAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTCT  
CTGTCTCTTGATAAAGGTTATAAATCATCACCAGACCAAGTTTGTGCGCATCTTTGCTCAGAATAGGCCAGAGTG  
GATCATCTCCGAATTGGCTTGTTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC  
CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATTGGTGCTGAT  
AGGGAATGTAGAGAAAGGCTTACCCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTTGATGATGACCTGAA  
GCAAGAGGGGAGAAGAGTGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCAG  
AAAACCTGTGCCTCTAGCCCAGAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAGG  
AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCCTTTCTCAAATGTGTGGAGCATGCTTATGAGCC  
CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAAGAGATTGTACAGGCTGTTGTGTA  
CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTGCGTTGCTGGCTGACGACATGAAGACTTTGAAGCC  
CACATTGTTTCCCGCGGTGCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCCT  
GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG  
TTTCTGGGACAAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGGTTCGTGTAATTGTCACCTGGAGC  
TGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGCAGCAATGGGATGTCAGGTGTATGAAGCTTATGGTCA  
AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGGACTGGACATCAGGTACGTTGGGGTGGCCCTGGC  
TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTTTTACAGTGAATAATGAAGGAGAGGTCTGCAT  
CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG  
GCTTCACACAGGAGACATTTGGTCTGCTGGCTCCCGAATGGAACCTGAAGATCATCGACCGTAAAAAGAACATTTT  
CAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAAATATCTACAACAGGAGTCAACCAAGTGTACA  
AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCTGACACAGATGTACTTCCCTC  
ATTTGCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAAGTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT  
AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTTAAACCTTTTGAACAGGTCAAAGCCATTTTTCTCATCC  
AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACTT  
TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGGCCCACTG  
TGCACCTGCTTGTGAGAAAATGGATTAAAAACTATTCTTACATTTGTTTTGCCTTTCCTCCTATTTTTTTTTTAAAC  
TGTTAAACTCTAAAGCCATAGCTTTTGTTTTATATTGAGACATATAATGTGTAAACTTAGTTCCCAAATAAATCA  
ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTCAA  
GATCCCAGTTTATGTTCTGTGTCTTCCCTCATGATTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT  
CAAAGGGACCCCTCTGTGCCTTCTTCTTTGTTTTGTGATAAACATAACTTGCCAACAGTCTCTATGCTTATTTACA  
TCTTCTACTGTTCAAATAAGAGATTTTTAAATCTGAAAACTGCTTACAATTCATGTTTTCTAGCCACTCCAC  
AAACCACTAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT  
CTGCGTAAATTAAATTGTGTACTGAAGGGAAAAGTTTGATCATACCAAAACATTTCTTAACTCTCTAGTTAGATA  
TCTGACTTGGGACTATTAAAAATTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATATTTA  
CAGTAGGAAGTGGGAGTAAATCTGTTCCCTACAGTTTGCTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA  
GGTGGGCCCAAGTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAACCTCCTGAAGTGGGAACAAAGATCT  
ACAGGCAAGCAAGATGCCACACAACAGGCTTATTTCTGTGAAGGAACCAACTGATCTCCCCACCCCTTGATT  
AGAGTTCTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAAGTCTTTAAATAAAC  
TATTACAGATAAAAAA

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**FIGURE 478**

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFNF  
LFSPLPTPALICILTFGAAIFLWLITRPQPVLPDLLNNSVGIEGGARKGVSQKNNDLTSCC  
FSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQ  
FVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKALVLIG  
NVEKGFTPSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPEDLSVIC  
FTSGTTGDPKGAMITHQNIVSNAAFLKCV E HAYEPTPDDVAISYLPLAHMFERIVQAVVYSC  
GARVGFFQGDIRLLADDMKTLKPTLFPAPVPRLLNRIYDKVQNEAKTPLKKFLLKLAVSSKFKE  
LQKGIIRHDSFWDKLIFAKIQDSLGGVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTEC  
TGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFKGYLKDPEKT  
QEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNRSQPV LQIFVH  
GESLRSSLVGVVVPD TDVLP SFAAKLG VKGSFEELCQNQVVREAILEDLQKIGKESGLKTFEQ  
VKAIFLHPEPFSIENGLLTPTLKA KRGE LSKYFRTQIDSLYEHIQD

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622

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**FIGURE 479**

GGAGGCGGAGGCGCGGCGAGCCGGGCGGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGGC  
CCGGGGCCCCCTAAGCCATTTCCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAATCC  
GGT**ATG**GACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGGAGC  
TGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCAGACA  
GGGGCCGTGCTTTTCCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCCTGGACACTCGG  
CGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCCCTAGGC  
CGCCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTTGACGTAGAGGTGTAT  
TCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATGAGGCCCGG  
GAGCAGGGCCGGGGCATCCATGTCAATTGTCTCAACCAGGCCACGGGCCACGTGATGGCAAAA  
CGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTCAACATGGTA  
GCGCCCGGGCAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACCTCAAGGACACA  
GCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGCTGGAGGGACACA  
TGGGCCTTCGTGGGACGAAAAGGAGGTCCTGTCTTCGGGGAGAAACATTCTAAGTCACCTGCC  
CTCTCTTCCTGGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGAGCTCAGCAGAAGAG  
GCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGCTTCTGCAGCAAAGTT  
GAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGAGTTCAGCCCTGACCCA  
CTCCAGACAACAAGGTCCTCAATGTGCCTGTGGCTGTCAATTGCAGGGAACCGACCCAATTAC  
CTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCAGGGGGTGTCTCCTCAGATGATAACAGTT  
TTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACTGTTTGGTCTGAGGGGCATC  
CAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGCACTACAAGGCCAGCCTCACT  
GCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGTGTGGTTCTGGAAGAGGACCTGGACATT  
GCTGTGGATTTTTTTCAGTTTCTGAGCCAATCCATCCACCTACTGGAGGAGGATGACAGCCTG  
TACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACACGGCTGAGGACCCAGCACTACTG  
TACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTCAGGAGGTCTTGTACAAGGAGGAG  
CTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGATTGGGACATGTGGATGCGGATGCCT  
GAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACGTTTCCCGATCCTACCACTTTGGCATC  
GTCGGCCTCAACATGAATGGCTACTTTCACGAGGCCTACTTCAAGAAGCACAAAGTTCAACACG  
GTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCTGAAGAAAGAAGCTTATGAAGTGGAAAGTT  
CACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACCACAGCAAGAACCCTTGTGAAGACTCTTTC  
CTGCCAGACACAGAGGGCCACACCTACGTGGCCTTTATTTCGAATGGAGAAAGATGATGACTTC  
ACCACCTGGACCCAGCTTGCCAAGTGCCCTCCATATCTGGGACCTGGATGTGCGTGGCAACCAT  
CGGGGCCTGTGGAGATTGTTTCGGAAGAAGAACCCTTCCTGGTGGTGGGGTCCCCGGCTTCC  
CCCTACTCAGTGAAGAAGCCACCCTCAGTCACCCCAATTTTCTGGAGCCACCCCAAGGAG  
GAGGGAGCCCCAGGAGCCCCAGAACAGACAT**GA**GACCTCCTCCAGGACCTGCGGGGCTGGGT  
ACTGTGTACCCCCAGGCTGGCTAGCCCTTCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTA  
GGGGCTGGGGCTACCTTGTTTTTAACATGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCC  
CTGCTCCAACACCCCGTTCTTGAGTTAAAAGTCTATTTATTTACTTCTTGTGGAGAAGGGC  
AGGAGAGTACCTGGGAATCATTACGATCCCTAGCAGCTCATCCTGECCTTTGAATACCCCTCAC  
TTTCCAGGCCTGGCTCAGAATCTAACCTATTTATTGACTGTCCTGAGGGCCTTGAAAAAGGC  
CGAACCTGGAGGGCCTGGATTTCTTTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTC  
TACTCAGGAACTGCTGTGCCCCAACCCATGGACAGGCCCAGCTGGGGCCCACATGCTGACAC  
AGACTCACTCAGAGACCCTTAGACACTGGACCAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGA  
TTTCCAAAGCTGGATAAGTTGGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAA  
AAAAA

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**FIGURE 480**

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTIVIVNIKLILDTRR  
AISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEARE  
QGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLKDTA  
KALLRSLGSQAGPALGWRDWFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSSAEEA  
ECHWADTELNRNRRRRFC SKVEGYG SVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGNRPNYL  
YRMLRSLLSAQGVSPQMITVFIDGYEPMDDVVALFGLRGIQHTPISIKNARVSQHYKASLTA  
TFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLY  
RVETMPGLGWVLRRLSYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVSRSYHFGIV  
GLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSLKEAYEVEVHRLLSAEVLDHSKNPCEDSFL  
PDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDL DVRGNHRGLWRLFRKKNHFLVVGVPASP  
YSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

**Important features:****Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

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**FIGURE 481**

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCA  
GGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT  
GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTT  
CCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGTATCA  
TTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCA  
GCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCTCTGGAA  
TTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATT  
ATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATC  
TGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAA  
AACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGGGGCATATTA  
ATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTC  
CTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGAT  
CATATATTTTGTTCACCATTCCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAG  
CAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAATATTCTAA  
AATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAA  
GCATTTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAA  
ATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTT  
TGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTA  
AATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCA  
ACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT  
TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTTTAA  
AAAAAAAAAAAAAAAAAAAAA

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**FIGURE 482**

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPN  
REATEISHVLLCNVTQRVSFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFL  
KIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCENM  
ITIENGIPSDPLDMKGGILMMPS

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**FIGURE 483**

CGTCTCTGCGTTTCGCCATGCGTCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGGC  
CCTGGCTTGGGCCGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGGTGGTGT  
TTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACTGATGTCACCCG  
GGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGGGGAA  
CAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCACTGCCTTCCCTGCAAAGATTTCGTGCGA  
CGGCGTGGAGTGCGGGCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCGCCCGCGCTGCGAGTG  
CGCGCCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCGCCACCTA  
CCGCGACGAGTGCGAGCTGCGCGCCGCGCGCTGCCGCGGCCACCCGGACCTGAGCGTCATGTA  
CCGGGGCCCGCTGCCGCAAGTCCTGTGAGCACGTGGTGTGCCCCGCGGCCACAGTCGTGCGTCTGT  
GGACCAGACGGGCAGCGCCCACTGCGTGGTGTGTGAGCGGCGCCCTGCCCTGTGCCCTCCAG  
CCCCGGCCAGGAGCTTTGCGGCAACAACAACGTACCTACATCTCCTCGTGCCACATGCGCCA  
GGCCACCTGCTTCCTGGGCCGCTCCATCGGCGTGCGCCACGCGGGCAGCTGCGCAGGCACCCC  
TGAGGAGCCGCCAGGTGGTGAAGTCTGCAGAAGAGGAAGAGAACTTCGTGTGAGCCTGCAGGAC  
AGGCCTGGGCCTGGTGGCCGAGGCCCCCATCATCCCTGTTATTTATTGCCACAGCAGAGTC  
TAATTTATATGCCACGGACACTCCTTAGAGCCCGGATTTCGGACCACTTGGGGATCCCAGAACC  
TCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGGCGGGCTGGTGGGTGGGAT  
AGACCTGCGTTCCGGACACTGAGCGCCTGATTTAGGGCCCTTCTCTAGGATGCCCCAGCCCT  
ACCCTAAGACCTATTGCCGGGGAGGATTCCACACTTCCGCTCCTTTGGGGATAAACCTATTAA  
TTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATTCCTGAAGAGGCATGACTGC  
TTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGTGTACGGA  
GGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGT  
GAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAGCCTGGGTGAGTATGGAGGGTCT  
AGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTAT  
GGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTG  
GGTGTGTACGGAGGGTCTAGTCTGAGTGCGTGTGGGGACCTCAGAACACTGTGACCTTAGCCC  
AGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGCCACCATTCCTGCCAGCCCCAAGAACT  
CCAGCTTCCCCACTGCCTCTGTGTGCCCCCTTTGCGTCCTGTGAAGGCCATTGAGAAATGCCCA  
GTGTGCCCCCTGGGAAAGGGCACGGCCTGTGCTCCTGACACGGGCTGTGCTTGGCCACAGAAC  
CACCCAGCGTCTCCCCTGCTGCTGTCCACGTCAGTTCATGAGGCAACGTCGCGTGGTCTCAGA  
CGTGGAGCAGCCAGCGGCAGCTCAGAGCAGGGCACTGTGTCCGGCGGAGCCAAGTCCACTCTG  
GGGGAGCTCTGGCGGGGACCACGGGCCACTGCTCACCCACTGGCCCCGAGGGGGGTGTAGACG  
CCAAGACTCACGCATGTGTGACATCCGGAGTCCTGGAGCCGGGTGTCCCAGTGGCACCCTAG  
GTGCTGCTGCCTCCACAGTGGGGTTACACCCAGGGCTCCTTGGTCCCCCACAACCTGCCCC  
GGCCAGGCCTGCAGACCCAGACTCCAGCCAGACCTGCCTCACCCACCAATGCAGCCGGGGCTG  
GCGACACCAGCCAGGTGCTGGTCTTGGGCCAGTTCTCCACGACGGCTCACCTCCCCCTCCAT  
CTGCGTTGATGCTCAGAATCGCCTACCTGTGCCTGCGTGTAACCACAGCCTCAGACCAGCTA  
TGGGGAGAGGACAACACGGAGGATATCCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGAGC  
TTGGGCATCCTCCTCCAGCCTCCTGCAGCCCCCAGGCAGTGCCTTACCTGTGGTGCCCAGAAA  
AGTGCCCTAGGTTGGTGGTCTACAGGAGCCTCAGCCAGGCAGCCACCCACCCTGGGGCC  
CTGCTCACCAAGGAAATAAAGACTCAAGCCATAAAAAAA

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**FIGURE 484**

MRPGAPGPLWPLPWGALAWAVGFVSSMSGGNPAPGGVCWLQQGQEATCSLVLQTDVTRA ECCA  
SGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVECGPGKACRMLGGRPRCECAPDCS  
GLPARLQVCSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCHEHVVCPRPQSCVVDQTGS  
AHCVV CRAAPCPVPSSPGQELCGNNNVTYI ISSCHMRQATCFLGRSIGVRHAGSCAGTPEEPPG  
GESAE EEEENFV

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation sites.**

amino acids 73-77, 215-219

**Osteonectin domain proteins.**

amino acids 97-130, 169-202



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**FIGURE 485**

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCCC  
GAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGGGA  
AACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATCATC  
GTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGATCATG  
GAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGCGCCGTGGAGCTGAAGAAGAAC  
GAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGCCACAAC  
TTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAATAACATC  
ACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGAGGAATTAC  
GGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAGAGGAAGTTC  
TCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTGTGAGGAGCGA  
ATAGAAGAGGTCACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGAGTGAAAACAAC  
GACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAGGCAGCAGGCCTG  
CCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAACAGCAAGTCCCAGACACCA  
GCCCCCAGTTCCGAAGTGTTTTTGGATTCAAAGAGACAAGTTGAGAAAGAGGAAACCAATGAG  
ATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAGCCAGGCCGGGAGCAG  
GTGGTGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGGAGAACTGGGCCAGACC  
CCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGATGGAGGGCCCTGAGCGA  
GACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCTGCCGGGGAAGGGAGAAAC  
CAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAATGAAGCAGAATCTGAGACA  
GACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATGTTTTTAATGTTGAAGATCAG  
AAAAGAGACACCATAAAATTTACTTGATCAGCGTGAAAAGCGGAATCATACACTCTGAATTGAA  
CTGGAATCACATATTTTCAACAGGGCCGAAGAGATGACTATAAAATGTTTCATGAGGGACTGA  
ATACTGAAAATGTGAAATGTACTAAATAAAATGTACATCTGA

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**FIGURE 486**

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGAV  
ELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQLKT  
LQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVASRD  
LSENNDQRQQQLQALSEPQPRQLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLD SKRQVEK  
EETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQENPEM  
EGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGNDRNIDVF  
NVEDQKRDTINLLDQREKRNHTL

**Important features:****Signal peptide:**

amino acids 1-29

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**FIGURE 487**

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGGG  
TGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGTAT  
GGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGGCCT  
ATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGCTCGG  
TTAAATGCACCTTTCTCCAGCTTTGCCCCTGTGGGTGATGCTCTAACAGTGACCTGGAATTTT  
CGTCCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTCCAACCC  
ATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGATGCCTCC  
ATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATAACCTGCCAGGTGAAGAACCCA  
CCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCT  
GAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCATAATAGTAATT  
GTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTCATAAAGTGGTG  
GAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCTGTTTATTTAGAA  
GACACAGACTTAACAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAAGAACCCTAGTATT  
TCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGTTTTCCAACCAGTTC  
TGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCACAGTGCTCCTCCATAT  
CACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCAGAGTGTAATTTTTTCAA  
GTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCTTAAGACACTACTTACAGTGT  
TATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCCAATTTGTCTGTTACATTT  
CCTTTCACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTAATGTGTTTACTCTCTTTCC  
TTCCACATTCTCAATTAAAAGGTGAGCTAAGCCTCCTCGGTGTTTCTGATTAAACAGTAAATC  
CTAAATTCAAACGTGTTAAATGACATTTTTATTTTTATGTCTCTCCTTAACTATGAGACACATC  
TTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATTTTTTGTCG

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**FIGURE 488**

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVTW  
NFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQVK  
NPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLFFQHYRKKRWAERAHK  
VVEIKSKEEERLNQEKKVSVYLEDTD

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**FIGURE 489**

[illegible]

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**FIGURE 490**

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDSFDGRLTFHPGSQVVKLPFINFM  
KTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQKF  
GKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNWLRK  
EAINYTEPFVIYLGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLSEMHP  
VDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIYSSDHG  
ELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVSVLDIYPTMLDIAGIPLPQNLSG  
YSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGASILPQLFD  
LSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIGQNYSNVIA  
NLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

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**FIGURE 491**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA  
GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATGGC**  
CTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGT  
TGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCTGGTGCCAGCATTGTGACAGCAGT  
TGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGA  
CATCTATAGCACCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCCAGGCCATGATGGTGAC  
ATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTT  
CTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTCATCCTTGG  
AGGCCTCCTGGGATTCAATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTC  
ACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTTC  
TTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCCCAGAGAAATCG  
CTCCAATACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGG  
TCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGTATGTG**TGA**AGAAC  
CAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCA  
CAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGG  
CCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAA  
GGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTCCCCTGCCCTAAGTCCCC  
AACCCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGQT  
TTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTGACTGACCCTCTGTGATCAA  
AGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGT  
GGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC  
TGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCCAGACTAATTTGTGCATGAACTG  
AAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAA  
GGCAGCCTGGGACATTTAAAAAATA

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**FIGURE 492**

MASLGLQLVG YILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQ  
CDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIIISVGMRICTVFCQESRAKDRVAVAGGVFFI  
LGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQR  
NRSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV

**Important features:****Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59



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**FIGURE 493**

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGCT  
TATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAGAA  
CCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAGTGC  
TGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCACCTTC  
TGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCCCTTTGGCCTCACAAACGATTTTGTGTGAAG  
CTGAAGGTTTCAGGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGTGAAAGC  
AGAAGACGTTTTCCCTTGAGAAGACATAGAAAGAAAATCAACTTTACTAAGGCATCTCAGAAA  
CATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATGATGCAGCT  
CCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGTAGATTATCA  
GGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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**FIGURE 494**

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSET  
RQCGPPCTFWPCFELCCLDSFGLTNDFFVVKLVQGVNSQCHSSPISSKCESRRRFP

**Important features:**

**Signal peptide:**

amino acids 1-25

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**FIGURE 495**

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATTT  
TCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCTGA  
TGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTTGCT  
ATGATGATGCCGTCGTGCCCTTGCCAGGACCCAGACGTGTGGAACTGCACCTTCAGAGTCT  
GCTTTGAGCAGTGCTGCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGACTCAG  
CCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTCAGCTAATGGAACATCAGGGGAACGATGA  
CTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTTACCTGAGATCTGGGA  
TGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATTCTGTGACC  
TGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAGAATTCTGGA  
CAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGATGACCCCTATG  
GCCAACATCAACCCGGCACCAACCCCAAGGCTGGCTGGGGAACCCTTCACCCTTCTGTGAGATT  
TTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAATAAATTTATGTA  
CTTTATAAATGAAAA

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**FIGURE 496**

MAPRGCIVAVFAIFCISRLCSHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVPL  
ARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCD SARTSDDRLCRSVS

**Important features:**

**Signal peptide:**

amino acids 1-24

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**FIGURE 497**

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACTC  
CTTGGCCTCCGCAGCCGATCACATGAAGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTGGC  
ACAGGTGTGGCTGGTACCCGGCTTGGCCCCCAGTCCTCAGTCGCCAGAGACCCCAGCCCCCTCA  
GAACCAGACCAGCAGGGTAGTGCAGGCTCCCAGGGAGGAAGAGGAAGATGAGCAGGAGGCCAG  
CGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTTGCCAA  
GGAGACTTCAAACCTTCGGATTACAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGGCAACAT  
GGTCTTCTCTCCATTTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCACAGGGCC  
GACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAGCCCGGGCT  
CCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCTCTCCCGCAACCTGGAACCTGGGCCTCTC  
ACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCTTCAATTTATC  
CAAGAGGTATTTTGATACAGAGTGCCTGATGAATTTTCGCAATGCCTCACAGGCCAAAAG  
GCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTTCCCAAACCTGTTTGATGAGAT  
TAATCCTGAAACCAAATTAATTCTTGTGGATTACATCTTGTTCAAAGGGAAATGGTTGACCCC  
ATTTGACCCTGTCTTACCAGAAGTCGACACTTTCCACCTGGACAAGTACAAGACCATTAAGGT  
GCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAATTTTCGTTGTCATGT  
CCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCCCTCATGGAGAAAATGGGTGA  
CCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACATGGCTCAGAAACATGAA  
AACCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCAGAAGTATGAGATGCATGA  
GCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCCTTTGCTGACCTTAGTGAACCTCTC  
AGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGAACAGTGATTGAAGTTGATGA  
AAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTACTGCTTATTCCATGCCTCCTGT  
CATCAAAGTGACCGGCCATTTCAATTCATGATCTATGAAGAAACCTCTGGAATGCTTCTGTT  
TCTGGGCAGGGTGGTGAATCCGACTCTCCTATTAAATTCAGGACATGCATAAGCACTTCGTGCTG  
TAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGATACCAGCAATGGATGGCAGGGGAG  
AGTGTTCCCTTTTGTCTTAACTAGTTTAGGGTGTCTCAAATAAATACAGTAGTCCCCACTTA  
TCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGCCTGAAACGGTGGACAGTGCTGAACCT  
TATATATATTTTTTCTACACATACATACCTATGATAAAGTTTAAATTTATAAATTAGGCACAG  
TAAGAGATTAAACAATAATAACAACATTAAGTAAATGAGTTACTTGAACGCAAGCACTGCAAT  
ACCATAACAGTCAAACCTGATTATAGAGAAGGCTACTAAGTGACTCATGGGCGAGGAGCATAGA  
CAGTGTGGAGACATTGGGCAAGGGGAGAATTCACATCCTGGGTGGGACAGAGCAGGACGATGC  
AAGATTCCATCCCCTACTCAGAATGGCATGCTGCTTAAGACTTTTAGATTGTTTATTTCTGG  
AATTTTTCATTTAATGTTTTTGGACCATGGTTGACCATGGTTAACTGAGACTGCAGAAAGCAA  
AACCATGGATAAGGGAGGACTACTACAAAAGCATTAATTTGATACATATTTTTTAAAAAAA  
AAAAAAA

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**FIGURE 498**

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E E  
E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I K R  
G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F D T E  
C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P V F T E  
V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L A L E D Y  
L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A T G R N L Q  
V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F L G R V V N P  
T L L

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**FIGURE 499**

[illegible]

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**FIGURE 500**

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRRKQEMLKEMPLQDPRSREEAARTQQLLAT  
LQEAATTQENVAWRKNWMVGEGGASGRSP

**Important features:**

**Signal peptide:**

amino acids 1-18



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**FIGURE 501**

[illegible]

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**FIGURE 502**

MGPSTPLLILFLLSWGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKML  
PLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGRRN  
EKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRLRDF  
TLAMAARKASRVVPFPWVGTLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLANRTVV  
DSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDEQQWDTP  
CPRENAEAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAHASLRYN  
PRERQLYAWDDGYQIVYKLEMRRKKEEV

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

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**FIGURE 503**

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGGT  
CTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGGCC  
CTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAAGAA  
CGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTCAGCA  
CGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGGGTGTT  
TGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGACTATGC  
CATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGTACAGTCT  
GACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGCCTGGGCTT  
CCTGTCACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGATCCTTCTGTG  
AGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCAGTGTCCACCC  
ACCTCGCTCAGCGGCTCCCGGGGCCCAGCACCAGCTCAGAATAAAGCGATTCCACAGCA

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**FIGURE 504**

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVTL  
TPENNLRTLSSQHGLGGCDQSVMDLIKRN'NSGWVFENPSIGVLELWVLATNFRDYAIIIFTQLEF  
GDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Important features:**

**Signal peptide:**

amino acids 1-20

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**FIGURE 505**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCACA  
GCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAATC  
CTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTTCGAGTGC  
AAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGGGGCG  
ACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCACTGCCTCAAGCCCCGCTACATAGTT  
CACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCCACTGAG  
TCCTTCCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATG  
CTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCTCTCCTCA  
CGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCCAGCCCCCAG  
TTACGCCTGCCTCACACCTTGCATGCGCCAACATCACCATCATTGAGCACCAGAAGTGTGAG  
AACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGGAAGGGGGCAAG  
GACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTTCAAGGCATTATC  
TCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAA  
TATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCACCCACCACAGCCCA  
TCACCCTCCATTTCCACTTGGTGTTTGGTTCCCTGTTCACTCTGTTAATAAGAAACCCTAAGCC  
AAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATGCTGTCACTTAATAATC  
AACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTTGAAATATTGTGACTCTG  
GGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCAAAGACAGCTCCTGGCCAT  
ATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAA

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**FIGURE 506**

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHC  
LKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITWAV  
RPLTLSSRCVTAGTSC LISGWGSTSSPQLRLPHTLRCANITIIHQKCENAYPGNITDTMVCA  
SVQEGGKDSCQGDSSGGLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

**Important features:****Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

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**FIGURE 507**

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACCATGAGG  
AGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAGCA  
CCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAGGCC  
TGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTTCCCTGTC  
CAGAAGCCGAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCATCCTT  
CCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCTGAGTCCCAGAGCCC  
GACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCCCCGGTTG  
TGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACATCTACCAC  
CCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCCAGGCTGTTGGGA  
CTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCCAGCAGGCAAAAAAAAAAAAAA  
AAAAAA

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**FIGURE 508**

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL  
F  
PVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEERP  
RLWVMPNHQVLLGPEEDQDHIYHPQ



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**FIGURE 509**

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCCC  
ACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCGCG  
CTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCCATG  
GCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAACAGAG  
ACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAACCACCA  
ACTTCAGTTGCCTCAGACTCCAGTAATAACAACGGTCACCACCATGAAACCTACAGCGGCATCT  
AATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTCTACACCC  
AAAACAACAAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCGTAACCCAC  
AATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACATATGCATTCTGAAGCA  
AAGAAAGGATCAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAACGCTGGGAGTT  
TTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTGGGTATCGAACC  
ATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGAATACAGATTGAT  
GCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAACAATATTCTCTTTTGGAAATA  
GTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTAAAGATTCTTCAAGG  
TAACAAGGGTTTGGGTTTGAATAAACATCTGGATCTTATAGACCGTTCATACAATGGTTTT  
AGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCTGGGGTGGGGGCATTGG  
TCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAATGCCATCTGGGCATACA  
AATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTGTAGCTCACATAAAGAACTT  
CAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACACAGAAATTATACAATCAAA  
CTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTGTGCTTTAACTGTAGTAGTT  
GGTCTAGAAACAAAATACTCC

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**FIGURE 510**

MGLGARGAWAALLLGTLQVLALLGAAHESAAMAASANIENSGLPNSSANSTETLQHVPDHT  
NETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQNTS  
QISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIGCKM  
YYSRRGIRYRTIDEHDAII

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**FIGURE 511**

GACTTTGCTTGAATGTTTACATTTTCTGCTCGCTGCCTACATATCACAATATAGTGTTTACGTTTTGTAAAAAC  
TTTGGGGTGTGAGGAGTTGAGCTTGCTCAGCAAGCCAGCATGGCTAGGATGAGCTTTGTTATAGCAGCTTGCCAA  
TTGGTGCTGGGCCTACTAATGACTTCATTAACCGAGTCTTCCATACAGAATAGTGAGTGTCACAACTTTGCGTA  
TGTGAAATTCGTCCCTGGTTTACCCACAGTCAACTTACAGAGAAGCCACCACTGTTGATTGCAATGACCTCCGC  
TTAACAAGGATTCCCAGTAACCTCTCTAGTGACACACAAGTGCTTCTCTTACAGAGCAATAACATCGCGAAGACT  
GTGGATGAGCTGCAGCAGCTTTTCAACTTGACTGAACTAGATTTCTCCCAAAACAACCTTTACTAACATTAAGGAG  
GTCGGGCTGGCAAACCTAACCCAGCTCACAACGCTGCATTTGGAGGAAAATCAGATTACCGAGATGACTGATTAC  
TGTCTACAAGACCTCAGCAACCTTCAAGAACTCTACATCAACCACAACCAAATTAGCACTATTTCTGCTCATGCT  
TTTGCAGGCTTAAAAAATCTATTAAGGCTCCACCTGAACTCCAACAAATTGAAAGTTATTGATAGTCGCTGGTTT  
GATTCTACACCCAACTTGAAATTCTCATGATCGGAGAAAACCTGTGATTGGAATTCTGGATATGAACTTCAAA  
CCCCTCGCAAATTTGAGAAGCTTAGTTTTGGCAGGAATGTATCTCACTGATATTCCTGGAAATGCTTTGGTGGGT  
CTGGATAGCCTTGAGAGCCTGTCTTTTTATGATAACAAACTGGTTAAAGTCCCTCAACTTGCCCTGCAAAAAGTT  
CCAAATTTGAAATCTTAGACCTCAACAAAAACCCATTCAAAAATCCAAGAAGGGGACTTCAAAAATATGCTT  
CGGTTAAAGAAGTGGGAATCAACAATATGGGCGAGCTCGTTTCTGTCGACCGCTATGCCCTGGATAACTTGCCT  
GAACTCACAAGCTGGAAGCCACCAATAACCTAACTCTCTTACATCCACCGCTTGGCTTTCCGAAGTGTCCTT  
GCTCTGGAAGCTTGATGCTGAACAACAATGCCTTGAATGCCATTTACCAAAAGACAGTCGAATCCCTCCCCAAT  
CTGCGTGAGATCAGTATCCATAGCAATCCCTCAGGTGTGACTGTGTGATCCACTGGATTAACTCCAACAAAACC  
AACATCCGCTTCATGGAGCCCTGTCCATGTTCTGTGCCATGCCGCCGAATATAAAGGGCACCAGGTGAAGGAA  
GTTTTAATCCAGGATTCGAGTGAACAGTGCCTCCCAATGATATCTCACGACAGCTTCCCAAATCGTTTAAACGTG  
GATATCGGCACGACGGTTTTCTTAGACTGTCTGAGCCATGGCTGAGCCAGAACCTGAAATTTACTGGGTCACTCCC  
ATTGGAATAAGATAACTGTGGAACCCCTTTCAGATAAATACAAGCTAAGTAGCGAAGGTACCTTGGAATATCT  
AACATACAAATTGAAGACTCAGGAAGATACACATGTGTTGCCAGAATGTCCAAGGGGCAGACACTCGGGTGGCA  
ACAATTAAGGTTAACGGGACCCCTTCTGGATGGTACCCAGGTGCTAAAAATATACGTCAAGCAGACAGAATCCCAT  
TCCATCTTAGTGCTGGAAGTTAATTCGAATGTCATGACGTCAAACCTAAAAATGGTCGTCTGCCACCATGAAG  
ATTGATAACCCCTCACATAACATATACTGCCAGGGTCCCAGTCGATGTCCATGAATACAACCTAACGCATCTGCAG  
CCTTCCACAGATTATGAAGTGTGTCTCACAGTGTCCAATATTCATCAGCAGACTCAAAAGTCATGCGTAAATGTC  
ACAACCAAAAATGCCGCCTTCGCAGTGGACATCTCTGATCAAGAAACCAGTACAGCCCTTGCTGCAGTAATGGGG  
TCTATGTTTGCCGTATTAGCCTTGCGTCCATTGCTGTGTACTTTGCCAAAAGATTTAAGAGAAAAAACTACCAC  
CACTCATTAaaaaaAGTATATGCAAAAACCTCTTCAATCCCACTAAATGAGCTGTACCCACCACTCATTAACCTC  
TGGGAAGGTGACAGCGAGAAAGACAAAGATGGTTCTGCAGACACCAAGCCAACCCAGGTGACACATCCAGAAGC  
TATTACATGTGGTAACTCAGAGGATATTTTGCTTCTGGTAGTAAGGAGCACAAAGACGTTTTTGTCTTATTCTGC  
AAAAGTGAACAAGTTGAAGACTTTTGTATTTTGACTTTGCTAGTTTGTGGCAGAGTGGAGAGGACGGGTGGATA  
TTTCAAATTTTTTTAGTATAGCGTATCGCAAGGGTTTGACACGGCTGCCAGCGACTCTAGGCTTCCAGTCTGTGT  
TTGGTTTTTTATTCTTATCATTATTATGATTGTTATTATATTATTTTATTATTAGTTGTTGTGCTAAACTCAAT  
AATGCTGTTCTAACTACAGTGCTCAATAAATGATTAATGACAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

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**FIGURE 512**

MARMSFVIAACQLVLGLLMTSLTESSIONSECPQLCVCEIRPWFTPQSTYREATTVDCNDLRL  
TRIPSNLSSDTQVLLLQSNNIAKTVDELQQLFNLTELDQSQNNFTNIKEVGLANLTQLTTLHL  
EENQITEMTDYCLQDLSNLQELYINHNQISTISAHAFAGLKNLLRLHLNSNKLKVIDSRWFDS  
TPNLEILMIGENPVIGILDMNFKPLANLRSLVLAGMYLTDIPGNALVGLDSLESLSFYDNKL  
KVPQLALQKVPNLKFLDLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDYALDNLPELT  
KLEATNNPKLSYIHLAFRSVPALESMLNNNALNAIYQKTVESLPNLREISIHNSNPLRCDV  
IHWINSNKTNIRFMEPLSMFCAMPPEYKGHVKEVLIQDSSEQCLPMISHDSFPNRLNVDIGT  
TVFLDCRAMAEPEPEIYWVTPIGNKITVETLSDKYKLSSEGTLEISNIQIEDSGRYTCVAQNV  
QGADTRVATIKVNGTLLDGTQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDNPH  
ITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVTTKNAFAVDISDQETST  
ALAAVMGSMFAVISLASIAVYFAKRFRKKNYHHSLLKKYMQKTSSIPLNELYPPLINLWEGDSE  
KDKDGSADTKPTQVDTSRSYYMW

**Important features:****Signal peptide:**

Amino acids 1-25

**Transmembrane domain:**

Amino acids 508-530

**N-glycosylation sites:**

Amino acids 69-73;96-100;106-110;117-121;385-389;517-521;

582-586;611-615

**Tyrosine kinase phosphorylation site:**

Amino acids 573-582

**N-myristoylation sites:**

Amino acids 16-22;224-230;464-470;637-643;698-704

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**FIGURE 513**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC  
CAGCAAT**ATG**CATCTTGACAGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT  
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT  
GAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGGAATCACGCATGC  
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA  
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA  
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG  
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG  
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT  
GGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC  
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG  
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA  
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCT**TAA**ACTGG  
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGACATGACCTGGAGGGG  
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTGGGATTTGTGAATAAA  
CTTGATACACCA

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**FIGURE 514**

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR  
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA  
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN  
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features:****Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

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**FIGURE 515**

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCTT  
TTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCGAA  
CCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCGGAG  
AAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTTGGGG  
CCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCGGTGTG  
CGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGGTTCGCCG  
GCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCGCTGCTACCCCTGCGCCCCG  
TGCGAGCCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTGGCGGCGGC  
GCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCCCGCCCCGCGCGG  
GACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCAGTTCCCTCCT  
GGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAGAAGCTGGCCCA  
GGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGGCCCCGGGGCGGGT  
GAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACTGGAAGAGCAAGAG  
CGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCCTGGGTCTCCAGGG  
CGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACACCCCGCAGGCGGAAGC  
CCTGGCCGCAGCCGCCCAGGACGCGATTGGCCCCGGAACCTCGCGCCCACGCCCCGAGCCACCCGA  
GGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAGAGCGGCTTCGTGTACGC  
GATCGGGGAGAAGTTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCCTGTGCACCGAGGAGGGGCC  
GCTGTGCGCGCAGCCGAGTGCCCCGAGGCTGCACCCGCGCTGCATCCACGTGCACACGAGCCA  
GTGCTGCCCGCAGTGCAAGGAGAGGAAGAACTACTGCGAGTTCCGGGGCAAGACCTATCAGAC  
TTTGGAGGAGTTTCGTGGTGTCTCCATGCGAGAGGTGTCGCTGTGAAGCCAACGGTGAGGTGCT  
ATGCACAGTGTACGCGTGTCCCCAGACGGAGTGTGTGGACCCTGTGTACGAGCCTGATCAGTG  
CTGTCCCATCTGCAAAAATGGTCCAAACTGCTTTGCAGAAACCGCGGTGATCCCTGCTGGCAG  
AGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTACTTATGAGGAAGGCACATGGAGAAT  
CGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGCAAATGTAGACGCTTCCCAGAACACA  
AACTCTGACTTTTTCTAGAACATTTTACTGATGTGAACATTCTAGATGACTCTGGGAACTATC  
AGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAATTGTTGGTACTTTTCCTTTTCTTGATA  
ACAGTTACTACAACAGAAGGAAATGGATATATTTCAAACATCAACAAGAACTTTGGGCATAA  
AATCCTTCTCTAAATAAATGTGCTATTTTACAGTAAGTACACAAAAGTACACTATTATATAT  
CAAATGTATTTCTATAATCCCTCCATTAGAGAGCTTATATAAGTGTTTTCTATAGATGCAGAT  
TAAAAATGCTGTGTTGTCAACCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 516**

MPSSTAMAVGALSSSLLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNELG  
RPARDEGGSGRDWKS KSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDT PQAEALAAA  
AQDAIGPELAPTPEPP EYVYPDYRGKGCVDES GFVYAIG EKFA PGPSAC PCLCTEEGPLCAQ  
PEC PRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVS PCERCRC EANGEVLCTVS  
ACPQTECVDPVYEPDQCCPICKNGPNCFAETAVI PAGREVKTDECTICHCTYE EGTWRIERQA  
MCTRHECRQM

**Important features:****Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 11-30

**Glycosaminoglycan attachment site.**

amino acids 80-83

**N-myristoylation sites. .**

amino acids 10-15, 102-107, 103-108

**Cell attachment sequence.**

amino acids 114-117

**EGF-like domain cysteine pattern signature.**

amino acids 176-187



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**FIGURE 517**

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCCT  
TTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCTAC  
GGACGACGCCTATGAAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTGTGC  
CGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATACAAG  
TTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATCTAACT  
CTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTACACATG  
GAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACAACCTTCC  
CTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCCATTTCTGGT  
CGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTGAAAATGAAG  
AGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATGTTGCCAGTTG  
TTACTGAATCATCTACAAGTCCATATGTTACCTCATAACAAGTCACCTGTCACCACTTTAGATA  
AGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCTCAGGTGAACTG  
CGATAGAAAAACCCGAAGAGTTTGGAAGCACCCAGAGAGTTGGAATAATGATGACATTTTGA  
AAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGACACCAGCAACCCAG  
CATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCCTTGCTCTAGCAGCAG  
CAGCAGAACATAAATTA AAAACAATGTATAAGTCCCAGTTATTGCCAGTAGGACGAACAAGTA  
ATAAAATTGATGACATCGAAACTGTTATTAACATGCTGTGTAATTCTAGATCTAACTCTATG  
AATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAGCTGCTACAGTATTCAATA  
CATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTAAAAGTTTATTAAACAATAA  
TATAAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGATTTAAGCAAACCTGCATTTTT  
TCACAGGAGAAATAATCATATTCGTAATTTCAAAAGTTGTATAAAAATATTTTCTATTGTAGT  
TCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACAATTTTCATATGCACTAAAAACC  
TAATTTAAATAAAATTTTGGTTCAGGAAAAAA

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**FIGURE 518**

MKPLVLLVALLLPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPKH  
VYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTTFPTGGFTPEIGKKKHTESTPFWSIKP  
NNVSIVLHAEOPYIENEEPEPEPEPAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDKSTG  
IEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNPAYRE  
DIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKLYEYLD  
IKCVPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Important features:****Signal peptide:**

amino acids 1-19

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**FIGURE 519**

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTTG  
GATTTGAAAGTTGAGAGCAGC**ATG**TTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTACTG  
GATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTGGGT  
GATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGATAGAC  
TGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCAATCTC  
AGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGGACATCTTATGCAATGAT  
GGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGC  
CTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCC  
AAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGATGGGATGTGTTTTCCAGAGCACAGAA  
GTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGAGGAGATTGTA  
TTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGGGCCACTTCCAG  
AATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCATCATGCTTCAAGGAGTG  
AGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAAA  
ACCATTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGG  
CCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTG  
CTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCT  
ACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCTGCCATTTT  
GAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAA  
GAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTG  
AGGTCAGATCGGAACAACTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA  
GCCTTT**TGA**GAAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGT  
GTCCTGGGCCACTCTACCAGTGATTTGAGACTCCCGCTCTCCAGCTGTCCTCCTGTCTCATT  
GTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGAGACTGGACAGCTCTGGA  
GGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTG  
GGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTTGGATCAGACCTCCTGTGGGCAGGG  
TTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAACCAACCCAAATCAA

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**FIGURE 520**

MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPGE  
HAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGESQV  
FKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKL  
RMSVEYSQSWGHEFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIVLHVS  
PEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLPVLLILIVKKTCGNKSSVNSTVLVKNT  
KKTNP EIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLRSDRNN  
LEKKSGGGMPKTQQAF

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**FIGURE 521**

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATGG  
TTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGGAA  
ACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCAGGA  
TGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTGGCCC  
TGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGGATGGT  
TGTCGGGCTGGTGGCTCTGGGGATTTGGTCTGTTCATGCAGCGCAATTACCTACAAGATGAGAA  
TGAAAATCGCACAGGAAGCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGGTAAAACA  
ATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAACTGGAGATA  
TTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAGTAAGCAGTA  
CTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGGAGTACATCAA  
AGCCAGGACTCATTTAATTCGTTGGGTGCGATTATCTCGCCAGAAGTCGAATGAGGTCTGGAA  
GTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGAAGATGGAAAAGGAAA  
TATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTGAGAACAAACATTA  
TTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCTTAATGCAAAGAGGT  
GGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGTATGAATGCATCAGTA  
GCTGAAAAAAAAAAAAA

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**FIGURE 522**

MQDEDGYITLNIKTRKPALVSVGPASSSWVRMALILLILCVGMVVGLVALGIWSVMQRNYLQ  
DENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWEES  
KQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDG  
KGNMNCAYFHNGKMHPTFCENKHLYLMCERKAGMTKVDQLP

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**FIGURE 523**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGGC**  
AAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAA  
GAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCTAAT  
TGTCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGA  
GCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAG  
AACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAA  
CGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGT  
GATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACTTT  
CTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAA  
AAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAAT  
ATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTTCCTGCCAACGA  
AAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCG  
TCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAATGGAATAGA  
ATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTA  
TTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATACTGCTACCAAGGAGG  
ACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCCGCATGCTGGGGAGGGT  
**CTAA**TAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATATAATAAATGCATGCTATT  
CAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAG  
GTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACCAAAAAAAAAAAAAAAAAA

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**FIGURE 524**

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTILIVLFWGSKHFWPEVPPKKAYD  
MEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQI  
KVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWINPT  
LISVSELQDFEEEGEDLHFPA NEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENG  
IEFDPMLDERGYCCIIYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWWVARMLGRV

**Important features:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14



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**FIGURE 525**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGTC  
TCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCCAA  
AAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCACAT  
ACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACCGAGA  
GCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCATGGAC  
ATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTGAGTTTC  
TTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTGACTGAAT  
GGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCATTTTTTTTTT  
TAACACGTCAATAAAAAAATAATCTCCCAGA

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## **FIGURE 526**

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNE  
CHLCTESLKSNQGRVQFLHDGSC

**Important features:**

**Signal peptide:**

amino acids 1-19

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**FIGURE 527**

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTGG  
CTGCGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTTCTAGAGCCGAGGGACCCGGTGGCCT  
CGTCGCTCAGCCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTATTGT  
CGGGCCCCGAGGCTCCGTGGCGGGACCCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTGCAGC  
TGGTCGCCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCTGAGGC  
AGCTGCACGGGTGCTGTCAGGCCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCGGCAGCC  
GCGACCTGGGTGCAGCGCTGGCCGACTGGCCCTTTGTGGTACGCGGACTGGATGGACGGGCAGC  
TAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCTCTTCCCGG  
CCCTTTTTCAGCCGTGAGAACTACGGCCGCTGCGGGCTCATCACCAGTTCCAAGCACCGCTGCA  
TGGATAGCAGCGCCGCTTCCTGCAGGGGCTGTGGCAGCACTACCACCTGGCTTGCCGCCGC  
CGGACGTCGCAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAATGAGATTTTTTG  
ATCACTGTGAGAAGTTTTTAAGTAGAAAAAATGCTACAGCTCTTTATCACGTGGAAG  
CCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCTACTTTGCAAGTGC  
CAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTCACCTGTTCAATTTGACCTGG  
CAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATGATGCAAAGGTATTAG  
AATATTTAAATGATCTGAAACAATATTGGAAGAGGATATGGGTATACTATTAACAGTCGAT  
CCAGCTGCACCTTGTTTTCAGGATATCTTTTCAGCACTTGGAACAAGCAGTTGAACAGAAACAAA  
GGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATGCAGAGACTCTTCTCCAC  
TGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACAGCGTACAATTACAAAAAAC  
AAATGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGCCTCGAACCTGATATTTGTGC  
TTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACAAATCCGAGTGCAGATGTTATTAAATG  
AAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCATTTTATGAAGATCTGAAGAACC  
ACTACAAGGACATCCTTCAGAGTTGTCAAACAGTGAAGAATGTGAATTAGCAAGGGCTAACA  
GTACATCTGATGAAGTATGAGTAAGTGAAGAACATTTTTAATTCTTTAGGAATCTGCAATGAG  
TGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATTACAGGAAGCTTTTATATTACTTGAG  
TATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTCTCTGGGTTTGGACATGAAATGTAAGA  
AAAGATTTTTCAGGAGCAGCTCTCTTAAGGAGAAACAAATCTATTTAGAGAAACAGCTGGC  
CCTGCAAATGTTTACAGAAATGAAATTCTTCTACTTATATAAGAAATCTCACACTGAGATAG  
AATTGTGATTTTATAATAACACTTGAAAAGTGTGAGTAACAAAATATCTCAGTTGGACCAT  
CCTTAACCTGATTGAAGTGTCTAGGAACCTTACAGATTGTTCTGCAGTTCTCTCTTTCTTTCC  
TCAGGTAGGACAGCTCTAGCATTCTTAATCAGGAATATTGTGGTAAGCTGGGAGTATCACT  
CTGGAAGAAAGTAACATCTCCAGATGAGAATTTGAAACAAGAAACAGAGTGTGTAAAAGGAC  
ACCTTCACTGAAGCAAGTCGGAAGTACAATGAAAATAAATATTTTTGGTATTTATTTATGAA  
ATATTTGAACATTTTTTCAATAATTCCTTTTTACTTCTAGGAAGTCTCAAAGACCATCTTAA  
ATTATTATATGTTTGGACAATTAGCAACAAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCC  
ATTGCTTAGCTAACTTTTTTCACTTCTGTCACCTGGCTTCGATTTTTATATTTTCTATTATATG  
AAATGTATCTTTGGTTGTTGATTTTTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCA  
AATGCCGTGAAAGTATTTGCTATAATAAGAAAATCTTGTGACTTTAAAAA

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**FIGURE 528**

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPLYFGTKTRYEDVNPVLLSG  
PEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGSRD  
LGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHRCMD  
SSAAFLQGLWQHYPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYHVEAF  
KTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTC SFDLAIKGVKSPWCDVFDIDDAKVLEY  
LNDLKQYWKRGYGTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAETLLPLL  
SLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRVQMLLNEK  
VLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

**Important features:****Signal sequence**

amino acids 1-30

**N-glycosylation sites.**

amino acids 242-246, 481-485

**N-myristoylation sites.**

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

**Endoplasmic reticulum targeting sequence.**

amino acids 484-489

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**FIGURE 529**

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTGG  
CGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGGGA  
CGCGGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGGGCG  
GTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGGTGGCGGCGGCGCTTGGGCTC  
TTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAAATGGT  
ACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTC  
TCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTTTCCACTACTCCCAAGGG  
CAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAGACCTTGAC  
AAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACCTATATCTGT  
GATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTATGTCGTAGAA  
AAAGAGAATTTGCCTGTGTTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTGCTGTGGTCTTA  
GGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAAACTCTAAACGG  
GATTACACTGGCTGCAGTACATCAGAGAGTTTGTACCAGTTAAGCAGGCTCCTCGGAAGTCC  
CCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACCAGGGCCCAGTCATA  
TATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAACAAGTCAGAGTCTGTG  
GTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATCCTCAGCAAGAAACAAA  
ACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCCATTAACCATGTAGCCTTGGAGACCCAGG  
CAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGTACAAAGGATATGTATAAA  
TATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGATGAAAAGATGGTATGATTC  
TACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTCAGGTCATTTACAATTGGGAG  
ATTTTCAGAAACATTCCTTTACCATCATTTAGAAATGGTTTGCCTTAATGGAGACAATAGCAG  
ATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAGGGCTTAAGACTGATTAGTCTTA  
GCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAAGCATACCCAGGGTGGCCTTTAGC  
ACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAAAATACCCATTGGCTATGCCACTTG  
AAAACAATTTGAGAAGTTTTTTTTGAAGTTTTTCTCACTAAAATATGGGGCAATTGTTAGCCTT  
ACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTGAAATGTGTATATCAATTTCTGGATT  
CATAATAGCAAGATTAGCAAAGGATAAATGCCGAAGGTCATTCTGACACAGTTGGAT  
CAATACTGATTAAAGTAGAAAATCCAAGCTTTGCTTGAGAACTTTTGTAACGTGGAGAGTAAAA  
AGTATCGGTTTTTA

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**FIGURE 530**

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKST  
STTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKKDASINIENMQ  
FIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMILAV  
LYRRKNSKRDTGCTSESLSPVKQAPRKSPDTEGLVKSLPSGSHQGPVIYAQLDHSGGHHS  
DKINKSESVVYADIRKN

**Important features:****Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

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**FIGURE 531**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCGA  
GGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGCTC  
TTGCTGATGGCGGTAGCAGCGCCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACTGGT  
GCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCTGCTG  
GAGCACTCATTTGAGATCGATGACAGTGCCAACCTCCGGAAGCGGGGCTCACTGCTCTGGAAC  
CAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGCCGACTC  
CGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGGGGCCCTG  
GATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGGTGGAGTCG  
CACCTGTCCGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGCGTGTCCGTG  
GTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGAGCTGTTCAAC  
ACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGGCCTTCATTGAG  
CGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAGTCCTTCTTCGCC  
AAATACTGGATGTACATCATTCCCGTCGTCTCTGTTCCCTCATGATGTCAGGAGCGCCAGACACC  
GGGGGCCAGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCCTTTGCTGTGTGCCA  
CCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTGTGAACGTTTAAAA  
GCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGGTCCTGATGTACAAGCT  
TGATTGAAATTCAGTCTCACTTGATACGTTATTCAGAAACCAAGGAATGGCTGTCCCCATC  
CTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTATTAAACTGTCCCCAGATC  
GACACGCAAAAAAAAA

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**FIGURE 532**

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEID  
DSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIIPRRPGALDGLEAGG  
YVSSFVPACSLVESHLSQDLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQLQP  
PTTAPGPETAAFIERLEMEQAQKAKNPQEKSFFAKYWMYIIPVVLFLMMSGAPDTGGQGGGG  
GGGGGGGSGLCCVPPSL

**Important features:****Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243





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**FIGURE 534**

MELALLCGLVVMAGVPIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWC  
CQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDL SQRYCLMAVFNVIIYLENEDESE

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

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**FIGURE 535**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTG  
AACTGGGTGCTCATCACGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCC  
CCAAATTGCGTGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTT  
TTTTTAACCGCCCCCTCCCCACCCCCCAAAAAAAGTGTAAAGATGCAAAAACGTAATATCCAT  
GAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTT  
GTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAG  
GGGTCCAATTTTTCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGG  
CTGTCATGCAACTGGCCCCCTAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAACAATACAA  
AGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCC  
ACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAA  
GGCAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGT  
TGCTTAGGTTTGTCCTTCGCTATAACAGCCTTCAAAAAGTAAAGTATAATCAATTTAAAGGG  
CTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATATTGACGAAAATGCT  
TTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAATCTCCTATTTTCTT  
AACAATACCTTCAGACCTGTGACAAATTTACGGAAGCTTGGATCTGTCTTATAATCAGCTGCAT  
TCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTTACATTTACGGTCTAAC  
TCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACCTGGAAGTTTGGACCTG  
GGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGCATGATCAGACTCAAAGAA  
CTTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCTTTTTTCCAAGGTTGGTCAGC  
CTTCAGAACCTTTACTTGCAGTGAATAAAATCAGTGTATAGGACAGACCATGTCTTGGACC  
TGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATCGAAGCTTTCAGTGGACCCAGT  
GTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGATTCCAACAAGCTCACATTTATT  
GGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAGTCTTGCTGGGAATATATGG  
GAATGCAGCAGAAATATTTGCTCCCTTGTAAGTGGCTGAAAAGTTTTAAAGGTCTAAGGGAG  
AATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTGATCGATGCAGTGAAG  
AACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAGGGCTCTCCCAAAG  
CCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCCCTTTGCCCCCGACG  
GTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCTTTCCATAAA  
ATCATCGCGGGCAGCGTGGCGCTTTTCCTGTCCGTGCTCGTCATCCTGCTGGTTATCTACGTG  
TCATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAAGGCAC  
AGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCAGCACCCAGGAATTTTATGTAGAT  
TATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCTGCACCTAT  
AACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTGTGATAAAAAGAGCTCTTAAAGC  
TGGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTC  
CCCTTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCTTGTCGTTTTAGTGCATTCATA  
ATACTGGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGT  
GAAGCTTGAAGTCCGGTTTAAATATAATACCTATTGTATAAGACCCTTTACTGATTCCATTAAT  
GTCGCATTTGTTTTAAGATAAACTTCTTTCATAGGTAAAAA

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**FIGURE 536**

MGFNVIRLLSGSAVALVIAPT VLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGC  
LGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLN  
NTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELLDLG  
YNRIRSLARNVFAGMIRLKEHLEHNQFSKLNALFPRLVSLQONLYLQWNKISVIGQTMSWTW  
SSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIQEILDSWISLNDISLAGNIWE  
CSRNICSLVNWLKSFKGLRENTIICASPKELOQGVNVIDAVKNYSICGKSTTERFDLARALPKP  
TFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKI IAGSVALFLSVLVILLVIYVS  
WKRYPASMKQLQQRSLMRRHRKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLNGTGPCTYN  
KSGSRECEV

**Important features:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

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**FIGURE 537**

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGGAAGTGTCTTGTCATCATTACGGATTTCGC  
AGACAAGTGACCCAGGATCGAGTGGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT  
CCAGAGCCAATCCAGATTTTCGCAATTCTTCTTTCCACTTAAACTCTGAAACAGGCACCTTGGTGTTCACTGCTG  
TTCACAAGGACGACTCTGGGCGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGTCTTGTCTGACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCTTAATCTGTTTCTGGCCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTTGCTCACGTAAACGCGCGTGTGGGCGCTGTGAAGCCAGCATGTTACCACCTGGTCGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGAAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCACTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG  
GTAAATTGGTTGCTGGAAGAGGGATCTTGCTGAGGAACCTGCTGTCCAACAGGGGTGTGAGGATTTAAGGAAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT  
TACATCTAAATTTTGTCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATTGT  
CATACAATGTTAAATAACCTATTTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT  
TGGAATAATCAATAATTAAGAGTATTTTACCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTCT  
CACACAAGTTTTAGCCTTTTTTACAAAGGGAATCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATCCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT  
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG  
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT  
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAACAGACCTCT  
TTTTGGTTATGGATGGCTCACAAAATAGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTTTAATTATTTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT  
CCCAGTGTCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAACCAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG  
TGAAACGCCTGAATCAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGAGACACTGCTCCATT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCTGGA  
GAATGGCTCTCACTACTCACCTTGTCTTTCAGCTTCCAGTGTCTTGGGTTTTTATACTTTGACAGCTTTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTTTAGTTATGTGAAACACTTTGCCGCAGGCCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGGTAGAGAGGATGGCTCCCCACCCTCAGCGTTGGGATTACGCTCCAGCCTCCT  
TCTTGGTTGTATAGTATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACCTTCTACACTAGTGCCA  
TGGGAACCAAGTCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTAATAACACACCGTAATTTGGCATTGTTTAAAC  
CTCATTTATAAAAGCTTCAAAAAACCCA

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**FIGURE 538**

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS DP  
RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTS LKIWNVTRRDSALYRCEVVARNDRKEI  
DEIVIELTVQVKPVPVPCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPR  
FRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDL NIGGIIGGVLVV  
LAVLALITLGICCA YRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

**Important features:****Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

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**FIGURE 539**

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCTCAGAGGCCGGGGAAGAGAAGCAAAGC  
GCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAA  
CTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGG  
CACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTCTGGGCAGCTGG  
GCTCGGGCGGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTCGCGGG  
CTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCGCGCA  
**TG**AGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCC  
GCCGCGTGGTCAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGG  
CCTACTTCCATGAAGTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTG  
AGGGAGGAGTCTCTCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGC  
AAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTCTGGATAGGGCTTTGGAGGA  
ATGGAGATGGGCAAACATCTGGTGCCTGCCCAGATCTCTACCAGTGGTCTGATGGAAGCAATT  
CCCAGTACCGAACTGGTACACAGATGAACCTTCTGCGGAAGTGAAGAGTGTGTTGTGATGT  
ATCACCACCAACTGCCAATCTGGCCTTGGGGGTCCCTACCTTTACCAGTGGAAATGATGACA  
GGTGTAAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTAATCCAACAGCCCCCTG  
TAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAATGTGGTTGTTACTGAAG  
CAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACCCCTGCTCTTACTGATAC  
TGTTTGCTTTTGGAACCTGTTGTTTCCAGATGCTGCATAAAAGTAAAGGAAGAACAAAACTA  
GTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAAGAAAGTGGCATGGAAGTAT  
**AA**TAACTCATTGACTTGGTTCAGAATTTTGTAATCTGGATCTGTATAAGGAATGGCATCAG  
AACAATAGCTTGAATGGCTTGAAATCACAAAGGATCTGCAAGATGAACTGTAAGCTCCCCCT  
TGAGGCAAATATTAAAGTAATTTTTATATGTCTATTATTTTCAATTAAGAATATGCTGTGCTA  
ATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAACTTCAAACCTCAAGCAAA  
TGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTATGTGTGTTAGAAGCAAT  
TCCTTTTTATTTCTTTACCTTTTCATAAGTTGTTATCTAGTCAATGTAATGTATATTGTATTGA  
AATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAAATGAACTGTTCTA  
ATATTTATTTTTATGGCATCTCATTTTTCAATACATGCTCTTTTGATTAAAGAACTTATTAC  
TGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGTCTCTCGAA  
ATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGAAATAAGA  
AGCTATTTTCATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGATTGTCT  
AATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTCTAGCTTAAATTAACAGATTTTG  
TAATAATGTAACCTTGTAAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAGT  
GACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTG  
AGGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTT  
GGGATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGC  
CTCTGACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAG  
TGTGGAGACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACCTACGAAATCGTGTGAAA  
ATGGGTTGGAACCCATCAGTGATCGCATATTCATTGATGAAGGTTTGCTTGAGATAGAAAATG  
GTGGCTCCTTTCTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGA  
AAGTTGTAACCTCTGGTCTTCATATGTCCCTGTGCTCCTTTTAACCAAATAAAGAGTTCTTG  
TTTCTGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 540**

MSRVVSLLLGAALLCGHGAFRRVVSQKVCFADFKHPCYKMAYFHELSSRVSFQEARLACES  
EGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSACPDLYQWSDGSN  
SQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAP  
VEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRKT  
SPNQSTLWISKSTRKESGMEV

**Important features:****Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89 and 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145  
and 212-217



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**FIGURE 541**

GGAGAAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG  
CCACAGCCACTGGGCCCCAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTCGTGTGCGAGGCCGGCAGGTGG  
GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCTGACC  
GGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCTAC  
AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCAACGGAAAACAGCAGATCTTCTCCGTTTCAGAGGACT  
GCCTGGTCTCAACGTCTATAGCCCAGCTGAGGTCCCCGAGGGTCCGGTAGGCCGGTCATGGTATGGGTCCATG  
GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGG  
TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTTCAGACTGGAGATGAGCATGCACCTGGCAACCAGGGCT  
TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA  
CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTC  
ACAGAGCCATCACACAGAGTGGGGTCAACACCCAGGGATCATCGACTCTCACCTTGGCCCCCTAGCTCAGA  
AAATCGCAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG  
AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCTCTCACCGTTGATGGCACTGTCTTCCCCAAAA  
GCCCCAAGGAACCTTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTTCA  
GCTGGCTCATCCCCAGGGGCTGGGGTCTCCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT  
CAACACCCGTCTTGACCACTGTGGATGTGCCCCCTGAGATGATGCCACCGTCATAGATGAATACCTAGGAAGCA  
ACTCGGACGCACAAGCCAAATGCCAGGCGTTCAGGAATTCATGGGTGACGTATTCATCAATGTTCCACCGTCA  
GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTCTATGAGTTCAGCATCGACCCAGTTCTTTTG  
CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGTCTTTGTGTTCCGAGGTCCCTTCTCA  
TGGACGAGAGCTCCCGCTGGCCTTTCAGAGGCCACAGAGGAGAGAAGCAGCTAAGCCTCACCATGATGGCCC  
AGTGGACCCACTTTGCCCCGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGCCCCCAATTCAACCAGGCGG  
AACAATATCTGGAGATCAACCCAGTGCCACGGGCCGACAGAAGTTAGGGAGGCCCTGGATGCAGTTCTGGTCAG  
AGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAACAGGAAGGCCCAGGAGGACCTCTGAGGCC  
AGGCCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAGTCCCAGCACGGCAGCCCGCCTCTC  
CCCCTGCTGAGACTTTAATCTCCACAGCCCTTAAAGTGTGGGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA  
ATGTCAACAAGCCGCTCCCACCTCTGGGGCATTGTACAAGTTCTTCCCTCTCCCTGAAGTGCCTTTCCTGCTTT  
CTTCGTGGTAGGTTCTAGCACATTTCTAGCTTCTCTGGAGGACTCACTCCCAGGAAGCCTTCCCTGCCTTCTC  
TGGGCTGTGCGGCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT  
CCCCCTCAGAGGAGCTCTCTCAAATGGGGATTAGCTAACCCCACTCTGTACCCACACCAGGATCGGGTGGGA  
CCTGGAGCTAGGGGGTGTGTTGCTGAGTGAGTGAGTGAAACACAGAATATGGGAATGGCAGCTGCTGAACCTGAAC  
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCCACCACATTGTCCACCCTGGCCAGAAGGGTGCATGCC  
AATGGCAGAGACCTGGGATGGGAGAGTCTTGGGGAGCCAGGGGATCCAGCCTAGAGCAGAGCTTAGCCCCGTGAC  
TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTCTGCTGCCAGTCTTGGCCCCCTGCACAAGACAACAGA  
ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCTCACCAATTCCAGCCCCCTGACCTCAGGACGCTGGATG  
CCAGCTCCCAGCCCCAGTGCCGGGTCTCCTCCTCCTTCTGGCTTGGGGAGACCAGTTCTGGGGAGCTTCCAAG  
AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTCCGGGCTATTGTACA  
GAGAAAAGAAGAGACCCACCACTCGGGCTGCAAAAGGTGAAAAGCACCAAGAGTTTTCAGATGGAAGTGAGAG  
GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGTTGCTCTCCTGCCGCTCTGCCTGGGCTCCCCTTTGGCA  
GCACTTGAGGAGCCCTTCAACCCGCGCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAGGCCGAGCCAGCT  
CCCTCAGCTTGGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGGGGGCCAG  
AGTGAGTTCGGGTGGCGTGGGCTCGGGCGGGGCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCCT  
TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTCTCGCTGGGCCTTAGCTGCCTCCCCGCGGGGAGGGCTCGG  
GACCTGCAGCCCTCCATGCCTGACCTCCCCCACCCTGGGCTCCTGTGCGGCCGAGCCTCCCCAAGGAG  
CGCCGCCCCCTGTCCACAGCGCCAGTCCCATCGACCAACCAAGGGCTGAGGAGTGCGGGTGCACAGCGCGGGA  
CTGGCAGGCAGTCCACCTGCTGCCCCAGTGTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG  
GGACTTGGAGAACCTTTATGTCTAGCTAAGGGATTGTAAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTT  
TGTAACACACCAATCAGCACCCCTGTGTCTAGCTCAGTGTGTTGTGAATGCACCAATCCACACTCTGTATCTGGCT  
ACTCTGGTGGGACTTGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT  
TTGTACTAGCTCAGGGATCGTAACGACCAATCAGCACCTGTCAAACAGACCACTGACTCTCTGTAAAAAT  
GGGCAATCAGCGAGTGTGGGTGGGGCGAGACAGAGAATAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC  
CCCTCGGGTCCCCCTCCACGCGCTGGAAGCTTTGTTCTTTGCTCTTTGCAATAAATCTTGCTACTGCCAAAAA

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**FIGURE 542**

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVVRGRQVGKGTDRLVNVFLGI  
PFAQPPLGPD RFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDCLV  
LNVYSPAIEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAAYGDVVVVTVQYRLGVLGFFSTG  
DEHAPGNQGFLDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIISGLVLSPVAAGLFHRAI  
TQSGVITTPGIIDSHPWPLAQKIAN TLACSSSSPAEMVQCLQQKEGEELVLSKKLKNTIYPLT  
VDGTVFPKSPKELLKEKPFHSPFLMGVNNHEFSWLI PRGWGLLD TMEQMSREDMLAISTPVL  
TSLDVPPPEMMPTVIDEYLG SNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGSPVFFYEF  
QHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTMM AQWTHFA  
RTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQWHQKQKNRKA  
QEDL

**Important features:****Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 226-245

**N-glycosylation site.**

amino acids 105-109

**N-myristoylation sites.**

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,  
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,  
461-467

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

**Carboxylesterases type-B serine active site.**

amino acids 216-232

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**FIGURE 543**

TGTCGCCTGGCCCTCGCC**ATG**CAGACCCCGCGAGCGTCCCCTCCCCGCCCCGCCCTCCTGCTTCTGCTGCTGCTA  
CTGGGGGGCGCCACGGCCTCTTTCTGAGGAGCGCCGCGCTTAGCGTGGCCCCAGGGACTACCTGAACCAC  
TATCCCGTGTTTGTGGGCAGCGGGCCCGGACGCCTGACCCCGCAGAAGGTGCTGACGACCTCAACATCCAGCGA  
GTCCTGCGGGTCAACAGGACGCTGTTCATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCAGC  
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTGTGTCGGATGAAG  
GGCAAACAGGAGGGCGAGTGTGAAACTTCGTAAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC  
GGTTCCAACGCCCTTCAACCCGGTGTGCGCCAACTACAGCATAGACACCCTGCAGCCCGTGGAGACAACATCAGC  
GGTATGGCCCGCTGCCCCGTACGACCCCAAGCAGCCTAATGTTGCCCTCTTCTCTGACGGGATGCTCTTCACAGCT  
ACTGTTACCGACTTCTTAGCCATTGATGCTGTCTATCTACCGCAGCCTCGGGGACAGGCCACCCCTGCGCACCGTG  
AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC  
TTCCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCGCGTGGCCCGAGTGTGCAAGAAC  
GACGTGGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGTCTTCTGAAGGCGCGGCTCAACTGCTCTGTA  
CCCGGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGCGTGGTCAAGCTCGGGGGCGGGCCGTG  
GTCTTGGCCGTTTTCACGCCCCAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG  
GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCCGAGTCCATCTGGACGCCGCTGCCGGAGGATCAG  
GTGCCTCGACCCCGGGCGGGTGTGCGCAGCCCCGGGATGCAGTACAATGCCTCCAGCGCCTTGGCCGATGAC  
ATCCTCAACTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG  
CGGACCCTGATGAGGCACCGAGTGAAGTGGCTGTGGACGTGGGAGCCGCCCCCTGGGGCAACCAGACCGTT  
GTCTTCTCGGTTCTGAGGCGGGGACGGTCCCAAGTTCCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT  
GGGCTCAGTGTCTTCTGAGGAGTTTGAAGCTACCGGCCGGACAGGTGTGGACGGCCCGGGCTGGCGAGACA  
GGGCAGCGGCTGCTGAGCTTGGAGCTGGACGCAGCTTCCGGGGGCTGCTGGCTGCCTTCCCCCGTGCCTGGTC  
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGC  
GGGTGGGCCCCCGACGGCTCCTGCATCTTCTCAGCCCGGGCACCAGAGCCGCTTTGAGCAGGACGTGTCCGGG  
GCCAGCACCTCAGGCTTAGGGGACTGCACAGGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGT  
TCGGTGAACCTGCTGGTAACGTGCTCGGTGGCGGCCTTCTGTTGGGAGCCGTGGTGTCCGGCTTACCGTGGGC  
TGGTTCTGGGCCCTCCGTGAGCGGGCGGAGTGGCCCGGCGCAAGGACAAGGAGGCCATCCTGGCGCAGCGGGCG  
GGCAGGCGGTGCTGAGCGTCAGCCGCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCGGGGCGGAGGCGGT  
GGCGGTGGCGCCGGGTTCCCCCGAGGCCCTGCTGGCGCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG  
CTGCAGGGCGGGCCCCACGACCTGGACTCGGGGCTGCTGCCACGCCCCGAGCAGACGCCGCTGCCGCAGAGCGC  
CTGCCCACTCCGCACCCCGCACCCCCACGCCCTGGGCCCCCGCGCTGGGACCACGGCCACCCCTGCTCCCCGCC  
TCCGCTTCATCTCCTCCTGCTGCTGGCGCCCGCCGGGCCCCGAGCAGCCCCCGCGCTGGGGAGCCGACC  
CCCGACGGCCGCTCTATGCTGCCCGCCCGCGCCTCCACCGCGACTTCCCGCTACCCCCCAGCCAGC  
CCGACCGCCGGCGGGTGGTGTCCGCGCCACGGGCCCTTGGACCCAGCCTCAGCCGCCGATGGCTCCCCGCG  
CCCTGGAGCCCGCCCCGACGGGCGAGCTGAGGAGGCCACTGGGCCCCACGCCCTCCGGCCGCCACCCTGCGC  
CGCACCCACAGTTCAACAGCGCGAGGCCCGGCTGGGGACCGCCACCGCGGCTGCCACGCCCGCGGGGACA  
GACTTGGCCACCTCCTCCCCTATGGGGGGCGGACAGGACTGCGCCCCCGTGGCC**TAG**CGCGGGGGCCCCCG  
ATGCCTTGGCAGTGCCAGCCACGGGAACAGGAGCGAGAGACGGTGCCAGAACGCCGGGGCCCGGGCAACTCCG  
AGTGGGTGCTCAAGTCCCCCGCGACCCACCCGCGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACAAACAG  
CTCGCCCTCCCCCTACCCGGGGCGCAGGACGCTGAGACGGTTTGGGGGTGGGTGGGCGGGAGGACTTTGCTATG  
GATTTGAGGTTGACCTTATGCGGTAGGTTTGGTTTTTTTTTGCACTTTGGTTTCTTTGCGGTTTCTAACC  
AATTGCACAACTCCGTTCTCGGGGTGGCGGCAGGCAGGGGAGGCTTGACGCCGGTGGGGAATGGGGGGCCACAG  
CTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCCAACCCAGGCCCCCTGGCGTGTGTGGGTGTGCG  
TGCGTGTGCGTGGCGTGTTCGTGTGCAAGGGGCCGGGAGGTGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG  
TGGGCGTGTGTGCAAGTGGGCCACGCTGCAGGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC  
TGGGCGTGTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCGGGGGTCTCCGAGGTGCCGTTAGGAGTTTGAAC  
CCCCCCTCTGACAGGGGAAGCGGGGACAATGCCGGGTTTTCAGGACGAGACACGAGGAGGGCTGCCCGGA  
AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCTGGGGGCGCGGAAGGTGGGTGGGGCCCTCTGTAA  
ATACGGCCCCAGGGTGGTGAAGAGTCCCATGCCACCCGTCCCCCTGTGACCTCCCCCTATGACCTCCAGCTGA  
CCATGCATGCCACGTGGCTGGCTGGTCTCTGCCCTCTTGGAGTTTGCCTCCCCAGCCCCCTCCCATCAAT  
AAAACCTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 544**

MQTPRASPPRPALLLLLLLLGGAGHLFPEEPPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGAD  
DLNIQRVLRVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEGEC  
RNFVKVLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALFSDG  
MLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGS HVYFFFREIAMEF  
NYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTGVVSLG  
GRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTPVPEDQVPRPRPGCC  
AAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVAVDVGAGPWGN  
QTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPDRCGRPGGGETGQRLLSLELD  
AASGGLLAAPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPGTRAAFEQDV  
SGASTSGLGDCGTGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGWVGLRERREL  
ARRKDKEAILAHGAGEAVLSVSRLEGERRAQGPGRGGGGGGGAGVPPEALLAPLMQNGWAKAT  
LLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLLPASASSLLLLLAPA  
RAPEQPPAPGEPTPDGRLYAARPPGRASHGDFPLTPHASPDRRRVVSAPTGPLDPASAADGLPR  
PWSPPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPGTDLAHL L PYGGADR  
TAPPVP

**Important features:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 318-339, 598-617

**N-glycosylation sites.**amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,  
462-466**Glycosaminoglycan attachment sites.**

amino acids 51-55, 573-577

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation sites.**amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,  
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,  
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,  
668-674, 669-675, 670-676, 868-874, 879-885

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**FIGURE 545**

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCTTGTGGGTCTGAGGG  
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA  
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT  
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG  
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG  
GCTTGGCAGTTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCCTCTAGT  
CTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG  
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT  
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT  
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC  
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC  
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA  
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAG  
GAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCT  
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT  
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGATTGTCTTTATGCATCCCC  
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT  
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG  
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT  
ACAGTAAAAAAAACCTTGTAATTCTAGAAGAGTGGCTAGGGGGGTATTTCATTTGTAT  
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC  
TACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG  
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG  
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 546**

MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNKGATTCATNSHSDSELRPE  
IFSSREAWQFFLLWSPDFRPMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE  
IRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHY  
TLRKISSLANSLFTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQA AAVVKALGELDI  
LLQWMEETE

**Important features:****Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

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**FIGURE 547**

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTTCTCGGCCGGGACAGCA  
GAACGCCAGGGGACCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCCTGGGGTCGCG  
GAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTGCGA  
TCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTCATTT  
ATCGGTGGATCATTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATTGCTTC  
TTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCGGAGAAG  
AGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCTTCCCGCCCGCTATTTCTATATT  
CAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCTTCCAGGTG  
AAAGTCTCAGCACCAGAGGAGCAATTCAGTAGAGTTGGAGTCCAGGTTTTAGACCGAAAAGAT  
GGGTCCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGTGGAAATTTAA  
TTCCAAGGGCAACATGTGGCCAAATCCCCATATATTTTAAAGGGCCGGTTTACCATGAGAAC  
TGTGACTGTCCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGCCCTGAAACCATT  
GCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAAGATTGCAGTAGAA  
ATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAAAGGATAACAAGGTT  
TATATCAAGACTCATGGTGAACATGTAGGTTTTAGAAATTTTCATGGATGCCATACTACTTTCT  
TTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTTGGGAGACTGGCCTTTG  
GAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCTGGTGTGGCTCCACAGATTCC  
AAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTGGAAACCATGGGCCGGGTA  
AGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCCTCCCTGGGAAAGCAAAAATCCACT  
GCCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGCTGGTTAAACTCAGTAGAAAA  
CACCCAGAACTCATAGACGCTGCTTTACCAACTTTTTCTTCTTTAAACACGATGAAAACCTG  
TATGGTCCCATTTGTGAAACATATTTTCATTTTTTTGATTTCTTCAAGCATAAGTATCAAATAAAT  
ATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGCTAGTTGGTGACAGTGTTGTGCTG  
AAGCAGGATTCCATCTACTATGAACATTTTTTACAATGAGCTGCAGCCCTGGAAACACTACATT  
CCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAAACTTAAATGGGCGAAAGATCACGATGAA  
GAGGCCAAAAGATAGCAAAAGCAGGACAAGAATTTGCAAGAAATAATCTCATGGGCGATGAC  
ATATTCTGTTATTATTTCAAACCTTTTCCAGGAATATGCCAATTTACAAGTGAGTGAGCCCCAA  
ATCCGAGAGGGCATGAAAAGGTAGAACCACAGACTGAGGACGACCTCTTCCCTTGTAATTGC  
CATAGGAAAAAGACCAAAGATGAACTTGATATGCAAAATAACTTCTATTAGAATAATGGTGC  
TCTGAAGACTCTTCTTAACTAAAAAGAAGAATTTTTTTAAGTATTAATTCCATGGACAATATA  
AAATCTGTGTGATTGTTTGCAGTATGAAGACACATTTCTACTTATGCAGTATTCTCATGACTG  
TACTTTAAAGTACATTTTTTAGAATTTTATAATAAAACCACCTTTATTTTAAAGGAAAAAA

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**FIGURE 548**

MFGTLLLYCFFLATVPALAETGGERQLSPEKSEIWGPGLKADVVLPAFYFYIQAVDTSGNKFT  
SSPGEKVFQVKVSAPEEQFTRVGVQVLDRKDGSFIVRYRMYASYKNLKVEIKFQGQHVAKSPY  
ILKGPVYHENCDCPLQDSAOWLREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRFGQRQSL  
CHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLGDWPLEKKKSNSNIHP  
IFSWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMSVQANTGPPWESKNSTAVWRGRDSRKE  
RLELVKLSRKHPOLIDAAFTNFFFFFKHDENLYGPIVKHISFFDFFKHKYQINIDGTVAAYRLP  
YLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKSNSLDLLEKLKWAKDHDEEAKKIAKAGQE  
FARNNLMGDDIFCYFVKLFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRKKTKDEL

**Important features:****Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 302-306, 414-418

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 243-247, 495-499

**Tyrosine kinase phosphorylation site.**

amino acids 341-348

**N-myristoylation sites.**

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

**Endoplasmic reticulum targeting sequence.**

amino acids 499-504



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**FIGURE 549**

GGGTGATTGAACTAAACCTTCGCCGCACCGAGTTTGCAGTACGGCCGTCACCCGCACCGCTGC  
CTGCTTGCGGTTGGAGAAATCAAGGCCCTACCGGGCCTCCGTAGTCACCTCTCTATAGTGGGC  
GTGGCCGAGGCCGGGGTGACCCTGCCGGAGCCTCCGCTGCCAGCGACATGTTCAAGGTAATTC  
AGAGGTCCGTGGGGCCAGCCAGCCTGAGCTTGCTCACCTTCAAAGTCTATGCAGCACCAAAAA  
AGGACTCACCTCCCAAAAATTCCGTGAAGGTTGATGAGCTTTCACCTCTACTCAGTTCCTGAGG  
GTCAATCGAAGTATGTGGAGGAGGCAAGGAGCCAGCTTGAAGAAAGCATCTCACAGCTCCGAC  
ACTATTGCGAGCCATACACAACCTGGTGTCAGGAAACGTACTCCCAAACCTAAGCCCCAAGATGC  
AAAGTTTGGTTCAATGGGGGTTAGACAGCTATGACTATCTCCAAAATGCACCTCCTGGATTTT  
TTCCGAGACTTGGTGTTATTGGTTTTGCTGGCCTTATTGGACTCCTTTTGGCTAGAGGTTCAA  
AAATAAAGAAGCTAGTGTATCCGCCTGGTTTCATGGGATTAGCTGCCTCCCTCTATTATCCAC  
AACAAGCCATCGTGTTTGCCAGGTCAGTGGGGAGAGATTATATGACTGGGGTTTACGAGGAT  
ATATAGTCATAGAAGATTTGTGGAAGGAGAACTTCAAAGCCAGGAAATGTGAAGAATTCAC  
CTGGAACCTAAGTAGAAAACTCCATGCTCTGCCATCTTAATCAGTTATAGGTAAACATTGGAAA  
CTCCATAGAATAAATCAGTATTTCTACAGAAAAATGGCATAGAAGTCAGTATTGAATGTATTA  
AATTGGCTTTCTTCTTCAGGAAAACTAGACCAGACCTCTGTTATCTTCTGTGAAATCATCCT  
ACAAGCAAACCTAACCTGGAATCCCTTCACCTAGAGATAATGTACAAGCCTTAGAACTCCTCAT  
TCTCATGTTGCTATTTATGTACCTAATTAAACCCCAAGTTTAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

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**FIGURE 550**

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPPKNSVKVDELSLYSVPEGQSKYVEEARSQLEES  
ISQLRHYCEPYTTWCQETYSQTKPKMQSLVQWGLDSYDYLQNAPPGFFPRLGVIGFAGLIGLL  
LARGSKIKKLVYPPGFMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQKPG  
NVKNSPGTK

**Important features:****Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 111-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 36-44

**N-myristoylation sites:**

Amino acids 124-130;144-150;189-195